STIC-Biotech/ChemLib

From: Sent: Duffy, Patricia

Tuesday, January 25, 2005 7:26 AM

To: Subject:

STIC-Biotech/ChemLib

protein sequence search 09/993,292

In re: 09/993,292

Please search SEQ ID NO:24.
Please search in commercial and interference databases.
Please print out top 50 hits.

Thanks.

Patricia A. Duffy, Ph.D. Art Unit 1645, Remsen 3B05 571-272-0855

STA	FF	USE	ONL	ľ

Searcher: ______ Searcher Phone: 2Date Searcher Picked up: _____ Date Completed: _____ Searcher Prep/Rev. Time: ____ Online Time: _____

Type of Search	
NA Sequence: #	
AA Sequence :#	
Structure: #	
Bibliographic:	
Litigation:	
Patent Family:	
Other:	

endors and cost where applicable
STN:
DIALOG:
QUESTEL/ORBIT:
LEXIS/NEXIS:
SEQUENCE SYSTEM:
WWW/Internet:
Other(Specify):

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From: Sent:

Chan, Christina Tuesday, January 04, 2005 4:14 PM Duffy, Patricia; STIC-Biotech/ChemLib RE: rush sequence search

To: Subject:

Please rush. Thanks Chris

Chris Chan TC 1600 New Hire Training Co (5) Re

(571)-272-0841 Remsen, 3E89	diffator and SFE 1044	
		•
Original Message From: Duffy, Patricia Sent: Tuesday, January 04, 2005 To: Chan, Christina Subject: rush sequence search Importance: High	4:08 PM	
Christina,		
Please approve rush sequen	ce request. Amendment due this	; biweek.
IN re: 09/993,292		
	• .	1.4
Thank you.	1-30	75
Patricia A. Duffy, Ph.D. Art Unit 1645, Remsen 3BC 571-272-0855	28-30	05
**************************************	**************	. ****************
STAFF USE ONLY Searcher: Searcher Phone: 2- Date Searcher Picked up: Date Completed:	Type of Search NA Sequence: # AA Sequence :# Structure: # Bibliographic: Litigation:	Vendors and cost where applicable STN: DIALOG: QUESTEL/ORBIT: LEXIS/NEXIS: SEQUENCE SYSTEM:
Searcher Prep/Rev. Time: Online Time:	Patent Family: Other:	WWW/Internet: Other(Specify):
Date completed:	Search Site	Vendors
Searcher: Bevery e z	STIC	IG
Terminal time:	CM-1	STN
CPU time:		Dialog
o. o time	Type of Search	APS

N.A. Sequence

A.A. Sequence

Structure

Bibliographic

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SDC

Other CGN

DARC/Questel

PTO-1590 (9-90)

Total time: ___

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18, Appl 5793, Ap 1078, Ap 2, Appli 11, Appl 11, Appl 844, App 5599, Ap 20145, A

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1044, Ap

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Appl Appl: Appl:

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US-09-134-000C-4522
US-09-134-001C-5178
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'cgn2 6/ptodata1/iaa/PCTUS COMB.pep:*
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Compugen Ltd.
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PCT US94-05669-3
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US-09-117-522A-3347
US-09-134-010C-5080
US-09-134-010C-5080
US-09-134-010C-4820
US-09-134-000C-4820
US-09-134-000C-3594
US-09-114-000C-3594
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                                                                                                                                                           APPLICANT: King, Harold C.
APPLICANT: King, Harold C.
APPLICANT: Sathish, Mundayoor
APPLICANT: Shinnick, Thomas M.
TITLE OF INVENTION: Regulator of Contact-Mediated Hemolysin
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: Jones & Askew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 1376; DB 1; Length 309;
; :Pred. No. 2.6e-132;
16; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CARRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,115
FILING DATE: 26-JUN-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                          ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03063-0171US
                                                                                                         Sequence 3, Application US/08557115
Patent No. 5731151
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTONISY/AGENT INFORMATION:
NAME: Greene, Jamie L.
REGISTRATION NUMBER: 32,467
REFERENCE/DOCKET NUMBER: 0306
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 818-3700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91.1%;
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 309 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 90.4%
Matches 272; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                    STATE: Georgia
COUNTRY: U.S.A.
ZIP: 30303
                                                                                                                                                                                                                                                                                                                  CITY: Atlanta
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61 LVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRIL 120
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                                                                                                               APPLICANT: Sathish, Mundayoor
APPLICANT: Sathish, Mundayoor
APPLICANT: Shinnick, Thomas M.
TITLE OF INVENTION: OF MYCOBACTERIUM TUBERCULOSIS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Suite "...
STREFF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91.1%; Score 1376; DB 5; Length 309; 90.4%; Pred. No. 2.6e-132; ive 16; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05869
                                                                                                                                                                                                                                         CITY: Atlanta STATE: Georgia COUNTRY: USA
                                                                                                                              Sequence 3, Application PC/TUS9405869
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perryman, David G.
REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 1414
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 688-0770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (404) 688-9880
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 90.4*
Matches 272; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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ANTI-SENSE: NO
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301 P 301
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Sequence 3944, Application US/09107532A
Sequence 3944, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83 -----VYEWC--GVVTQLLSAYILLFDEYNEKKASAQKDILIRILDDGVNKLNEAQKS 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 DTTYSNDVYENISKGVVDSMSFGFVLGLDSFDKK-----EDGTIERSIDKIKALNEISVV 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172 TVPAYDSSNVQVNKRSYESFMSNNQAKQTNNSLESTSKAQKESNNMEKTLIDNEKTELRG 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 FVEVITP----BALKEVDLSNVFLLYGHDYSKPLASVKAGTLK-LNVDDTGLHFEAELT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30 YLDQVIPWKTFDETIKELS-----RFKQEYSQE-ASVLVGDIKVLLMDSQDKYFEATQT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.2%; Score 109; DB 4; Length 515
22.7%; Pred. No. 0.025;
tive 59; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               340 SAVNIVQEVKDQLAKLVENTDNKHIMDLLKTFTKKTAATLDDL 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  269 LMLSLLKGA----AKKMINTCNEY----QQRHGKKTLLEVPDI 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   235 DIDAAKLKLAT-----EIAAIGEIKTETETTRFYVDY----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . NAME/KEY: misc_feature;
; SEQUENCE DESCRIPTION: SEQ ID NO: 5317:
US-09-107-532A-5317
                                                                                                                                                                                                                              NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
                                                                                                       APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Enterococcus faecium
                                                                                                                                                                                FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 100 Beaver Street
                                                   FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 5317:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 7310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match Best Local Similarity 22.7*

Best Local Similarity 22.7*

T8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE
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                                                                                                                                                                             GENERAL INFORMATION:

APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT PELLING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   153 SQLTNDFSEKSSYFOSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELN 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35 FLAIADOFKRANKIEEYSORFKKFGYEGDS-----LLAAFRKETGAIDASL---- 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54 YSQEASVL-----VGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILL-FDEY 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105 NEKKASAQKDILIRILDD---GVNKLNEAQKSLLGSSQSFNNASGKLLA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

7.4%; Score 111.5; DB 4; Length
Best Local Similarity 21.0%; Pred. No. 0.041;
Matches 69; Conservative 62; Mismatches 117; Indels
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |::|||||::|||
----QSMFEHVANRMANTIAEWEKTHGK 450
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COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
COMPUTER: PC
OPERATING SYSTEM: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5317, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION:
                                                                                                                            Sequence 7736, Application US/09543681A
Patent No. 6605709
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Proteus mirabilis
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P 301
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STATE: Massachusetts
COUNTRY: USA
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CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249 AQLAKFNL-----ELGKLSESIQEQESILAKQRKENAQADRLIEKNQQVLLDLSEKLKQ 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           166 FQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNDRLKAVQNFFTSL 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   226 SVTVKQANKDIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDLMLSLLKGAAKK---- 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89;
                                COMPUTER: PC
COMPUTER: PC
COREATING SYSTEM: «Unknown»
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/031571
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 40,499
REGISTRATION NUMBER: 40,499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.2%; Score 108.5; I 20.1%; Pred. No. 0.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...1196
SEQUENCE DESCRIPTION: SEQ ID NO: 3944:
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221 LKETLTQTDVSLMVAEIKTAKKD-------
                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: GTC-012 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-134-001C-5080
; Sequence 5080, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION;
; APPLICANT: Lynn Doucette-Stamm et al
UTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1196 amino acids
                                                                                                                                                                                                                                                                                                                           TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 3944:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                              (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       325 QTSLAEAOK----KVK---
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                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 20.1
Matches 66; Conservative
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Sequence 5150, Application US/09107532A
Sequence 5150, Application US/09107532A
Sequence 5150, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: BUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: BUTEROCCCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SVLVGDIKVLLM-----DSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              161 EKSSYFQSQVDRIRK-EAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNDRLKAVQ 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               220 NFFTSLSVTVKQANKDIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDLMLSLLKGAAK 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 OKDILIRILDDGVNKLNEAOKSLLGSS-----OSFNNASGKLLALDSQLTNDFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---FKQEYSQ-EA
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   81;
                                                                                                                                                                                                                                                                                                                                                        Length 3696;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           11 EVVKSAIETADGALDFYNKYLDQVIPWKTFDETIKELSR-
                                                                                                                                                                                                                                                                                                                                                        Query Match
7.1%; Score 106.5; DB 3;
Best Local Similarity 21.5%; Pred. No. 1;
Matches 71; Conservative 49; Mismatches 129;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      280 KMINTCNEYQ-----QRHGKKTLLEVP 301
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COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: <Unknown>
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728 NHEATTEEQNEAIRQVEAHSSDA----
                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: GENOME THERAPE
STREET: 100 Beaver Street
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Sequence 4820, Application US/09134001C
Patent No. 6380370
EGBERAL INFORMATION:
APPLICANT: LYAND DOUGETE-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: BEDIERMIDIS FOR DIAGNOSTICS AND THERAFEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
FRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR PRILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NOS: 5674
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                                                              67 VLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDE--YNEKKASAQKDILIRI---- 119
                                                                                                                                                                             -----FDDAVYAEKRPGGGYRVVVAIADVSH 316
                                                                                                                                                                                                                                                           | :| :| ||: || :| ||: || 317 YVRLDSALNE--EAEER--GTSVYPPHF--VLPMLPEALSNGLCSLNPH-----VDRLCMV 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 LVGDIKVLLMDSQDKYFEATQTVYEWC------GVVTQLLSAYILLFDEYNE 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 - KGKRQON-----DYDIEKIN---YELVKATENYEQLSGKINVLEERKKNQSETNARYE 345
                                                                                                                                                                                                                                                                                                                                                                                                                                 226 SVTVKQANKDIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDL-----MLSLLKGAAKK 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    382 EVÓELESLLYISDEQHDEKLEEIKNSYYTLMSEQSVVNNDIRFLEHTINENEAKKSRLDS 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TVEVVKSAIETADGALDFYNKYLDQVIPWKTFDETIKELSRFKQ--EYSQEASVLVGDIK
                                                                                                                                                                                                                               120 ---LDDGVNKLNEAQKSLLGSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDRI---
                                                                                                                                                                                                                                                                                                                                 174 --RKEAYAGAAAGIVAGPFGL---IISYSIAAGVIEG--KLIPELNDRLKAVQNFFTSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 BQTVEVVK-----SAIETADGALDFYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 KKASAQKDILIRILDDGVNKLNEAQKSLLGSSQSFNNASGKLLALDSQLTND-----FS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161 EKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNDRL----K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     217 AVQNFFTSLSVTVKQANKDIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDLMLSLLKG
                                                                                                                                                                                                                                                                                                                                                                             367 CDLKLSRTGRVTGYEFYPAVMHSKARLTYTQVGQYFEGATDAIPKDRDIHKSLNTLF-QL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              245 MEQSDVIVTVSDIDHYTEDNQRLDERLNHLKSQQAEKEGQQAQINQLLQKY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.9%; Score 104; DB 3; Length 1211;
18.0%; Pred. No. 0.31;
tive 60; Mismatches 131; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       277 AAKKMINTCNEYQQ------RHGKKTLLEV 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 281 MINTC-----NEYQQRHGKKTLLEV 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   346 EELDNLESQIDSIKNEKAQNE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60; Conservative
                                                                                                                                                              :::|:|
280 LVTIDGEDARD----
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US-09-134-001C-4820
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Patent No. 6562958

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BADMANNII FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT PILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 4284

LENGTH: 815
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| SSKEPGAGGEPLIL-DVQSALYDSELRPAVIGGRYGLGSK-----DVTPDQISA---VF 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | | : : | | : | | : | | 379 DELKKDPSIRKKRFTIGIVDDVTYQSLEPKESLDLTEPQTFQAKFWGFGSDGTVGANKSA 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RFKQEYSQEASVLVGDIKVLLMDSQ-----DKYFEATQTVYEWCGVVTQLLSAYILLF 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEYNEKKASAQKDILIRILDDGVNKLNEAQKSL-LGSSQSFN-------NASGKL 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYSIAAGVIEGKLIPELNDRLKAVQNFFTSLSVTVKQ--ANKDI---DAAKLKLATEIAA 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     149 LALDSQLTNDFSEKSSYFQSQ-----VDRIR-----KEAYAGAAAGIVA--GPFGLII 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 AEQTVEVVKSAIETADGALD------FYNKYLDQVIPWKTFDE-----TIKELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 7.0%; Score 106; DB 4; Length 1231; Best Local Similarity 23.0%; Pred. No. 0.2; Matches 77; Conservative 60; Mismatches 124; Indels 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.9%; Score 104; DB 4; Length 815; 22.0%; Pred. No. 0.17; tive 47; Mismatches 123; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature

LOCATION: (B) LOCATION 1...1231
USCOUENCE DESCRIPTION: SEQ ID NO: 5150:
US-09-107-532A-5150
                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Enterococcus faecium
                                                                                                                                                 TELEPHONE: (781)893-5007
TELEPRA: (781)893-8277
INFORMATION FOR SEQ ID NO: 5150:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                         LENGTH: 1231 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77; Conservative
                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72; Conservative
                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
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Matches 72; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-328-352-4284
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                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE
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; TYPE: PRT
; ORGANISM: BOS taurus
US-09-914-259-66
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Best Local S:
Matches 70,
                                                            Query Match
Best Local 8
                                                                                               Matches
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Fatent No. 6703492

GENERAL INFORMATION:

APPLICANT: KINMERLY, WILLIAM JOHN

TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS

TITLE OF INVENTION: VOWBER: US/09/710,279

CURRENT APPLICATION NUMBER: 000/11-09

CURRENT FILING DATE: 1999-11-09

NUMBER OF SEQ ID NOS: 4472

SOFTWARE: PATENTIN VOR: 2.1

SEQ ID NO 1660

LENGTH: 885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 VKNGQKLQLVGDKETGSSYGFAVKKGQNPELIKKFNAGLKNJKDNGTYDKILNNYLATGD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EYNEKKASAQKDILIRILDDGVNKLNEAQKSLLGSSQS-----FNNASGKLLALDSQLT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157 NDFSEKSSY-----FQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLI 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTERCCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/99/134,000C
CURRENT FILING DATE: 1999-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .....KYFEATQTVYEWCGVVTQLLSAYILLFD 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 AVKVGGEGANFLEKNKEK-----YDYTIKNFDDATGLYKALENGEADAIVDDYPVLGYA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 AIBTADGALDFYNKYLDQVIPWKTFDBTIKEL----SRFKQBYSQBASVLVGDIKVL---
                                                                                                                                                                                                                                                                                                                                                                                                                                  6.8%; Score 103; DB 4; Length 284;
21.0%; Pred. No. 0.039;
tive 46; Mismatches 106; Indels 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169 KRAAELOGFTVEFKFIGFSSAVQAVE----SGQADGMVAG-
: | : : | | : : | | SELVEAFNQLKDIQQNITQTQKEYQSSKKSMEKV 474
                                                                                                   ; Sequence 3594, Application US/09134000C
; Patent No. 6617156
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                                                                                                                                                                                                                                                                                                                                                                                      Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 3594
LENGTH: 284
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Best Local Similarity 21.0
Matches 67; Conservative
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US-09-710-279-1660
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                                                                                           US-09-134-000C-3594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109 AS-----AQKDILIRILDDGVNK--LNEAQKSLLGSSQSFNNASGKLLALDSQLTND 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           159 FSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKL-----IPELN 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143 ----KLLAELKNKÇKQLNKEVQELESLLYISDEQHDEKLEEIKNSYYTLMSEQSDVNNDI 198
                                                                                                                                                                                                                                                                                            88 GVVTQLLSAYILLFDEYNEKKASAQKDILIRILDDGVNKLNEAQKSLLGSSQSFNNASGK 147
                                                                                                                                                                                                                                                                                                                                                                                       148 LLALDSQLTND-----FSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAG 201
                                                                                                                                                                                                                                                                                                                                                                                                                                          142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        257
                                                                                                                                                                                                                               2 EPLKEERAAIAKEYKQLSKEMEQSDVIVTVSDIDHYTEDNQRLDERLNHLKSQQAEKEGQQ 61
                                                                                                                                                                                                                                                                                                                               202 VIBGKLIPELNDRL----KAVQNFFTSLSVTVKQANKDIDAAKLKLATEIAAIGEIKTET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66; Gaps
                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      258 ETTRFYVDYDDLMLSLLKGAAKKMINTCNEYQQ------RHGKKTLLEV 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 199 RFLEHTINENEAKKSRLDSRLVEAFNQLKDIQQNITQTQKEYQSSKKSMEKV 250
; OTHER INFORMATION: Description of Artificial Sequence: synthetic; CTHER INFORMATION: amino acid sequence
US-09-710-279-1660
                                                                                                                                                     16;
                                                                                                                                                                                                                                                                                                                                                                                                                                       103 LNVLEBRKKNOSETNARYEEELDNLESQIDSIKNEKAQNE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 961;
                                                                                                        Length 885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 6.8%; Score 103; DB 4; Length 96
1 Similarity 22.0%; Pred. No. 0.27;
70; Conservative 53; Mismatches 129; Indels
                                                                                                     h
Similarity 18.2%; Pred. No. 0.24; Length 89
53; Conservative 52; Mismatches 111; Indels
                                                                                                                                                                                                     42 BTIKELSRFKQEYSQEASVLVGDIKVLLMDSQDKYFEATQTVYEWC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 EVVKSAIETADGALDFYNKYL-------DQVIPWKTFDE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hyman, Paul APPLICANT: Williams, Mark TITLE OF INVENTION: STRAGED ASSEMBLY OF NANOSTRUCTURES FILE REFERNCE: 8471-010-999 CURRENT APPLICATION NUMBER: US/09/914,259 CURRENT FILING DATE: 2000-11-21 NUMBER OF SEQ ID NOS: 180 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 66, Application US/09914259
Patent No. 6495336
GENERAL INFORMATION:
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                                                                                                                              ------ EHKKKKLEA 1144
                                                                                                                                                                                                                                                                                                                                       1145 QVQELQSKCSDGERARAELNDKVHKLQNEVESVTG---MLNEAEGKAI----KLAKDVAS 1197
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                                                                                                                                                                                            52 QEYSQEASVLVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASA 111
                                                                                                                                                                                                                                                                                           112 QKDILIRILDDG-----VNKLNEAQKSLLGSSQSFNNASGKLLALDSQLTNDFSE 161
                                                                                                                                                                                                                                                                                                                                                                                       162 KSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIE---GKLIPELNDRLKAV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 QEYSQEASVLVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162 KSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIE---GKLIPELNDRLKAV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  219 QNF---FTSLSVTVKQANKDIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDLMLSLLK 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112 QKDILIRILDDG-----VNKLNEAQKSLLGSSQSFNNASGKLLALDSQLTNDFSE 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:

APPLICANT: diot, Loic
APPLICANT: Mansfield, Traci A.

TITLE OF INVENTION Protein-Protein Complexes and Method of Using Same;
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT APPLICATION NUMBER: 60/127,352
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR PILING DATE: 1999-04-01
PRIOR PILING DATE: 1999-04-01
PRIOR FILING DATE: 2000-02-01
PRIOR FILING DATE: 2000-02-01
SOFTWARE: CLEAPERSEGFORMATER VERSION 0.9
SOFTWARE: CLEAPERSEGFORMATER VERSION 0.9
                                                                                                7 EQTVEVVKSAI--ETAD-----GALDFYNKYLDQVIPWKTFDETIKELSRFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 EQTVEVVKSAI--ETAD-----GALDFYNKYLDQVIPWKTFDETIKELSRFK
6.7%; Score 101.5; DB 4; Length 1857;
11.8%; Pred. No. 1.1;
ve 48; Mismatches 105; Indels 95;
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21.8%; Pred. No. 1.2;
tive 48; Mismatches 105;
                                                                                                                                                                                                                                           1112 ÓTLEKENADLAGELRVL------GQÁKÓBV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1084, Application US/09538092
Patent No. 6753314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1296 KAAAYDKLEKTKNRLQQ 1312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 276 GAA--KKMINTCNEYQQ 290
                           21.8%;
                                                    69; Conservative
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NAME/KEY: misc_feature
LOCATION: (0)...(0)
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Matches 69; Conserve
                             Local Similarity
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US-09-538-092-1084
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       Query Match
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                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.132
CURRENT APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR PILING DATE: 1998-08-13
PRIOR FILING DATE: 1998-08-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 DDGVNKLNEAQKSLLGSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDRIRKEAYAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 AAAGIVAGPFGLIISYSIAAGVIEGKLIPE-LNDRLKAVQN--FFTSLSVTVKQANKDID 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 DFYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVLVGDIKVLLMDSQDKYFEATQ---
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; Patent No. 6703204
; GENERAL INFORMATION:
    APPLICANT: Baak, Jan
    TITLE OF INVENTION: Prognostic Classification of Breast Cancer
    TITLE OF INVENTION: Prognostic Classification of Breast Cancer
    TITLE REFERENCE: B0801/7224 (JRV)
; CURRENT APPLICATION NUMBER: US/09/917,254
; CURRENT FILING DATE: 2001-07-27
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ 1D NOS: 102
; SOFTWARE: PatentIn version 3.0
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21.9%; Pred. No. 0.22;
tive 41; Mismatches 97; Indels
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----FKTDI----ETKLIKENKKLQLDYEDVLL 432
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                                                                                                                                                                 Sequence 20613, Application US/09248796A
Patent No. 6747137
    LLKGAAKKMINTCNEYQQ 290
                                --TVYEWCGVVTQL----
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ORGANISM: Homo Sapiens
US-09-917-254-91
                                                                                                                       RESULT 13
US-09-248-796A-20613
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LENGTH: 1857
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106 EKKASAQ---KDILIRILDD--GVNKLNBAQKSL-----LGSSQSFNNASG-KLLALD 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                205 GKLIPELNDRLKAVONFFTSLSVTVKOANKDIDAAKLKLATEIAAIGEIKTETTRFYV 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 TEVIQLEPEKGNMGKILPEYLSNWTMEKVRRE-----GVKVMPNAIVQS----VGVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 -----VIVGDIKVILMDSQD---KYFEATQTVYEWCGVVT----QILSAYILLFDEYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - CTHER INFORMATION: human apoptosis-inducing factor (hAIF isoform #2); OTHER INFORMATION: hAIF-exon-skip-Gold; mature polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89;
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                                                                                                                                                                                                                                                                                                                                      Length 526;
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                                                                                                                                                                                                                                                                                                                                         Query Match
6.7%; Score 100.5; DB 4;
Best Local Similarity 22.6%; Pred. No. 0.19;
Matches 68; Conservative 50; Mismatches 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Estimated, Couldo P.
APPLICANT: Siderovei, David P.
APPLICANT: Sanzami, Naoufal
APPLICANT: Susin, Santos A.
APPLICANTION NUMBER: US/09/447,497
CURRENT FILING DATE: 1999-11-23
EARLIER PELING DATE: 1998-11-23
NUMBER OF SEQ ID NOS: 25
NUMBER OF SEQ ID NOS: 25
SOSTWARE: PATENTIN Ver. 2.0
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Best Local Similarity 22.6%; Pred. No. 0.2;
Matches 68; Conservative 50; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 14, Application US/09447497 ; Patent No. 6773911
EARLIER FILING DATE: 1998-11-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Penninger, Josef M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                  NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver.
SEQ ID NO 15
LENGTH: 526
                                                                                                                                                                              ORGANISM: Homo sapiens
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US-09-447-497-14
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                                                                                                                                                     TYPE: PRT
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DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION:
DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER:
US/09/543,681A
CURRENT PILING DATE:
2000-04-05
PRIOR APPLICATION NUMBER:
US 60/128,706
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 8019
            487
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Patent No. 6773911
GRENEAL INFORMATION
APPLICANT: Penninger, Josef M.
APPLICANT: Siderovsi, David P.
APPLICANT: Siderovsi, David P.
APPLICANT: Siderovsi, David P.
APPLICANT: Siderovsi, Maoufal
APPLICANT: Snow, Bryan E. I.
TITLE OF INVENTION: APOPTOSIS-INDUCING FACTOR
FILE REFERENCE: 01017/36780
GURRENT PELLON NUMBER: 05/09/447,497
CURRENT FILING DATE: 1999-11-23
EARLIER APPLICATION NUMBER: 60/109,595
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                        1411 KAAAYDKLEKTKNRLOO 1427
                                                                                                                                                                                                                                276 GAA--KKMINTCNEYQQ 290
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-543-681A-8019
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APPLICANT: Kroemer, Guido P.
APPLICANT: Siderovsi, David P.
APPLICANT: Salestovsi, David P.
APPLICANT: Salestovsi, David P.
APPLICANT: Susin, Santos A.
APPLICANT: Susin, Santos A.
APPLICANT: Snow, Bryan E.L.
TITLE OF INVENTION: APPPROSIS-INDUCING FACTOR
FILE REFERENCE: 01017/36780
CURRENT APPLICATION NUMBER: 08/09/447,497
CURRENT FILING DATE: 1999-11-23
EARLIER APPLICATION NUMBER: 60/109,595
EARLIER APPLICATION NUMBER: 60/109,595
EARLIER APPLICATION NUMBER: 0980-11-23
NUMBER: OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
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                                                                                                                             211 -DRAGAEVKSRTTLFRKIGDFRSLEKISREVKSITIIGGGFLGSELAC--ALGRKARALG 267
                                                                                                                                                                         153 SQLTNDFSEKSS-----YFQS-QVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIE 204
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-----VLVGDIKVLLMDSQD---KYFEATQTVYEWCGVVT----QLLSAYILLFDEYN 105
                                                                                      EKKASAQ---KDILIRILDD--GVNKLNEAQKSL-----LGSSQSFNNASG-KLLALD 152
                                                                                                                                                                                                                                                                  205 GKLIPELNDRLKAVQNFFTSLSVTVKQANKDIDAAKLKLATEIAAIGEIKTETETTRFYV 264
                       | :|| | :: : | | : : | | SYVETLDSMIELFKDYKPGSITLENITRLCQTLGLESFTEELSNELSRLSTASKIIVIDV
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APPLICANT: Giot, Loic
APPLICANT: Giot, Loic
APPLICANT: Giot, Loic
APPLICANT: Giot, Loic
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT APPLICATION NUMBER: G0/127,352
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR PILING DATE: 1999-04-01
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CURAPALSeqFormatter Version 0.9
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NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number YPR070W
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Patent No. 6753314
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Matches 56; Conserv
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US-09-538-092-807
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106 EKKASAQ----KDILIRILDD--GVNKLNEAQKSL-----LGSSQSFNNASG-KLLALD 152
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                                                                                                                                                                                                              Gaps
; OTHER INFORMATION: human apoptosis-inducing factor (hAIF isoform #1; OTHER INFORMATION: ); hAIF-alt-exon-Gold; mature polypeptide US-09-447-497-12
                                                                                                                                                                                                           89;
                                                                                                                                     Query Match 6.7%; Score 100.5; DB 4; Length 609; Best Local Similarity 22.6%; Pred. No. 0.24; Matches 68; Conservative 50; Mismatches 94; Indels 89
                                                                                                                                                                                                                                                                             17 IETADGALDFYNKYLDQVIPWKTFDETIKELSRFKQEYSQEAS-
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APPLICANT: Samzami, Naoufal
APPLICANT: Susin, Santos A.
APPLICANT: Susin, Santos A.
APPLICANT: Susin, Santos A.
APPLICANT: Snow, Bryan E.L.
TITLE OF INVENTION: APOPTOSIS-INDUCING FACTOR
FILE REFERENCE: 01017/36780
CURRENT APPLICATION NUMBER: US/09/447,497
CURRENT FILING DATE: 1999-11-23
NUMBER OF SEQ ID NOS: 25
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Patent No. 6773911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Penninger, Josef M. APPLICANT: Kroemer, Guido P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Ver. 2.0
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; Seguence 12, Application US/09447497

US-09-447-497-12

RESULT 20

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Indels
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GENERAL INFORMATION:
APPLICANT: Penninger, Josef M.
APPLICANT: Kroemer, Guido P.
APPLICANT: Saderovsi, David P.
APPLICANT: Samzami, Naoudal
APPLICANT: Samzami, Naoudal
APPLICANT: Samzami, Naoudal
APPLICANT: Snow, Bryan E.L.
TITLE OF INVENTION: APOPTOSIS-INDUCING FACTOR
FILE REFERENCE: 01017/36780
CURRENT APPLICATION NUMBER: US/09/447,497
CURRENT FILING DATE: 1999-11-23
FARLIER PILING DATE: 1998-11-23
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PARCHILIN UNINE CONTRACTOR
SOFTWARE CONTRACTOR
SOFTW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 6.7%; Score 100.5; DE Best Local Similarity 22.6%; Pred. No. 0.25; Matches 68; Conservative 50; Mismatches
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Patent No. 6773911
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CRGANISM: Homo sapiens
US-09-447-497-8
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434 N 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GKLIPELNDRIKAVQNFFTSLSVTVKQANKDIDAAKLKLATEIAAIGEIKTETETTRFYV 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161 İVSEDPELPYMRPPLSKEL-WFSDDPNVTKTLRFKQMNGKERSİYFQPPSFYVSAQDLPH 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                220 IENGGVAVLTGK-KVVQLDVRDNWVKLNDGSQITYEKCLIATGGTFRSLSAI-----
                                                                                                                                                                                                                                                                    Gaps
                     LENGTH: 613
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human apoptosis-inducing factor (hAIF); hAIF-Gold;
COTHER INFORMATION: mature polypeptide
US-09-447-497-9
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22.6%; Pred. No. 0.25;
ive 50; Mismatches 94;
                                                                                                                                                                                                                 Query Match 6.7%; Score 100.5; DB 4; Best Local Similarity 22.6%; Pred. No. 0.24; Matches 68; Conservative 50; Mismatches 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THE OF INVENTION: APOPTOSIS-INDUCING FACTOR FILE REFERENCE: 01017/36780

CURRENT APPLICATION NUMBER: 08/09/447,497

CURRENT FILING DATE: 1999-11-23

EARLIER APPLICATION NUMBER: 60/109,595

EARLIER FILING DATE: 1998-11-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11, Application US/09447497
Patent No. 6773911
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Penninger, Josef M. APPLICANT: Kroemer, Guido P. APPLICANT: Siderovai, David P. APPLICANT: Samzami, Naoufal APPLICANT: Susin, Santos A. APPLICANT: Snow, Bryan E.L.
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ORGANISM: Homo sapiens
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US-09-447-497-11
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US-09-447-497-11
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Best Local S
Matches 68
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SEQ ID NO 9
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342 TEVIQLFPEKGNMGKILPEXLSNWTMEKVRRE-----GVKVMPNAIVQS----VGVSS 390
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230 IENGGVAVLTGK-KVVQLDVRDNMVKLNDGSQITYEKCLIATGGTPRSLSAI-----
                                 EKKASAQ---KDILIRILDD--GVNKLNEAQKSL-----LGSSQSFNNASG-KLLALD
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SEQ ID NO 1
LENGTH: 1939
TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Best Local Similarity 21.3%; Pred. No. 1.6;
Matches 71; Conservative 44; Mismatches 131; Indels 88; Gaps
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                                                       APPLICANT: Leinwand, Leslie A.
APPLICANT: Viketrom, Karen L.
TITLE OF INVENTION: TRANSGENIC MODEL FOR HEART FAILURE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,105
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1374 IEDLAVDVERSNAAA---AALDKKORNFDKILAE 1404
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                                                                                                                                                      ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln St., Suite 3500
                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: Crook, Wannell M.
REGISTRATION NUMBER: 31,071
REFERENCE/DOCKET NUMBER: 3595-4
TELECOMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
Sequence 3, Application US/08938105
Patent No. 6353151
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1886 amino acids
                                                                                                                                                                                                                                                                                                  Floppy disk
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                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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ZIP: 80203
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; Sequence 1, Application US/09310187A; Patent No. 6358751

US-09-310-187A-1

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1173 FQKMRRDLEEATLQHEATAAALRKKHADSV---AELGEQIDNLQRVKQKLEKEKS----B 1225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125 N----KLNEAQKSLLGSSQSFNNASGKLLALDSQLTNDFSEKS-----SYFQSQ 169
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APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REPERBNCE: 15966-542
CURRENT FILING DATE: 1000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR APPLICATION NUMBER: 60/177,352
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR APPLICATION NUMBER: 60/178,965
NUMBER OF SEQ ID NOS: 1387
SOPTWARE: CLEAPERGEFORMATE: 1000-02-01
NUMBER OF SEQ ID NOS: 1387
SOPTWARE: CLEAPERGEFORMATE: Version 0.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 6.6%; Score 100; DB 3; Length 193
Best Local Similarity 21.3%; Pred. No. 1.7;
Matches 71; Conservative 44; Mismatches 131; Indels
APPLICANT: Benichou, Gilles
APPLICANT: Fedoseyeva, Eugenia
TITLE OF INVENTION: Involvement of Autoantigens in Cardiac
TITLE OF INVENTION: Graft Rejection
FILE REFERENCE: UCSF-090
CÜRRENT APPLICATION NUMBER: US/09/310,187A
CÜRRENT FILING DATE: 1999-05-12
SOFTWARE: FastSEQ for Windows Version 4.0
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OTHER INFORMATION: Polypeptide Accession Number P13533
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Patent No. 6753314
GENERAL INFORMATION:
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181 AA-----AGIVAGPFGL-----IISYSIAAGVIEGKLIPELNDRL--KAVQNFFTSLSVT 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 YEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRILDDG------VNKINBAQKSLL 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 LDFYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVLVGDIKVLLMDSQDKYFEATQTV 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             136 GS---SQSFW-----NASGKLLALDSQLTW--DFSEKSSYFQSQVDRIRKEAYAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1066;
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22.5%; Pred. No. 0.73;
tive 58; Mismatches 109; Indels
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22.5%; Pred. No. 0.73;
.ive 58; Mismatches 109; Indels
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APPLICANT: Sakowicz, Roman
APPLICANT: Baraud, Christophe
TITLE OF INVENTION: Antifungal Assay
FILE REFERENCE: 1015
CURRENT APPLICATION NUMBER: US/09/723,820
CURRENT APPLICATION NUMBER: 09/541,782
PRIOR PILING DATE: 2000-11-28
PRIOR PILING DATE: 2000-14-03
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 8
                                                                                                                           APPLICANT: Niellow, Corey
APPLICANT: Sakowicz, Roman
APPLICANT: Beraad, Christophe
TITLE OF INVENTION: Antifungal Assay
FILE REPERENCE: 1015
CURRENT APPLICATION NUMBER: US/09/541,782
CURRENT APPLICATION DOTE: 2000-04-03
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                 FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/09723820; Patent No. 6468760; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                      ) ORGANISM: Drosophila melanogaster US-09-541-782-8
                                                              Sequence 8, Application US/09541782
Patent No. 6284480
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Best Local Similarity
Matches 65; Conserv
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Best Local Similarity
Matches 65; Conserv
                                                                                                                GENERAL INFORMATION:
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US-09-723-820-8
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Sequence 18798, Application US/09248796A

Sequence 18798, Application US/09248796A

Sequence 18798, Application US/09248796A

Sequence 18798, Application US. 6747137

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

APPLICANT: Keith Weinstock of all

TITLE OF INVENTION:

TITLE OF INVENTION: NUMBER: US/09/248,796A

CURRENT APPLICATION UNMBER: US/09/248,796A

CURRENT APPLICATION UNMBER: US 60/074,725

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NOS: 28208

SEQ ID NO 18798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         383 ----TSEIVNDLKSQIETIKANLNKL----EBEREIQNKKLDQVSELKELKELKVE--- 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145 ----SGKLLALDSQLTNDFSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIA 199
                                                                                                  1173 FQKMRRDLEEATLQHEATAAALRKKHADSV---AELGEQIDNLQRVKQKLEKEKS----E 1225
                                                                                                                                                                        1315 EDLKROLEEEGKAKNALA-----HALQSARHDCDLLREQYEEETEAKAELQRVLSKA 1366
                                                                                                                                                                                                                                                                                                                                                                                                                                         1367 NSEVAQWRİKYETDALQRIEBLEBAKKKLAQRLQDABBAVBAVNAKCSSLERİKHRLQNE 1426
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                                                                                                                                                                                                                                                                                                                                                                                                   215 LKAVQNPFTSLSVTVKQANKDIDAAKLKLATE-----IAAIGBIKTETETT--RFYVD 265
                    12;
                                                                                                                                             65 IKVILMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRILDDGV 124
                                                                                                                                                                                                                                                                                                                   -----LNDR 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38 KTFDETIKELSR----FKQEYSQEASVLVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQL
                                                        5 FAEQTVEVVKSAIETADGALDFYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVLVGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94 LSAYILLFDEYNEKKASAQKDILIRILDDGVNKLNEAQKSLLGSSQSFNNA--
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                                                                                                                                                                                                                                                                                                                   170 VDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 6.6%; Score 99.5; DB 4; Similarity 17.6%; Pred. No. 0.58; S0; Conservative 60; Mismatches 103;
Local Similarity 21.3%; Pred. No. 1.7; nee 71; Conservative 44; Mismatches 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YDDLMLSLLKGAAKKMINTCNEYQQRHGKKTLLE 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Candida albicans
US-09-248-796A-18798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 27
US-09-248-796A-18798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                431
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FEATURE
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                                                                                             214 KERRKTATTLMNA-----QSSRSHTVFSIVVHIRENGIEGEDMLKIGKLNLV--DLA 263
                                                                                                                                               GS---SQSFN-----NASGKLLALDSQLTN--DFSEKSSYFQSQVDRIRKEAYAG 180
                                                                                                                                                                                                                       181 AA----AGIVAGPFGL----IISYSIAAGVIEGKLIPELNDRL--KAVQNFFTSLSVT 228
                                                                                                                                                                                                                                                          324 RIKTSIIATISPGHKDIEETLSTLEYAHRAKNIQNK--PEVNQKLTKKTVLKEYTE---E 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 YEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRILDDG------VNKLNEAQKSLL 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 GS---SQSFN-----NASGKLLALDSQLTN--DFSEKSSYFQSQVDRIRKEAYAG 180
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                       84 YEWCGVVŢQLLSAYILLFDEYNEKKASAQKDILIRILDDG------VNKLNEAQKSLL 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 LDFYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVLVGDIKVLLMDSQDKYFEATQTV 83
LDFYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVLVGDIKVLLMDSQDKYFEATQTV 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Sakowicz, Roman
APPLICANT: Sakowicz, Roman
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: Antifungal Assay
FILE REFERENCE: 1015
CURRENT PILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: US/09/723,820
PRIOR PILING DATE: 2000-11-28
PRIOR PLING DATE: 2000-11-28
PRIOR PRICATION NUMBER: US/09/723,820
PRIOR PRICATION NUMBER: US/09/723,820
PRIOR PILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PastSEQ for Windows Version 4.0
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APPLICANT: Nislow, Corey
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US-10-270-085-8
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; Sequence 914, Application US/09538092

RESULT 31 US-09-538-092-914

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GREERAL INCORNATION:

APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: 1998-08-13
PRIOR APPLICATION NUMBER: 05 60/055,778
PRIOR FILING DATE: 1997-08-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 VGDIKVILIMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRILD 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      161 EKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNDRLKAVQN 220
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                            APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
TITLE REPERMER. 15966-542
CURRENT APPLICATION NUMBER. US/09/538,092
CURRENT FILING DATE: 2000-03-29
FRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR FILING DATE: 1999-04-01
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuraPatSeqFormatter Version 0.9
SEQ ID NO 914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 6.6%; Score 99.5; DB 4; Length 2349;
Best Local Similarity 18.5%; Pred. No. 2.5;
Matches 60; Conservative 49; Mismatches 104; Indels 111; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 DG-----VNKLNEAQKSLLGSSQSFNNASGKLLALDSQLTN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (0)....(0)
CTHER INFORMATION: Polypeptide Accession Number P12270
US-09-538-092-914
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1601 ALKSQYEGRISRLERELREHQERH 1624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              273 LLK----GAAKKMINTCNEYOORH 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4522, Application US/09134000C Patent No. 6617156
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ORGANISM: Enterococcus faecalis
FEATURE:
APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 4522
LENGTH: 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
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GENERAL INC. 037-101.

GENERAL INC. 037-101.

APPLICANT: GATY L. Breton et al.

APPLICANT: GATY L. Breton et al.

TITLE OF INVENTION: VOLZEIC ACID AND THERAPEUTICS

TITLE OF INVENTION: POR DIAGMOSTICS AND THERAPEUTICS

FILE REPERENCE: 2709-2005-001

CURRENT APPLICATION NUMBER: US/09/540,236

CURRENT FILING DATE: 2000-04-04

NUMBER OF SEQ ID NOS: 3840

SEQ ID NO 2753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 159 FSEKSSYFOSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNDRLKAV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         219 ONFFTSLSVTVKQANKDIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDLMLSLLKGAA 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58 ASVLVGDIKV---LLMDSQDKYFEATQTVYEWC--GVVTQLLSAYILLFDEYN-----E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     150 ASDKVETTKABAQSLKÜDATQTFBSAKQAVEGKVEAIKEQVLDQVDSLKÜDTDQDNTDQD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 718;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
6.5%; Score 97.5; DB 4; Length 7
Best Local Similarity 20.0%; Pred. No. 0.63;
Matches 66; Conservative 53; Mismatches 142; Indels
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APPLICANT: Lawlor, Elizabeth
TITLE OF INVENTION: No. 5750387el tRNA Synthetase
NUMBER OF SEQUENCES:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         279 KKMINTC-----NEYQQRHGKKTL 297
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              275 KGA-----AKKMINTCNEYQORHGKKTLL 298
                                                         300 ROATNOTLOVROALNTLREQSOWLGSSNLL 329
                                                                                                                                                                           US-09-540-236-2753; Application US/09540236; Patent No. 6673910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08785428; Patent No. 5750387; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM Compatible
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: King of Prussia
STATE: PA
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; ORGANISM: M.catarrhalis
US-09-540-236-2753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Components Componen
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; Sequence 8554, Application US/09489039A
; Sequence 8554, Application US/09489039A
; Patent No. 661086
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREDMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: PREDMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.204401
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: US 60/117,747
PRIOR PILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 8554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            152 NQLPQQQTDARRQLNEVERRI--GTQTGNNALAQAQNLALQAESARLKALVDEL--DLAQ 207
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                                                                                                                                                                                               10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        223 TSLSVTVKQANKDIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDLMLSLLKGAAKKMI 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 QTVEVVKS---AIETADGALDFYNKYLDQVIPW-KTFDETIKELSRFKQEYSQEASVLVG 63
                                                                                                                                                                                                                                                                                                                                                          141 FNN----ASGKLLALDSQ-----LTNDFSEK-----SSYFQSQVDRIRKEAYAG 180
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                                                                                                                                                                                                                                                                                        64 DIKVILMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRILD--
                                                                                                                                                                                                                                                   TQLLSAYILLFD-EYNEKKA---SAQKDIL-IRILDD-----GVNKLNEAQKSLLGSSQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----GKLIPELNDRLKAVQNFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
; NAME/KEY: MISC_FEATURE; LOCATION: (8)...(8); LOCATION: (9)...(8); OTHER INFORMATION: Amino acid 8 is Xaa wherein Xaa = any amino acid. US-09-134-000C-4522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96;
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57; Mismatches 109; Indels
                                                                                                                                            DB 4; Length 618;
                                                                                                                                                                                                     Indels
                                                                                                                                                                                                  51; Mismatches 104;
                                                                                                                                            6.5%; Score 98; DB 4. 20.8%; Pred. No. 0.44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 AAAGIVAGPFGLIISYSIAAGVIE------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             283 NT----CNEYQQRHGKKTLLEVPD 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Klebsiella pneumoniae
                                                                                                                                         Query Match
Best Local Similarity 20.8%;
Matches 55; Conservative
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Best Local Similarity
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US-09-489-039A-8554
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APPLICATION NUMBER: 9622617.0
FILING DATE: 30-CCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REPERRINCE/DOCKET NUMBER: P31354-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-134-001C-5178
; Sequence 5178, Application US/09134001C
; Patent No. 6380370
                                                                                                                                                                                                                                                                                                      AFILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 08/785,428
FILING DATE: 17-JAN-1997
APPLICATION NUMBER: 9601096.2
APPLICATION NUMBER: 9601096.2
APPLICATION NUMBER: 9601096.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 804 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144 ASGKL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
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                                                                                             COMPUTER READABLE FORM:
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                                                          19406-0939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                MEDIUM TYPE:
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Best Local Simi
Matches 69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63; Mismatches 106; Indels 133;
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Sequence 2, Application US/08996797
Patent NO. 5994111
GENERAL INFORMATION:
APPLICANT: Hodgson, John
APPLICANT: LAWLOY. Elizabeth
TITLE OF INVENTION: NO. 5994111e1 tRNA Synthetase
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 97.5; DB 1;
Pred. No. 0.75;
SOFTWARE: FastSEQ for Windows Version 2.0
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709 Swedeland Road
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                                                                                                        CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9601096.2
FILING DATE: 19-JAN-1996
APPLICATION NUMBER: 9622617.0
FILING DATE: 30-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REGISTRATION NUMBER: 38,891
REGISTRATION NUMBER: 38,891
REPERONCE/DOCKET NUMBER: P31354-5
TELEPHONE: 610-270-4478
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                           17-JAN-1997
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TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 18.6%
Matches 69; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 804 amino acid
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                           CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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                                                                                             FILING DATE:
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63 GDIKVLLMDSQDKYFEATQTVY-------EWGGVVTQLLSAYILLFDEYNE 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 K-----KASAQKDILIRILD--DGVNKLNEAQKSLLGSSQ----SF--NN 143
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18.6%; Pred. No. 0.75;
tive 63; Mismatches 106; Indels 133;
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,797
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Sequence 19055, Application US/09248796A

Sequence 19055, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:

GENERAL TOORN

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANE

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANE
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                                                                                                                                                                                                                                                                                           - I PELNDRLKAVQNFFTSLSVTVKQANKDIDAAKLKLATEIAA-----IGEI----- 253
                                                                                                                                                                                                                                                                                                                                    94 --LSAYILLFDEYNEK-KASAQKDILIRILDDGVNKLNEAQKSLLGSSQSFNNASGKLLA 150
                                                                                          151 LDSQLTNDFSEKSSYFQSQVDRIRKEAYAG--AAAGIVAGPFGLIISYSIAAGVIEGKL- 207
---TPNLEVEAAQTAAAEAALAAQRTAL 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 QTVEVVKSAIETADGALDFYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVLVGDIKV
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Pred. No. 0.22;
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US-09-248-796A-19212
Sequence 19212, Application US/09248796A
; Patent No. 6747137
   376 WRA-GETVKAEEQINMEDLMEAS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 19.1
Matches 53; Conservative
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ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 40
US-09-248-796A-19055
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                     GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: DEPERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----NDFSEKSSY----FQSQVDRIRKEAYAGAAAGIVAGPFGLISYSI 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KLFDKLQLDKSSYLSKLKEKKEQLNEIESSITNIDATLIDLNDKKDFVNEIKSAMSIGDT 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               105 --NEKK--ASAQKDILIRILDDGVNKLNEAQKSLLGSSQSFNNAS----GKLLALDSQLT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      199 AAGVIEGKLIPELNDRLKAVQNFFTSLSVTVKQANKDIDAAKLKLATEIAAIGEIKTETE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              677 ENEKTKDKL-NELNNKLKIEMNDQKHLTENLTQTSKEINNLELKMEKEMQQLG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KTFDETIKELSRF----YQEYSQEASVLVGDIKVLLMDSQDK----YFEATQTVYEW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1010;
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21.1%; Pred. No. 1.1;
tive 56; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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APPLICANT: Hyman, Paul
APPLICANT: Hyman, Paul
APPLICANT: Williams, Mark
IIILE OF INVENTION: STACED ASSEMBLY OF NANOSTRUCTURES
FILE REFERENCE: 8471-010-999
CURRENT APPLICATION NUMBER: US/09/914,259
CURRENT FILING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 180
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 19-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.5%; Score 97.5; DB 3;
18.6%; Pred: No. 1.1;
tive 54; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Drosophilia melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 19, Application US/09914259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 66; Conserv
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GENERAL INFORMATION:
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US-09-914-259-19
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Best Local &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55 SQEASVLVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKD 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 ILIRILDDGVNKLNRAQKSLLGSSQSFNNASGKLLALDSQLTNDFSEK-----SSYFQS 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                641 DLDRLKEEIEKSSKQRAMLAGATA--VYSQFITQLTDENGSCCPVCQRVFQTEAELQEVI 698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 VEVVKSAIETADGALDFYNKYLDQVIPWKTFDETIK------ELSRFKQEY
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                                                                                                                                                                                                                                                                                                                             Query Match 6.4%; Score 96.5; DB 2; Length 1312; Best Local Similarity 18.7%; Pred. No. 2.1; Matches 74; Conservative 54; Mismatches 99; Indels 169
                                                                                                                                                                                                                                    ORIGINAL SOURCE: RAGSO.pro-translation of SEQ ID NO:54
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CURRENT APPLICATION DATA:
APPLICATION NUBER: US/08/687,080
FILING DATE: 17-JUL-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         267 DDLMLSLLKGAAK-----KMINTCNEYQQRHGKK 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      169 QVDRIRKE-----AYAGAAGIVAGPF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSEE: Dehlinger & Associates
F: 350 Cambridge Avenue, Suite 250
Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/592,126
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Patent No. 5955427
GENERAL INFORMATION:
APPLICANT: Gregory Dolganov
TITLE OF INVENTION: Human RAD50 Gen
NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
    TELERAX: (415) 324-0880
INFORMATION FOR SEQ ID NO: 148:
SEQUENCE CHARACTERISTICS:
LENGTH: 1312 amino acids
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                    MOLECULE TYPE: protein HYPOTHETICAL: NO
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MEDIUM TYPE: Floppy
                                                                                                                           TYPE: amino acid
TOPOLOGY: linear
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STATE:
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, OTHER INFORMATION: Identity of amino acid sequences at the above locations are unkno
US-09-248-796A-19055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          549 KLIEYEKCITILQDELDQYKQPSDTTNTTNNNNNNNNNNNRSSYSSYNNHRNSSLNELNL 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----RILDDGVNKLNEAQKSLLGSS--QSFNNASGKLLALDSQLTNDFSEKSS 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        609 VNDYLQLQTSYSRINDELNQVNNDYK-LLNSSTLEKINN------LTSKLQEKSI 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165 YFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNDRLKAVQNFFT- 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 QTVEVVKSAIETADGALDFYNKY--LDQVIPWKTFDETIKELSRFKQEYSQEASVLVGDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 858;
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Patent No. 5821091
GENERAL INFORMATION:
APPLICANT: Gregory Dolganov
TITLE OF INVENTION: Transcripts Encoding Immunomodulatory
TITLE OF INVENTION: Polypeptides
NUMBER OF SEQUENCES: 151
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 6.4%; Score 96.5; DB 4; Length 8 Best Local Similarity 20.0%; Pred. No. 1; Matches 56; Conservative 46; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   224 --SLSVTVKQANKDIDAAKLKL--ATEIAAIGEIKTETET 259.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                686 RIQMSYTVDSLRKDNEALQLKVNKLTDLMTIDRTRAESNS 725
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patentin Release #1.0, Version #1.25
       FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1990-02-12
PRIOR PELLING DATE: 1998-02-13
PRIOR PELLING DATE: 1998-02-13
PRIOR PELLING DATE: 1998-08-13
PRIOR PELLING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 19055
LENGTH: 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,126
                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                  NAME/KEY: UNSURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----GLI-ISYSIAAGVIEGKLIPELNDRLKA 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       699 SDLQSKLRLAPDKLKSTESELKKKEKRRDEMLGLVPNRQSIID--LKEKEIPELRNKLQN 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               218 VONFFISLSVIVKQANKDIDAAKLKLATEIAAIGEIKTETETT------RFYVDY 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    V------NRDİQRLKNDIBEQETLLİGTİMPEBESAKVCLTDVTIMBRFQMBL 802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    502 MEVISLQNEKAD--LDRTLRKLDQEMEQLNHHTTTRTQMEMLTKDKADKDEQIRKIKSRH 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---ELSRFKQEY 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        115 ILIRILDDGVNKLNEAQKSLLGSSQSFNNASGKLLALDSQLTNDFSEK-----SSYFQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               560 SDELTSLIG------PINKKOLEDWLHSKSK------BINGTR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 169; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1312;
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Sequence 148, Application US/09168595
Sequence 148, Application US/09168595
Sequence 148, Application US/09168595
GENERAL INFORMATION:
TITLE OF INVENTION: Polypeptides
TITLE OF INVENTION: Polypeptides
NUMBER OF SEQUENCES: 151
CORRESPONDENCE ADDRESS:
ADDRESSEE: JSO Cambridge Avenue, Suite 250
STREET: JSO Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                   TRANS. OF RAD50 CDNA (SEQ. 54), NT. 389 TO 4324
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                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 VEVVKSAIETADGALDFYNKYLDOVIPWKTFDETIK--
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
6.4%; Score 96.5; DE
Best Local Similarity 18.7%; Pred. No. 2.1;
Matches 74; Conservative 54; Mismatches
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
RECISTRATION NUMBER: 4600-0111.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 1312 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              169 QVDRIRKE-----AYAGAAAGIVAGPF--
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                          ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE:
INDIVIDUAL ISOLATE:
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STATE: CA
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Sequence 18018, Application US/09248796A
Sequence 18018, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
GENERAL INFORMATION:
TILLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANE
TILLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
FILLE REPERBNICS: 107196-132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILLING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           641 DLDRLKEEIEKSSKQRAMLAGATA--VYSQFITQLTDENQSCCPVCQRVFQTEAELQEVI 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       218 VQNFFTSLSVTVKQANKDIDAAKLKLATEIAAIGEIKTETT------RFYVDY 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             757 V-------NRDİQRLKNDIBEQETLLĞTİMPEEESAKVCLTDVTIMERFÇMEL 802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SQEASYLVGDIKVLLMDSQDKXFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKD 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                502 MEVISLONEKAD--LDRTLRKLDQEMEQINHHTTTRTQMEMLTKDKADKDEQIRKIKSRH 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115 ILIRILDDGVNKLNBAQKSLLGSSQSFNNASGKLLALDSQLTNDFSEK-----SSYFQS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INDIVIDUAL ISOLATE: Rad50 pro-translation of SEQ ID NO:54
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DAIR:
APPLICATION NUMBER: US/09/168,595
FILING DAIE:
CLASSIPICATION:
PRIOR APPLICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: 08/592,126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         267 DDLMLSLLKGAAK-----KMINTCNEYQQRHGKK 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.4%; Score 96.5; DI
18.7%; Pred. No. 2.1;
Live 54; Mismatches
                                                                                                                                                                                               ATOCHEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION UNDERER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEPAK: (415) 324-0880
INFORMATION FOR SEQ ID NO: 148:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1312 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 18.7
Matches 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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US-09-248-796A-18018
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                                                                                                                                                                                       FILING DATE:
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1257 LQVKFNEGERVRTELADKVTKLQVELDNVTGLLSQSDSKSSKLTKDFSALBSQLQDTQEL 1316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 QEASVLVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDI 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 LIRILDDGVNKLNEAQKSLLGSSQSFNNASGKLLALD---SQLTNDFSEKSSYFQSQVDR 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        209 PELNDRLKAVQNFFTSLSV---TVKQANKDIDAAKLKLATEIAAIGEIKTETETTRFYVD 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 EQTVEVVKSAIE----TADGALDFYNKYLDQVIPWKTFDETIKE-----LSRFKQEYS
                                                                                                                                                                                                                                          TITLE OF INTERPLETATION: Process and Method of Using Same FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR APPLICATION NUMBER: 60/179,965
PRIOR PILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: Curapatseqformatter Version 0.9
SEQ ID NO 1077
LENGTH: 1960
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APPLICANT: Manafield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REPERENCE: 15966-542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION; (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P35579
US-09-538-092-1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1422 LDDLLVDL----DHQRQSACNLEKKÖKKFDQLLAE 1452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         266 YDDLMLSLLKGAAKKMINTCN-EYQQRHGKKTLLE 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
                                                                                                                         Sequence 1077, Application US/09538092
Patent No. 6753314
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 936, Application US/09538092
Patent No. 6753314
GENERAL INFORMATION:
                                                                                                                                                                                                                             Traci A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
                                                                                                                                                                                                 APPLICANT: Giot, Loic APPLICANT: Mansfield,
     626 SD 627
                                                                             RESULT 46
US-09-538-092-1077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 DIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKAS---AQKDILIRIL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 DDGVNKLNEAQKSLLGSSQSFNNASGKLLALDSQLTNDFS-----EKSSY-FQSQVDR 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 DDWNNKINENERYFISRVLAFFAASDGIVG--ENLIENFSTEVQLPEAKSFYGFQIMMEN 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88 GVVTQLLSAYILLFDEYNEKKASAQKDIL----IRILDDGVNKLNEAQKSLLGSSQSFN 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             473 -SIĞKLAEGLDAĞI-----EKIEELKRKQEDLKKSSDLĞGANK-----ĞISFYYTGDYE 520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 521 SFSAEVVKAR-----KDELQVTADLETK-----NRELEVTRKKMALLLDA--EVQKN 565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 QTVEVVKSAIETADGAL----DFYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVLVG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143 NASGKLL-ALDSQLTNDFSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISY----
                                                                                                                                                                                                                                                                                                      46; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 6.4%; Score 96; DB 4; Length 1086; Best Local Similarity 19.8%; Pred. No. 1.7; Matches 48; Conservative 56; Mismatches 76; Indels
                                                                                                                                                                                                                                                  Query Match 6.4%; Score 96; DB 4; Length 360;
Best Local Similarity 24.6%; Pred. No. 0.3;
Matches 46; Conservative 32; Mismatches 63; Indels
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 18018
LENGTH: 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 7696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Proteus mirabilis
                                                                                                                                                ; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-18018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173 IRKEAYA 179
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Best Local Similarity 19.2%; Pred. No. 4.9;
Matches 61; Conservative 52; Mismatches 101; Indels 103; Gaps
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1420 KTKNRLQQELDDLVVDL 1436
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TELECOMMUNICATION INFORMATION
TELEPHONE: (619) 552-8400
                                                                                7 EQTVEVVKSAIETA---
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APPLICANT: Matsawai, Yuzuru
APPLICANT: Matsadadi, Yuzuru
APPLICANT: Matsadadi, Katsuhito
APPLICANT: Tachabari, Katsuhito
APPLICANT: Sugahara, Michihiro
APPLICANT: Sugahara, Michihiro
APPLICANT: Sugahara, Michihiro
APPLICANT: Sugahara, Michihiro
APPLICANT: Ishiyama, Haruo
APPLICANT: Ishiyama, Haruo
APPLICANT: Ishiyama, Haruo
APPLICANT: Ishiyama, Haruo
APPLICANT: Ishiyama, Haruo
APPLICANT: Ishiyama, Haruo
APPLICANT: Ishiyama, Haruo
APPLICANT: Ishiyama, Haruo
APPLICANT: AN AGENT FOR TREATWENT OF ARTERIOSCLEROSIS COMPRISING THE
TITLE OF INVENTION: AN AGENT FOR TREATWENT OF ARTERIOSCLEROSIS COMPRISING THE
TITLE OF INVENTION: AN AGENT FOR TREATWENT OF ARTERIOSCLEROSIS COMPRISING THE
TITLE OF INVENTION: AN AGENT FOR TOPS
TITLE OF INVENTION: AN AGENT FOR TREATWENT OF ARTERIOSCLEROSIS COMPRISING THE
TITLE OF INVENTION: AN AGENT FOR TREATWENT OF ARTERIOSCLEROSIS COMPRISING THE
TITLE OF INVENTION: AN AGENT FOR TYPE FOR THE FORM TOPS
TITLE OF INVENTION: AN AGENT FOR TOPS
TITLE OF INVENTION: AN AGENT FOR TOPS
TITLE OF INVENTION: AN AGENT FOR TOPS
TITLE OF INVENTION NUMBER: PCT/JP96/00134
FRIOR RILING DATE: 1996-01-25
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q-----TVYEWCGVVTQLLSAYILLFDEYNEKKASAQ---KDILIRILDDGV---N 125
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Best Local Similarity 17.6%; Pred. No. 8;
Matches 59; Conservative 56; Mismatches 92; Indels 12
                                                                                                                                                                                                     FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number P15924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1461 -ESVRYKQSLDD-----AAKTIQDKNKEIER 1485
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                PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CurabatSeqFormatter Version 0.9
SEQ ID NO 936
LENGTH: 2871
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APPLICANT: Arakawa, Emi
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                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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US-08-875-435B-3
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Query Match

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13;
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                                                                                                                                                                                                                                                                                                                                     52 QEYSQEASVIJVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112 Q-KDILIRI------LDDGVNKLNBAQKSLLGSSQSFNNASGKLLALDSQLTNDFSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             162 KSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIE---GKLIPELNDRLKAV
                                                                                                            --DGALDFYNKYLDQVIPWKTFDETIKELSRFK
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Sequence 4, Application US/08434000A

Patent No. 6046037

GENERAL INFORMATION:
APPLICANT: K.-C. MA, THOMAS LEHNER
TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
TITLE OF INVENTION: PROTEINS IN PLANTS AND THEIR USES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: 633 West Fifth Street
STREET: Calite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/367,395
FILING DATE: 12/30/94
ATTORNEY/AGENT INFORMATION:
NAME: Guise, Jeffrey W.
REGISTRATION NUMBER: 34,613
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|-----GQAKQBV-----
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,000A
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TELEX: 67-3510
TELEX: SEQUENCE LISTING
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 746 amino acids
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11;
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                                                                                                                                                                                                                                                                                                      578 NKAIQDPRLF--AEEKAVA-----DTRDQADGSRASVDSGSSEEQGGSSRALVSTLVP 628
                                                                                                                                                                                           86 WCGV-----VTQLLSAYILLFDEYNEKKASAQKDILI-------RILDDGVNKLNEAQ 131
                                                                                                                                                                                                                                                                                                                                              190 FGLIISY-SIAAGVIEGKLIPELNDRLKAVQNFFISLSVTVKQ-----ANKDIDAAKLK 242
                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                     41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ANDREW C. HIATT, JULIAN
K.-C. MA, THOMAS LEHNER
TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
PROTEINS IN PLANTS AND THEIR USES
                                                      Human Polyimmunoglbulin Receptor
                                                                                                              Length 746;
                                                                                                                                                     Indels
                                                                                                                                                     69
                                                                                                              DB 3;
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FILING DATE: 14 May-1999
CLASSIPICATION: (UNKnown)
PRIOR APPLICATION NUMBER: 08/434,000
FILING DATE: (UNKnown)
ATTORNEY, AGENT INFORMATION:
NAME: Guise, Jeffrey W.
REGISTRATION NUMBER: 34,613
REFERENCE/DOCKET NUMBER: 212/127
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
                                                                                                            6.3%; Score 94.5; DE 20.7%; Pred. No. 1.3; tive 47; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 746 amino acids
TYPE: amino acid
STRANDEDMISS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (619) 552-8400
TELEFAX: (619) 552-0159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09312157
Patent No. 6303341
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             243 LATEIAAIGEIKTETETT 260
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                                  linear
DESCRIPTION:
                                                                                                                               Best Local Similarity 20.79
Matches 41, Conservative
                    single
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TYPE: amino acid
              STRANDEDNESS:
TOPOLOGY: lin
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US-08-434-000A-4
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                                                                                                                                                                                                                                                                                                                         86 WCGV-----VTQLLSAYILLFDEYNEKKASAQKDILI-------RILDDGVNKLNEAQ
                                                                                                                                                                                                                                                              578 NKAIQDPRLF--AEEKAVA-----DTRDQADGSRASVDSGSSEEQGGSSRALVSTLVP
                                                                                                                      Gaps
           Human Polyimmunoglbulin Receptor
                                                                                                                   41;
                                                                                  Length 746;
                                                                                                                    69; Indels
                                                                                  ; DB 3;
1.3;
                                                                                 Query Match 6.3%; Score 94.5; D
Best Local Similarity 20.7%; Pred. No. 1.3;
Matches 41; Conservative 47; Mismatches
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Job time : 43 secs
DESCRIPTION: Hume
; SEQUENCE DESCRIPTION: SEQ ID NO: 4
US-09-312-157-4
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ADE63514
ADE63518
ADU4603
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AAE10039
AAU27604
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ADE48157
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                   Abg73265 Salmonell
Abg73266 Salmonell
Abg73261 Novel hum
Abm68103 Photorhab
Abu18419 Protein e
Abg78617 N. gonorr
Abg78617 N. gonorr
Abj19025 Pathogen
Abj19025 Pathogen
Abu42396 Protein e
Abu42399 Protein e
Abu43311 Protein e
Abu43311 Protein e
Abu43311 Protein e
Abu43311 Protein e
Abu43311 Protein e
Abb77386 Amino aci
Ade56035 Rat Prote
Abb77386 Amino aci
Abb77386 Amino aci
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N. gonorr
Bacterial
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E. faeciu
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Protein e
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E. faeciu
Rat Prote
Rat Prote
                                                                  ; Search time 157 Seconds (without alignments) 692.325 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                              ....TCNEYQQRHGKKTLLEVPDI
                                                                                                                                                                                                   2002273
         GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                Potal number of hits satisfying chosen parameters:
                                                                                                                                                                               2002273 seqs, 358729299 residues
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Maximum Match 100%
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                                                protein search, using sw model
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Maximum DB s
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No.
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The present invention relates to a system for expressing a protein of interest. The system comprises an expression vector having an expression cassette comprises an expression cassette. Where the expression cassette comprises an export protein coding sequence genetically fused to a DNA sequence encoding the protein of interest, a host cell transformed host cell, where the expression vector, and a culturing environment for the transformed host cell, where the expression cassette expressing at expression vector protein of interest fusion protein which is exported out of the host cell. The system is useful for expressing agene in a bacterial cell, by providing an expression vector to a population of untransformed bacterial cells, and expressing the expression cassette such that the export protein of interest fusion protein is produced and exported into the culture medium. The protein of interest is preferably an antigen and this method is useful for the system is useful for the production of recombinant protein. The system is useful for the production of recombinant proteins inside a bacterial host cell, in a bioreactor, and various devices that facilitate the growth of bacteria. The system is also useful for preparing inmunogenic composition capable of facilitating the generation of an immune response in an animal manner and animal shows the for vaccinating animals, and even in the food animal for preparing animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         biomediation, waste disposal, and waste treatment industries. The system
  Drosophil
                    Amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel system for expressing protein of interest, has expression vector with cassette having export protein coding sequence fused to protein coding sequence, host cell transformed with vector, and culturing
                                                                                                                                                                                                                                                                                                                                       Protein expression vector; expression cassette; export protein; transformed host cell; bacterial cell; immune response; HlyE family; cytolysin A; ClyA; recombinant protein; bioreactor; bacterial growth; live vector immunogenic composition; animal feed; animal vaccination; food industry; nutritional supplement; biomediation; waste disposal;
Abb59245
Aag67418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for use in the food, nutritional supplement, animal feed,
                                                                                                                                                                                                                                                                                                    Salmonella typhi cytolysin A (ClyA) protein
                                                                                ALIGNMENTS
ABB59245
AAG67418
                                                                                                                                                                                ABG73265 standard; protein; 305 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Page 18; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                             waste treatment; host bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-NOV-2001; 2001US-00993292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-NOV-2000; 2000US-0252516P.
    4 4
                                                                                                                                                                                                                                                             17-APR-2003 (first entry)
  1048
1066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2003-228013/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GALE/) GALEN J E.
  9.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ABX15174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Salmonella typhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US2002146430-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-OCT-2002
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99.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Galen JE;
                                                                                                                                                                                                                       ABG73265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
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is very advantageous for protein expression, as proteins that are toxic to host bacterium can also be expressed. A population of recombinant host cells can be transformed with the expression vector, and then the population of bacterial host cells can be maintained in culture and used to produce proteins without having to harvest and lyse the host cells. The present represents Salmonella typhi ClyA protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LKLATEIAAIGEIKTETETTRFYVDYDDLMLSLLKGAAKKMINTCNEYQQRHGKKTLFEV 300
                                                                                                                                                                                                                                                                                         LVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRIL 120
                                                                                                                                                                                                                                                                                                                        61 LVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRIL 120
                                                                                                                                                                                                                                                                                                                                                        DDGVNKLNEAQKSLLGSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDRIRKEAYAG 180
                                                                                                                                                                                                                                                                                                                                                                                       121 DDGVKKINEAQKSILTSSQSFNNASGKILALDSQLTNDFSEKSSYFQSQVDRIRKEAYAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                         AAAGIVAGPFGLIISYSIAAGVIEGKLIPELNDRLKAVQNFFTSLSVTVKQANKDIDAAK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                            LKLATEIAAIGEIKTETETTRFYVDYDDLMLSLLKGAAKKMINTCNEYQQRHGKKTLLEV 300
                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                             1 MISIFAEQTVEVVKSAIETADGALDLYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASV
                                                                                                                                                                                                                          1 MTGIFAEOTVEVVKSAIETADGALDFYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein expression vector; expression cassette; export protein; transformed host cell; bacterial cell; immune response; Hlyß family; cytolysin A; ClyA; recombinant protein; bioresactor; bacterial growth; live vector immunogenic composition; animal feed; animal vaccination; food industry; nutritional supplement; biomediation; waste treatment; host bacterium; sacB; mutant; muttein;
                                                                                                                                                                                         Gaps
                                                                                                                                                                                         ö
                                                                                                                                                        Length 305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salmonella typhi ClyA-Bacillus subtilis sacB fusion protein.
                                                                                                                                                                                       Indels
                                                                                                                                                      97.1%; Score 1466; DB 6;
97.0%; Pred. No. 7.1e-114;
iive 2; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG73266 standard; protein; 749 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-NOV-2001; 2001US-00993292.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lethal levansucrase
                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Salmonella typhi.
Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 PDI 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PDV 303
                                                                                                                        Sequence 305 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GALE/) GALEN J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US2002146430-A1.
                                                                                                                                                                                         Matches 294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-OCT-2002
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301 PDV 303

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The present invention relates to a system for expressing a protein of interest. The system comprises an expression vector having an expression cassette, where the expression cassette comprises an export protein cassette where the expression cassette comprises an export protein coding sequence generically fused to a DNA sequence encoding the protein coding sequence generically fused to a DNA sequence encoding the protein coding sequence generically fused to a box cell. The system is useful, for expression of the host cell. The system is useful for expression of untransformed batterial cells, more expression vector cassette express the exported out of the host cell. The system is useful for the capression of untransformed batterial cells, and expression vector capped in a pacterial cell, by providing an expression vector of a population of untransformed batterial cells, and expression vector capported in special protein of interest spression cassette, such that the export protein of interest cusion protein. The export protein may be a member of the HIVE family such as cytolysin A cortain of interest is preferably an antigen and this method is useful for the production of recombinant proteins. The system is useful for the production of recombinant proteins can almade and an animal antigenic material against which an immune response may be mounted. The obtained recombinant bacterium (e.g. Salmonalla) con providing an animal antigenic material against which an immune response the generation of an immune response in an animal. The system is also useful for preparing immunogenic compositions for vaccinating animals, the generation of an immune response in an animal. The system is also be useful for preparing immunogenic compositions of recombinant host cells can be adapted by an expression, as proteins that are toxic to host bacterial may be expressed A population of pacterial host cells can be expressed. A population of produce proteins without having to harvest and lyor the host cells cells can be expressed. A popul
                                                                                 Novel system for expressing protein of interest, has expression vector with cassette having export protein coding sequence fused to protein coding sequence, host cell transformed with vector, and culturing
                                                                                                                                                                                                                      Example 3; Page 25-28; 33pp; English.
WPI; 2003-228013/22.
N-PSDB; ABX15191.
                                                                                                                                                                   environment
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Sequence 749 AA;

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240
                                                                                                                                                   61 LVGDIKVLIMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRIL 120
                                                                                                                                                                                  DDGVNKINEAQKSLLGSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDRIRKEAYAG 180
                                                                                                                                                                                                   181 AAAGIVAGPFGLIISYSIAAGVIEGKLIPELNDRLKAVQNFFTSLSVTVKQANKDIDAAK 240
                                                                                                                                                                                                                                                                                                       LKLATBIAAIGEIKTETETTRFYVDYDDLMLSLLKGAAKKMINTCNEYQQRHGKKTLLEV 300
                                                                                                                                                                                                                                                                                                                       LVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRIL 120
                                                              9
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                                                                                                                                                                                                                                                             1 MTSIPAEQTVEVVKSAIETADGALDLYNKYLDQVIPWKTPDETIKELSRFKQEYSQEASV
                                                             1 MTGIFAEQTVEVVKSAIETADGALDFYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASV
                                Gaps
                                ;
0
Score 1466; DB 6; Length 749;
Pred. No. 2.3e-113;
2; Mismatches 7; Indels C
 97.1%;
97.0%;
Query Match
Best Local Similarity 97.0°
Matches 294; Conservative
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The sequence represents the E. coli haemolysis regulator which may be used as an immunogen in a vaccine composition against tuberculosis (Wyoobacterium tuberculosis). (Updated on 25-MAR-2003 to correct FN field.) (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAGIVAGPFGLIISYSIAAGVIEGKLIPELNDRLKAVQNFFTSLSVTVKQANKDIDAAK 240
                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid encoding haemolytic regulator of E coli - and derived vectors, proteins etc used to transform Mycobacterium cells to produce antituberculosis vaccines providing improved immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 LVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DDGVNKLNEAQKSLLGSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDRIRKEAYAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 LKLATEIAAIGEIKTETETTRFYVDYDDLMLSLLKGAAKKMINTCNBYQORHGKKTLLEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MTGIFAEQTVEVVKSAIETADGALDFYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.7%; Score 1370; DB 2; Length 309; 90.0%; Pred. No. 7.3e-106; ive 16; Mismatches 14; Indels
                                                                                                                                         Haemolysin regulator; tuberculosis; vaccine; therapy.
                                                                                                                                                                                                                                                                                                  (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 9; Page 39-40; 46pp; English.
                       AAR67645 standard; protein; 309 AA
                                                                                                                                                                                                                                                                                                                            Sathish M;
                                                                                                                                                                                                                                                                          93US-00066830.
                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     271; Conservative
                                                                                                                                                                                                                                                                                                                           King CH, Shinnick TM,
                                                                          (revised)
                                                                                                                Haemolysin regulator.
                                                                                                                                                                                                                                                                                                                                                     WPI; 1995-022809/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 271; Conserv
                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAQ75857.
                                                                                                                                                                    Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 309 AA;
                                                                                                                                                                                                                                                24-MAY-1994;
                                                                                                                                                                                            WO9428137-A1
                                                                                                                                                                                                                                                                          24-MAY-1993;
                                                                                         06-JUL-1995
                                                                          25-MAR-2003
                                                                                                                                                                                                                      08-DEC-1994.
                                                  AAR67645;
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RESULT 3
          AAR6764
ID AA
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130 AQKSLLGSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDRIRKEAYAGAAAGIVAGP 61 AQKSLLVSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDKIRKEAYAGAAAGVVAGP 190 FGLIISYSIAAGVIEGKLIPELNDRLKAVQNFFTSLSVTVKQANKDIDAAKLKLATEIAA

301 P 301

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Claim 20; SEQ ID NO 55580; 103pp; English.
                                                                                                                                                                                                                                                                                                                             ftp.wipo.int/pub/published_pct_sequences
                                           Novel human diagnostic protein #25212.
           ABG25221 standard; protein; 1035 AA.
                                                                                                                   31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                        30-MAR-2001; 2001WO-US008631
                                18-FEB-2002 (first entry)
                                                                                                                                                         WPI; 2001-639362/73.
                                                                                                                                               Drmanac RT, Liu C,
                                                                                                                                    (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                         Sequence 1035 AA;
                                                                                                                                                               N-PSDB; AAS89408.
                                                                                  WO200175067-A2
                                                                        Homo sapiens.
                                                                                             11-OCT-2001.
                      ABG25221;
RESULT 4
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The invention relates to the isolation of genes and their encoded proteins from Photorhabdus luminescens. The isolated sequences are proteins from Photorhabdus luminescens. The isolated sequences are proteins for detecting the genome of P. luminescens and are attacked species; to study polymorphisms; for gene analysis and for detection/amplification of the genes. Antibodies (Ab) raised against the polypeptides encoded by the genes are used for detection/dentification of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that carry a gene-containing vector are used to select compounds that carry a gene-containing vector are used to select compounds that carry a gene-containing vector are used to select compounds that corresponds or mincrogramisms other than P. luminescens and are able to alter response or sensitivity to toxins and antibiotics produced by P. creombinant production of the proteins, particularly toxins and antibiotics proteins are useful for treombinant production of the proteins, particularly toxins and antibacterials useful as insecticides, bactericides and fungicides. The therapeutically (to treat microbial infection by bacteria or fungi that are sensitive to P. luminescens encoded toxins or antibiotics) and as are sensitive to P. luminescens encoded toxins or antibiotics) and as are sensitive to P. luminescens and the proteins are as virulence factors and for identifying targets of human diseases for which P. cequence represents one of the isolated P. luminescens proteins
                                                                                                                                                                                                                                                                                                                       Antibacterial; fungicide; insecticide; polymorphism; genetic analysis; detection; food; gene expression; plant; animal; microorganism; toxin; antibiotic; biopesticide; virulence factor; disease model; plague;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomic sequence of Photorhabdus luminescens and encoded polypeptides, useful e.g. as therapeutic antimicrobials and agricultural pesticides.
                                                                                                                                                                                                                                                               Photorhabdus luminescens protein sequence #1200.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glaser P, Frangeul L,
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                                                              ABM68103 standard; protein; 582 AA
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(CNRS ) CNRS CENT NAT RECH SCI.
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                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Photorhabdus luminescens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-148459/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                          whooping cough.
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Buchrieser C;
                                                                                                                                                                                                   20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-NOV-2002.
                                                                                                                                    ABM68103;
                                         ABM68103
RESULT
                                                                                                 The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed cativity of (II) is useful in gene therapy techniques to restore normal activity of (II) is useful in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a useful for generating antibodies against it, detecting or quantitating of supplement. (II) and its binding partners are useful in medical imaging of supplement protein expression or biological activity. The involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in addisorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. Absolution-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of th
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      Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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Best Local Similarity 91.3
Matches 210; Conservative
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Danchin A;

Kunst F,

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                                                                                                                                 333 KIVELKŠSL-NSLNEDAQFITNEIERINNK--------YITDDDAVKKG 372
                                                                                                                                                                                                                                                                 -KLATEIAAIGEIKTETETTRFYVDYDDLMLSLLKGAAKKMI-NTCNEYQQRHGKKTLLE 299
                                                                                                                                                                                                                                                                           107 ITGDFSKGPSDLVNPKMKLPNRGDGNLETPPPAYYFLPFYIDQIKSWSSPWNSFENLGQY 166
                                                                                                                                                         -----SAQKDIL------IRILDDGVNKLNEAQKSLLGSSQSFNNASG 146
                                                                                                                                                                         284 DYKFAVESIPTDYLECPLCGTLHDNSLPNRALLLSEKDSLINEA------NSIAS 332
                                                                                                                                                                                           KLLALDSQLTNDFSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGK 206
                                                                                                                                                                                                                                             373 LIAQVIDTLSTENVSKNIQIKIDNEDLAISKAANSSIKELKKOOQKKLLSTKEKEELNSSFM 432
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                                                                                                 SNWKGPLIKYFTGYLKPEHFDIEENIYEYSEIKKESAHKIEKFQSAVEVIVDNTVDSPIT
                                                  1 MTGIFAEQTVEVVK-----SAIETADGALDFYNKYLDQV----IPWKTF----
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Xu HH;
                                  Gaps
                                                                                     -----DETIKELSRFKQEYSQEASVLVGDIKVL-----
               8.4%; Score 126.5; DB 6; Length 582;
19.0%; Pred. No. 0.089;
ative 55; Mismatches 132; Indels 155;
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                   Protein encoded by Prokaryotic essential gene #3946.
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                              ABU18419 standard; protein; 941 AA
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Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-2002; 2002WO-US009107.
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                                 Conservative
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-029926/02.
N-PSDB; ACA22289.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus anthracis.
                        Local Similarity
Sequence 582 AA;
                                                                                                                                                                                                                                                                                                                   493 PP 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200277183-A2.
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08-FEB-2002;
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                 Query Match
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The invention fracters to an instruction where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense ancience are in similar and in the state of the nucleic acid operation of its fragment whose expression is inhibited by the antisense antisense confirmation of the polypeptide of specifically binding the polypeptide of its fragment whose expression is inhibited by the antisense ancience acid; (3) a nost cell containing the vector; (3) an isolated of the polypeptide of its fragment whose expression is inhibited by the antisense ancience acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular composition or the activity of a gene in an operon required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profilling a compound; eactivity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent of the strains is present in a culture or collection of an organism. The antisense nucleic acids are useful for genetifying proteins or screening for homologous nucleic acids required for proliferation to isolate candidate molecules for rational culture dear or obliferation of an organism, or for screening homologous nucleic acids required for proliferation in the process of the strains in the proliferation of an organism. The antisense nucleic acids required for proliferation is screening for homologous nucleic acids required for proliferation is an event of the screening for homologous nucleic acids required for proliferation is a present earning the present earning to a process or obliferation is a present earning the present earning the present earning the present earning the present earning the 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64
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                                                  proliferation to
                                             for homologous nucleic acids required for cellular proliferation isolate candidate molecules for rational drug discovery programs
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                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid comprising
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                                                                                                                                                                                      Claim 25; SEQ ID NO 46343; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : ||
LSQA 795
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gonorrhoeae amino acid sequence SEQ ID 180.
                                                                                                                                              Claim 1; Page 197; 815pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                ABP78617 standard; protein; 1015
                                                            12-FEB-2002; 2002WO-IB002069
                                                                       12-FEB-2001; 2001GB-00003424
                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                     Conservative
                         Neisseria gonorrhoeae
                                                                                               Fontana MR, Pizza M,
                                                                                                           WPI; 2003-058415/05.
N-PSDB; ABZ37795.
                                                                                                                                                                                                                              Local Similarity
hes 75; Conserv
                                                                                    (CHIR-) CHIRON SPA
                                                                                                                                                                                                               Sequence 1015 AA;
                                    WO200279243-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                       07-MAR-2003
                                                10-OCT-2002
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present invention relates to proteins from Neisseria gonorrhoeae
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loament for treating or preventing N. gonorrheae infection
                                              Antibacterial; infection; vaccine; gene therapy
            N. gonorrhoeae amino acid sequence SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 460; 815pp; English
                                                                                                                                                                                           12-FEB-2002; 2002WO-IB002069
                                                                                                                                                                                                                            12-FEB-2001; 2001GB-00003424
                                                                                                                                                                                                                                                                                                Fontana MR, Pizza M,
                                                                                    Neisseria gonorrhoeae
                                                                                                                                                                                                                                                                                                                                  WPI; 2003-058415/05.
N-PSDB; ABZ39587.
                                                                                                                                                                                                                                                               (CHIR-) CHIRON SPA
                                                                                                                       WO200279243-A2
                                                                                                                                                        10-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 DIKVLL---MDSQD--KYFEATQTVYEWCGV------VTQLLSAYILLFDEYNEK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108 KASAQKDILIRIL-----DDGVNKL-NEAQ-----KSLLGSSQSFNNASGKLLALD 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       221 SISEAAPILLDTIAEYMGKSRDEIKKLGSEGKLTADVIFKAISGASEKFGEQAARMFVTM 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                338 APTLALNLALLANPFGII---AVAIGTVVG-LIAKFGDEIDVFGCGWSNLS-----D 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------AYAGAAA- 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63
                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to proteins from Neisseria gonorrhoeae. Also disclosed are the nucleic acid molecules encoding the proteins and antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy. Sequences given in records ABP76736-ABP81046 represent nucleic acid molecules of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163 TSRALKDYGYTQQEILKFTEAANNAMTIGGVGAQQQAAALMQLSQALGSGVLQGDEF--K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 TVEVVKSAIETADGALDFYNKYLDQVIPWKT-----FDETIKELSRFKQEYSQEASVLVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----GIVAGPFGLIISYSIAAGVIEGKLIPELNDRLKAVQNFFTSLSVTVKQANKD
                                                                                                                                                                                                                                                                                                                                                                          븅
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54; Mismatches 113; Indels 102; Gaps
                                                                                                                                                                                                                                                                                                                                                                     new protein from Neisseria gonorrheae, useful for the manufacture medicament for treating or preventing N. gonorrheae infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.5%; Score 113; DB 6; Length 1015; 21.8%; Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : | :: | | : | | 386 VIRAVWQIITETVGEAVGTVKSW------PDGLTGRLNEGA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IDAAKLKLATEIA--AIGEIKTETETTRFYVDYDDLMLSLLKGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         153 SQLTNDFSEKSSYFQSQVDRIRKE-----
                                      Antibacterial; infection; vaccine; gene therapy
                                                                                                                                                                                                                                                                                     Monaci E;
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ы Monaci

Masignani V,

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338 APTLAINLALLANPFGII---AVAIGTVVG-LIAKFGDEIDVFGGGWSNLS-----D 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 221 SISBAAPILLDTIAEYMGKSRDEIKKLGSEGKLTADVIFKAISGASEKFGEQAAKMPVTM 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----GIVAGPFGLIISYSIAAGVIEGKLIPELNDRLKAVQNFFTSLSVTVKQANKD 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 DIKVLL---MDSQD--KYFEATQTVYEWCGV------VTQLLSAYILLFDEYNEK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           163 TSRALKDYGYTQQEILKFTEAANNAWTIGGVGAQQQAAALMQLSQALGSGVLQGDEF--K 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 KASAQKDILIRIL-----DGVNKL-NEAQ-----KSLLGSSQSFNNASGKLLALD 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GOALTVFSNN----WOSMVSKLLNDSGTMSGIAAVIKLIADNLNLVVPIVAGFAVAVAAAV 337
Also disclosed are the nucleic acid molecules encoding the proteins and antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy. Sequences given in records ABP76736-ABP81046 represent nucleic acid molecules of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 TVEVVKSAIETADGALDFYNKYLDQVIPWKT-----FDETIKELSRFKQEYSQEASVLVG
                                                                                                                                                                                                                                                                                                                                                                                                                  113; Indels 102;
                                                                                                                                                                                                                                                                                                                                           7.5%; Score 113; DB 6; Length 1015; 21.8%; Pred. No. 2.5; cive 54; Mismatches 113; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     386 VIRAVWQIITETVGEAVGTVKSW------FDGLTGRLNBGA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          236 IDAAKLKLATEIA--AIGEIKTETETTRFYVDYDDLMLSLLKGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADF07451 standard; protein; 1036
                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 21.8°
Matches 75; Conservative
                                                                                                                                                                                                                                                                                      Sequence 1015 AA;
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ADF07451;

ABJ19025 standard; protein; 2681 AA.

RESULT 10

ABJ19025

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The invention relates to new Proteus mirabilis polypeptides and polymucleotides. The invention also relates to antibodies against the polymetides, amethod of generating the polypeptides, amethod of generating vaccines for immunising an individual against P. mirabilis, a method for evaluating a compound for the ability to bind a P. mirabilis activity. The polypeptides and polymucleotides are useful as molecular targets for diagnosing, preventing and treating pathological conditions resulting from bacterial infection, as reagents for diagnosis of bacterial diseases, as components of antibacterial vaccines, as targets for antibacterial diseases, as components of antibacterial vaccines, as targets sequence represents a Proteus mirabilis polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                      New Proteus mirabilis polypeptides and polynucleotides, useful as reagents for diagnosis of bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for plants.
                                                                    Proteus mirabilis infection; bacterial infection; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 7736; 870pp; English
                                                                                                                                                                                                                                                                                                             (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                         99US-0128706P.
                                                                                                                                                                                                                                     05-APR-2000; 2000US-00543681
                                   Bacterial polypeptide #3564.
12-FEB-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-895291/82.
                                                                                                                           Proteus mirabilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1036 AA;
                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ADF03279
                                                                                         immunostimulant.
                                                                                                                                                                                                                                                                         09-APR-1999;
                                                                                                                                                             US6605709-B1
                                                                                                                                                                                                 12-AUG-2003
                                                                                                                                                                                                                                                                                                                                                 Breton GL;
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14; 105 NEKKASAQKDILIRILDD---GVNKLNEAQKSLLGSSQSFNNASGKLLA-----LD 152 153 SQLTNDFSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELN 212 FLAIADOFKRANKIEEYSORFKKFGYEGDS-----LLAAFRKETGAIDASL---- 380 DRLKAVQNFFTSLSVTVKQANKDIDAAKLK--LATEIAAI-----GEIKTETETTRFYVD 265 54 YSQEASVL------VGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILL-FDEY 104 277 TGTKAAAGVELTTKVLGNVGKAVSQYILAQRVAQGLSTS--AASAGLIASAVTLAISPLS 334 2 TGIFAEQTVEVVK-----SAIETADGALDFYNKYLDQVIPWKTFDETIKELSRFKQE 53 81; Gaps Length 1036; Indels 7.4%; Score 111.5; DB 7; 21.0%; Pred. No. 3.4; ative 62; Mismatches 117; Conservative Local Similarity 69; 335 213 Query Match 381 Best Loca Matches g ò 셤 ò g ò ò ద ઠે 셤

|::||:|| ----QSMFEHVANRMANTIAEWEKTHGK 450

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producing Myperimmune serum-reactive antigens from a pathogen, tumour, allergen, a tissue or host prone to auto-immunity, where the antigens are allergen, a tissue or host prone to auto-immunity, where the antigens are used in a vaccine, comprises providing antibody preparation from a plasma pool of a type of animal, or individual sera with antibodies against the specific pathogen, tumour, allergen, tissue or host prone to auto-immunity. The hyperimmune serum-reactive antigens comprising any of the car immunity. The hyperimmune serum-reactive antigens comprising any of the car their hyperimmune fragments are useful for the manufacture of a pharmaceutical preparation, particularly a vaccine against taphylococcal infections or colonisation against S. aureus or S. epidermidis. The preparation of antibodies is useful for the manufacture of a medicament or against S. aureus or S. epidermidis. The actions or colonisation against S. aureus or colonisation against S. aureus or colonisation can amine a methody preparations may also be used for diagnostic and imaging purposes. Other conditions that can be treated include cancer, autoimmune diseases or infections caused by viral (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This sequence represents a staphylococal protein relating to the method for identifying and producing pathogen specific antigens of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dentifying, isolating and producing hyperimmune serum-reactive antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from a pathogen, for preparing vaccine or medicament for treating or preventing e.g. staphylococcal infections, comprises providing antibody
                                                                                                                                             Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV; hyperimmune; serum-reactive; antigen; pathogen; tumcur; allergen; auto-immunity; vaccine; staphylococcal infection; antibody; cancer; autoimmune disease; HIV; hepetitis.
                                                                                                       Pathogen specific antigen related staphylococcal protein SEQ ID No 274.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a novel method for identifying, isolating and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 TGIFAEQTVEVVKSAIETADGALDFYNKYLDQVIPWKTFDET------IKELSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50 FKQEY-----SQEASVLVGDIKVL-----LMDSQDKYFEATQTVYEWC--G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zauner W;
Hafner M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Von Ahsen U, Klade C, Henics T,
O, Etz H, Dryla A, Weichhart T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.3%; Score 110.5; 20.7%; Pred. No. 14; ive 52; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 7; Page 200; 252pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CIST-) CISTEM BIOTECHNOLOGIES GMBH
                                                                                                                                                                                                                                                                                                                                                                                  21-JAN-2002; 2002WO-EP000546.
                                                                                                                                                                                                                                                                                                                                                                                                                            26-JAN-2001; 2001AT-00000130.
                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 20.7 nes 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Meinke A, Nagy E, Vor
Minh DB, Vytvytska O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-075410/07.
                                                                                                                                                                                                                                                         Staphylococcus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2681 AA;
                                                                                                                                                                                                                                                                                                 WO200259148-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rempelmaier B;
                                                             36-MAR-2003
                                                                                                                                                                                                                                                                                                                                           01-AUG-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        preparation.
                   ABJ19025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Matches
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YMKKYDNCILEISKKYSNDAADKVLGDFTAIATELQNDFQDVKDNWAEFKQTTLESFKDG 1116
                                                                                                                                                                                                                     the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8)
                                                                                                                                                               162 TA-----SRSPYLSVHAS-LRK------VIEOIIADGKVDESEK 1193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                    VVTQLLSAYILLFDEYNEKKASAQKDILIRILDDGVNKLNEAQKSLLGSSQSFNNASGKL 148
                                                                                                                           149 LALDSQLTNDFSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLI 208
                                                                                                                                                                                                209 PELNDRLKAVQNFFTSLSVTVKQANKDI-----DAAKLKLATEIAAIGEIKTETETTRF 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antisense, prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                       1254 QRDGAVITYÝYSGVPTĽSNDPÁKSW--ŤTŇDĽKDĽHIKDMYĽD 1294
                                                                                                                                                                                                                                                                      263 YVD-----YDDLMLSLLKGAAKKMINTCNEYQQRHGKKTLLE 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haselbeck R, Ohlsen KL,
Yamamoto R, Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein encoded by Prokaryotic essential gene #28523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 25; SEQ ID NO 70920; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                               ABU42996 standard; protein; 1189 AA
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Carr GJ,
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2001US-0342923P.
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06-SEP-2001; 2001US-00948993.
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06-MAR-2002; 2002US-0362699P,
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Trawick JD,
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N-PSDB; ACA46866.
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pathway in which a proliferation-required gene or its gene product lies or agene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed of (12) determining the extent to which ach of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the strains; or (13) identifying the target of a compound that inhibits the strains; or organism. The antisense nucleic acids required for cellular proliferation to isolate candidate molecules for rational for did discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, C. The target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained to the electronic formed directly from NIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 KKASAQKDILIRILDDGVNKLNEAQKSILGSSQSFNNASGKLLALDSQLTND-----FS 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   161 EKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNDRL----K 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AVQNFFTSLSVTVKQANKDIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDLMLSLLKG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            360 EVQELESLLYVSDEQHDEKLEEIKNSYYTLMSEQSDVNNDIRFLEHTINENEAKKSRLDS 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --GVVTQLLSAYILLFDEYNE 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -KGKRQQN-----DYDIEKIN---YELVKATENYEQLSGKINVLEERKKNQSETNARYE 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 EQTVEVVK-----SAIETADGALDFYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASV 60
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.3%; Score 110; DB 6; Length 1189;
                                                                                                                                                                                                                                                                                                                                                                                                                            60; Mismatches 130; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             420 RLVEAFNOLKDIOONITOTNKAYOSSKKSMOKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 LVGDIKVLLMDSQDKYFEATQTVYEWC----
                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E. faecium protein sequence SEQ ID 5317.
                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADC95690 standard; protein; 515
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                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                        Sequence 1189 AA;
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14-MAY-1998;
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Best Local S
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ADC95690
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E. faecium protein sequence SEQ ID 3944.

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Entercoccus faccium encoding an Entercoccus faccium polypeptide having one of 10 fully defined sequences given in the (or comprising 40 sequences the form and the comprising 40 sequences hybridising to it). Also included are a recombinant vector comprising the nucleic acids, its complement or sequences hybridising to it). Also included are a recombinant vector comprising the nucleic acid operably linked to transcription regulatory element, a cell comprising the vector and a chosen from 3654 disclosed sequences encoding 3654 disclosed proteins. The nucleic acids is useful for diagnosing pathological conditions resulting from E. faecium bacterial infection (e.g. urinary tract infection) and for screening drugs such as agonists and antagonists. The nucleic acid is useful for recombinant production of Candida albicans mucleic acid is useful for recombinant production of Candida albicans and vaccines containing the nucleic acid are useful for preventing or treating Entercoccus faecium infections. The present sequence represents
                                                                                                                                                                                  New isolated nucleic acid derived from Enterococcus faecium encoding a
Enterococcus faecium polypeptide useful for detection, prevention and
treatment of a pathological condition resulting from a bacterial
                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid derived from
                                                                                                                                                                                                                                                                                                          Example 1; SEQ ID NO 5317; 243pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           one if the disclosed E. faecium proteins.
                      (GENO-) GENOME THERAPEUTICS CORP.
                                                                      Doucette-Stamm LA,
                                                                                                                                          N-PSDB; ADC92036
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Sequence 515 AA;

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-----VYEWC--GVVTQLLSAYILLFDEYNEKKASAQKDILIRILDDGVNKLNEAQKS 133
                                                                                                                                                                           134 LL----GSSOSFNNASGKLLALDSQL--TNDFSEKSSYFQSQVDRIRK------ 175
                                                                                                                                                                                                                                                           : | | : : | | : : | | 1.2 TVPAYDSSNVQVNKRSYESFMSNNQAKQTNNSLESTSKAQKESNNMEKTLIDNEKTELRG 231
                                                                                                                                                                                                                                                                                                             -EAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNDRLKAVQNFFTSLSVTVKQANK 234
                                                                                                                                                                                                                                                                                                                                                                                          DIDAAKLKLAT------EIAAIGEIKTETETTRFYVDY-------DD 268
                                                                                                                                                                                                                                                                                                                                                                                                                              --GOGKYPVATNQQAVLATKAELAEIGDIDAEMFTS---VDYKVETRAGKIALSNEVVED 339
                                                                                                                                                                                                                                                                                                                                                  232 YERYIRSQGEVRDG-----VITVNAAAVVPEEVIGEVFDLKRS--NYNLAQYATVKTVSN 284
                                                                              82
                                                                            30 YLDQVIPWKTFDETIKELS-----RFKQEYSQE-ASVLVGDIKVLLMDSQDKYFEATQT
                                      92; Gaps
7.2%; Score 109; DB 7; Length 515; 22.7%; Pred. No. 2.2; ive 59; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LMLSLLKGA----AKKMINTCNEY----QQRHGKKTLLEVPDI 303
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              Local Similarity
nes 78; Conserv
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  Query Match
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ADC94317 standard; protein; 1196 AA

01-JAN-2004 (first entry)

ADC94317;

RESULT 13
ADC94317
ID ADC94;
XX
AC ADC94;
XX
DT 01-JAI

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The invention relates to an isolated nucleic acid derived from Enterococcus faecium encoding an Enterococcus faecium polypeptide having one of 10 fully defined sequences given in the (or comprising 40 complement or sequences hybridising to it). Also included are a recomplement or sequences hybridising to it). Also included are a recomplement vector comprising the nucleic acid operably linked to transcription regulatory element, a cell comprising the vector and a single-stranded probe comprising the nucleic acid. The nucleic acids are chosen from 3654 disclosed sequences encoding 3654 disclosed proteins. The nucleic acids is useful for diagnosing pathological conditions resulting from E. faacium bacterial infection (e.g. urinary tract infection) and for screening drugs such as agonists and antagonists. The nucleic acid is useful for recombinant production of Candida albicans derived peptides or antisense polypeptides. Pharmaceutical compositions and vaccines containing the nucleic acid are useful for preventing or and vaccines containing the nucleic acid are useful for preventing or and vaccines containing the nucleic acid are useful for preventing or and acid as useful for acid are useful for preventing or and acid as a page and a preventing or and acid are useful for preventing or and acid as useful for preventing or and acid are useful for preventing or and acid as acid are useful for preventing or and acid are useful for preventing or and acid as acid are useful for preventing or acid as acid as acid are useful for preventing or acid and acid as acid are acid as acid are useful for preventing or acid and acid as acid as acid as acid as acid are useful for preventing or acid and acid as acid as acid as acid as acid are useful for preventing or acid and acid as acid as acid as acid as acid as acid as acid as acid as acid as acid as acid as acid as acid as acid as acid as acid as acid as acid as acid as acid as acid as acid as acid as acid as acid as acid as acid as acid as acid as acid as acid as acid as acid 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     faecium infections. The present sequence represents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid derived from Enterococcus faecium encoding an Enterococcus faecium polypeptide useful for detection, prevention and treatment of a pathological condition resulting from a bacterial
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                                              Vaccine, urinary tract infection, bacteraemia, endocarditis, wound, abdominal-pelvic infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89; Indels 133;
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98US-0085598P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Doucette-Stamm LA, Bush D;
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                                                                                                                                      Snterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-799836/75.
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                                                                                                                                                                                                                                                                                                           10-JUN-1998;
                                                                                                                                                                                           JS6583275-B1
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Matches 66;
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Page 10.

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proliferation or that has an excivity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underspressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids cequired for proliferation in cells other than S. aureus, S. typhimurium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid, (2) a host cell containing the vector, (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid, (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of
  357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                 Antisense; prokaryotic essential gene; cell proliferation; drug design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zyskind JW;
Xu HH;
  ----HFEKLQESLMKAAAEKETEIQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ohlsen Forsyth
                                                                                                                                                                                                                                                                                                        Protein encoded by Prokaryotic essential gene #11126.
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 25; SEQ ID NO 53523; 1766pp; English
                                        ----MINICNEYQ--QRHGKKTLLEVPD 302
                                                               | : | | : | : | | : | KAEANLIKTQOELEKYQKSTKELLAELRD
                                                                                                                                                                                    ABU25599 standard; protein; 742 AA
  OTSLAEAOK----KVK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-MAR-2001; 2001US-00815242.
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2001US-0342923P.
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                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                         Clostridium difficile.
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-029926/02.
N-PSDB; ACA29469.
                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200277183-A2
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25-OCT-2001;
08-FEB-2002;
                                                                                                                                                                                                                                                                  19-JUN-2003
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                                                                                                                                                                                                                            ABU25599
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                                                                                                                                                                                                                                                                                                                                                                                   one of
                                                                                                                                                                                                                                                                132 KSLLGSSQSFNNASGKLLALDSQLTN------DFSEKSSYFQSQVDRIRKEAYA 179
K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
the target prokaryotic essential genes. Note: The sequence data for this
patent did not form part of the printed specification, but was obtained
in electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                          77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antisense; prokaryotic essential gene; cell proliferation; drug design
                                                                                                                                                                             36 KIVDLASDATSKLSDIVKDIKSDLPTIKKT-----LNDIKLLSSDLKKFLEDINDNLD
                                                                                                                                                                                                              78 EATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRILD-----DGVNKLNEAQ
                                                                                                                                                                                                                             -DAAKLK-----LATEIAAIGEIKTETETTRFYVDYDDLMLSLLKGAAKKMINTCNEY
                                                                                                                                                         18 ETADGALDFYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVLVGDIKVLLMDSQDKYF
                                                                                                                                                                                                                                                                                                                   GAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNDRL-KAVQNFFTSLSVTVKQANKDI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zyskind JW;
Xu HH;
                                                                                                                                  Gaps
                                                                                                                                  63;
                                                                                                        Length 742;
                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Äξ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ohlsen Forsyth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein encoded by Prokaryotic essential gene #28838
                                                                                                       7.1%; Score 107.5; DB 6;
21.2%; Pred. No. 4.7;
ive 49; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ц,
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABU43311 standard; protein; 3692 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
06-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-MAR-2001; 2001US-00815242.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus epidermidis
                                                                                                                                                                                                                                       ELSPLIKSDLNLMVDL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                  66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         289 QQRHGKKTLLEV 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                SNGEDMKKLVSL 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-029926/02.
                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; ACA47181.
                                                                                Sequence 742 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200277183-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-OCT-2002.
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                                                                                                                                                                                                                                                                                                                   180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 502
                                                                                                       Query Match
Best Local
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Wall D,
                                                                                                                                 Matches
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Staphylococcus epidermidis; open reading frame; ORF; bacterial infection; antibacterial; gene therapy.

Staphylococcus epidermidis.

JS6380370-B1

Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5080.

(first entry)

24-JUL-2002

Wed Feb

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The invention relates to an isolated mucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the mucleic acid inhibite proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) and best cell containing the vector; (3) an isolated polypeptide; (5) producing the polypeptide; (5) producing the polypeptide; (6) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway the gene product or that has an activity against a biological pathway in which a proliferation-required gene product lies cequired for proliferation or the biological pathway in which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiocic; (10) profiling a compound; a activity; (11) a culture comprising strains in which the gene compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiocic; (10) profiling a compound; a activity; (11) a culture comprising strains in which the gene conduct is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational
isolate candidate molecules for rational drug discovery programs
                                                          Claim 25; SEQ ID NO 71235; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences
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Novel isolated nucleic acid encoding a Staphylococcus epidermis polypeptide, useful for diagnosing and treating bacterial infections.

(GENO-) GENOME THERAPEUTICS CORP.

Noucette-Stamm LA, Bush D;

WPI; 2002-381255/41

N-PSDB; ABN92780

97US-0055779P. 98US-00134001

14-AUG-1997;

38-NOV-1997;

13-AUG-1998;

10-APR-2002.

Sequence 3692 AA;

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SVLVGDIKVLLM-----DSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASA 111
                                                                                                                                                                                                                                                               QKDILIRILDDGVNKLNEAQKSLLGSS------QSFNNASGKLLALDSQLTNDFS 160
                                                                                                                                                                                                                                                                                                       SNNIDDELTDDGVERVKEAGLHTLESDTPHPVTKPNARQVVNNRA-----DQQKTLIRN 723
                                                                                                                                                                                                                                                                                                                                                  EKSSYFQSQVDRIRK-EAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIFELNDRLKAVQ 219
                                                                                                                                                                                                                                                                                                                                                                            NFFTSLSVTVKQANKDIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDLMLSLLKGAAK 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                               | : | : : | : | : | : | : | NGTKLIATDVPNPTKKAEA---RAAVTNSANSKIKDINNNTQATLDERNDAIALVNRSKD 821
                                                                                       11 EVVKSAIETADGALDFYNKYLDQVIPWKTFDETIKELSR------FKQEYSQ-EA 58
                                                                                                                  EQVNKDIIPSNYTLASYNKY------NKLKERAQTVLDEETNNTPFNQRYSQTQI
                                            81; Gaps
Query Match
7.1%; Score 106.5; DB 6; Length 3692;
Best Local Similarity 21.5%; Pred. No. 46;
Matches 71; Conservative 49; Mismatches 129; Indels 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : | | | | : | | EAIQNINTEAQNNGTNTIQQVP 851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KMINTCNEYQ------QRHGKKTLLEVP 301
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ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               568 EQVNKDIIPSNYTLASYNKY------NKLKERAQTVLDEETNNTPFNQRYSQTQI 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SVLVGDIKVLLM-----DSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QKDILIRILDDGVNKLNEAQKSLLGSS-----QSFNNASGKLLALDSQLTNDFS 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161 EKSSYFQSQVDRIRK-EAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNDRLKAVQ 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NFFTSLSVTVKQANKDIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDLMLSLLKGAAK 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   728 NHEATTEEQNEAIRQVEAHSSDA-------IAKIGEAETDTTVNE---ARD 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EVVKSAIETADGALDPYNKYLDQVIPWKTFDETIKELSR------FKQEYSQ-EA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 5; Length 3696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.1%; Score 106.5; DB 5; Length 21.5%; Pred. No. 47; tive 49; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           280 KMINTCNEYQ-----QRHGKKTLLEVP 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : | | | | : : | | EAIQNINTAQGNDDVTEAQNNGTNTIQQVP 855
                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 5080; 267pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3696 AA;
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ABP40235 standard; protein; 3696 AA.

RESULT 16

ABP40235

ABP40235 ID ABP4 XX AC ABP4 XX

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14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-033347P.
                                                                                                                                                                                                                                                                                                                                                                                                                                              14-AUG-2002; 2002WO-US025765.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GEHO ) GEN HOSPITAL CORP. (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                   (first entry)
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GENBANK; BAA05026.
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                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                          WO2003016475-A2.
                                                                                                                                                                                                                                                                    29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                   27-FEB-2003.
                                                                                                                                                                                                                                           ADE56031;
                                                               195
                                                                                          498
                                                                                                                                                                                      RESULT 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enterococcus facetium encoding an Enterococcus facetium polypeptide having one of 10 fully defined sequences given in the (or comprising 40 capturisting 40 capturisting 10 capturisting 10 complement or sequences hybridising to it). Also included are a recombinant vector comprising the nucleic acids its complement or sequences hybridising to it). Also included are a recombinant vector comprising the nucleic acid operably linked to transcription regulatory element, a cell comprising the vector and a single-stranded probe comprising the nucleic acid. The nucleic acids are chosen from 364 disclosed sequences encoding 3654 disclosed proteins. The nucleic acids is useful for diagnosing pathological conditions cresulting from E. facetium bacterial infection (e.g. urinary tract infection) and for screening drugs such as agonists and antagonists. The nucleic acid is useful for recombinant production of Candida albicans derived peptides or antisense polypeptides. Pharmaceutical compositions and vaccines containing the nucleic acid are useful for preventing or treating Enterococcus faccium infections. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | | | : : : | : | | | | | | ABEVIVSMGSVAQTIEQTIDYLNANGRKTGFLNIHLYRPFFVETFVQKLPHTVKTIAVLD 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEYNEKKASAQKDILIRILDDGVNKLNEAQKSL-LGSSQSFN-----NASGKL 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               379 DELKKOPSIRKKRFTIGIVDDVTYQSLEPKESLDLTEPQTFQAKFWGFGSDGTVGANKSA 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | |: : | | : | | | 329 RSKEPGAGGEPILL-DVQSALYDSELRPAVIGGRYGLGSK-----DVTPDQISA--VF
                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid derived from Enterococcus faecium encoding a
Enterococcus faecium polypeptide useful for detection, prevention and
treatment of a pathological condition resulting from a bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RFKQEYSQEASVLVGDIKVLLMDSQ-----DKYFEATQTVYEWCGVVTQLLSAYILLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 AEQTVEVVKSALETADGALD------FYNKYLDQVIPWKTFDE-----TIKELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74; Gaps
                                                                                                                     urinary tract infection; bacteraemia; endocarditis; wound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention relates to an isolated nucleic acid derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.0%; Score 106; DB 7; Length 1231; 23.0%; Pred. No.:12; ative 60; Mismatches 124; Indels 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; SEQ ID NO 5150; 243pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      one if the disclosed E. faecium proteins.
                                                                                            E. faecium protein sequence SEQ ID 5150
           ADC95523 standard; protein; 1231 AA
                                                                                                                                                                                                                                                                                                               (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                      97US-0051571P.
98US-0085598P.
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                                                                                                                                                                                                                                                                                                                                        Bush D;
                                                                                                                                   abdominal-pelvic infection
                                                                  (first entry)
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                                                                                                                                                             Enterococcus faecium.
                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-799836/75.
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tes 77; Conserv
                                                                                                                                                                                                                                                                                                                                          Doucette-Stamm LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1231 AA;
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                                                                                                                                                                                         US6583275-B1
                                                                                                                                                                                                                                              30-JUN-1998;
                                                                                                                                                                                                                                                                         02-JUL-1997;
                                                                                                                                                                                                                                                                                  14-MAY-1998;
                                                                  01-JAN-2004
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                                      ADC95523;
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Matches
ADC95523
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1963 DCIRYLGRISALEKTVKALEFVHTESQKDLDATKGNLAQAVEHHKKAQAELSSFKILLDD 2022
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                                                                                                                                                                                                                                                      1748 AEATLLANSAKPGVSETFSSHDDINNYLQQLDQLK---GRIAELEMEKQKDRELSQTLEN 1804
                                                                                                                                                                                                                                                                                                                    1805 EKNALLTQISAKDSELKLLEEEVAKINMINQOIQEELSRVTKL------KETAE 1852
                                                                                                                                                                                                                                                                                                                                                                                         1853 EEKDDLEERL---MNQLAELNGSIGNYYQDVTDAQIKNEQLESEMQNLKRCVSELEEEKQ 1909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            254
                                                                                                                                                                                                                                                                                       64 DIKVLL-----MDSQDKYFE-----ATQTVYEWCGVVTQLLSAYILLFDEYNEKKAS 110
                                                                                                                                                                                                                                                                                                                                                       111 AQXDILIRILDDGVNXLNBAQKSLLGSSQSFNNASGKLLALDSQLTN-----DFSEKSS 164
                                                                                                                                                                                                                                                                                                                                                                                                                          165 YP---QSQVD-RIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNDRLKAVQ- 219
injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                      6 AEQTV--EVVKSAIETADGALDFYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVLVG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----AAIGEIK------
                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            255 TETETTRFYVD------YDDLMLSLLKGAAKKMINTCNEYQQRHGKK 295
                                                                                                                                                                                       86;
                                                                                                                                                  7:0%; Score 106; DB 7; Length 3187; 22.2%; Pred. No. 42; ve 53; Mismatches 134; Indels 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Costigan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rat Protein BAA05026, SEQ ID NO 1874.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADE56035 standard; protein; 3187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-AUG-2002; 2002WO-US025765.
                                                                                                                                                                  22.28;
                                                                                                                                                                    Local Similarity 22.23
les 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GEHO ) GEN HOSPITAL CORP. (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D'urso D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-268312/26.
GENBANK; BAA05026.
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                                                                                                                    Sequence 3187 AA;
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                                                                                                                                                    Query Match
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The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a ckit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the composition, a method for producing a pharmaceutical composition, a compound to an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more computed to the compound that modulates its activity is useful for preparing a medicament for treating colypeptides or their antibodies. The polynucleotide or the compound injury (CCI) and spared nerve injury (SMI) in an animal (e.g. spin et therapy). The sequence presented is a rat protein (shown in Table 2 of the sequence data for this patent did not form part of the printed specification) which is differentially expressed during pain. Sore:

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1910 QLVKEKTKVESEIRKE-YMEKIQGAQKGPGSKIHAKELQ-----ELLKEKQQEVKQLQK 1962
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .963 DCIRYLGRISALEKTVKALEFVHTESQKDLDATKGNLAQAVEHHKKAQAELSSFKILLDD 2022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 DIKVLL-----MDSQDKYFE-----ATQTVYEWCGVVTQLLSAYILLFDEYNEKKAS 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111 AQKDILIRILDDGVNKLNEAQKSLLGSSQSFNNASGKLLALDSQLTN-----DFSEKSS 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                165 YF---QSQVD-RIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNDRLKAVQ- 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----NFFISLSVTVK------ QANKDIDAAKLKLATEI-----AAIGEIK---- 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 AEQTV--EVVKSAIETADGALDFYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVLVG
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2023 TQSEAARVIADNIKIKKELQSNKESIKSQIKQKDEDLIRRLEQAEEKHRKE 2073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 7; Length 3187;
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53; Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster polypeptide SEQ ID NO 40632.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.0%; Score 106;
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                        Claim 1; Page; 1017pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22.2%;
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Matches
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pharmaceutical.

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABBS7137) ABB72072). The sequence data for this patent did not form part of printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid detection reagent for detecting 1000 or more
genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77 FEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRILDDGVNKLNEAQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --KSLLGSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDRIRKEAYAGAAAGIVAGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------TFD-----ETIKELSRFKQEYSQEASVLVGDIKVLLMDSQDKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.0%; Score 105.5; DB 4; Length 588; 0.5%; Pred. No. 5.1; .ve 44; Mismatches 87; Indels 125;
                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 40632; 21pp + Sequence Listing; English
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                                                                                                                            23-MAR-2001; 2001WO-US009231.
                                                                                                                                                             23-MAR-2000; 2000US-0191637P
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                                                                                                                                                                                                                                           Ë
                             Drosophila melanogaster.
                                                                                                                                                                                                                                             Adams M,
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                                                                                                                                                                                                            (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                             N-PSDB; ABL15383
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                                                               WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                            interactions.
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                                                                                               27-SEP-2001
                                                                                                                                                                                                                                             Venter JC,
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415 131

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38

Gaps

189 497

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The specification describes a method for directing integration of a nucleic acid of interest to a pre-determined site, where the nucleic acid of nucleic acid of interest to a pre-determined site, in a cutaryote with a preference for non-homologous recombination. The method comprises comprises an integration pathway towards homologous recombination. The preference for non-homologous recombination. The method is useful for directing integration of a nucleic acid of interest to a subtelomeric and/or telomeric region in an eukaryote with a preference for non-homologous recombination. The nucleic acid of interest comprises an inactive gene to replace an active gene, or view eversa, is a portion of a gene delivery vehicle, confers a desired property to the cukaryotic cell, or encodes a therapeutic proteinaceous substance or a substance conferring resistence for an antibiotic substance or a cell.

The method is useful for improving gene targeting efficiency. The method is useful in the replacement of an active gene by an inactive gene, for e.g. for the inactivation of genes controlling undesired side branches of metabolic pathways, to increase the quality of bulk products such as starch, or to increase the production of specific secondary metabolites controlling senescence in fruits and flowers or that determine flower pigments. The method is also useful for replacing an inactive gene for engineer the replacement of a defective p33 by an intact p53. Many tumours acquire and often correlates with a poor cintact p53. Many tumours acquire and often correlates with a poor tract p53. Many tumours acquire and effect p53 by an intact p53. Many tumours acquire and effect p53 by an intact p54. Changes of succeeding. The method is also useful for therapy have better changes of succeeding. The method is also useful for therapy have better changes of succeeding. The method is also useful for therapy and the context therapy, conventional anticidada genes of succeeding. The method is also useful for therapeut of the apredetermined 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Directing integration of nucleic acid of interest to a sub-telomeric region in an eukaryote with preference for non-homologous recombination, by steering an integration pathway towards homologous recombination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----IPWKTFDETIKE
                                                                                                 Nucleic acid integration; homologous recombination; telomeric region;
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                                                        Amino acid sequence of an Arabidopsis RAD50 homologue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.9%; Score 104.5;
15.0%; Pred. No. 17;
tive 93; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 EQTVEVVKSAIETADGALDFYNKYLDQV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bundock P;
                                                                                                                                                                                                                                                                                                                                                                                                           STICHTING BINAIR VECTOR SYSTEEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 5; 63pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              non-homologous recombination
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hooykaas PJJ, Van Attikum H,
                                                                                                                                                                                                                                                                                                    22-DEC-2000; 2000EP-00204693.
                                                                                                                                                                                                                                                                                                                                             22-DEC-2000; 2000EP-00204693
                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                         RIJKSUNIV LEIDEN
                                                                                                                                                                        Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-550409/59.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1292 AA;
                                                                                                                                                                                                                   EP1217074-A1.
                      22-OCT-2002
                                                                                                                                                                                                                                                            26-JUN-2002.
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Matches
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ABB77986 standard; protein; 1292 AA.

ABB77986

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Similarity
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                                          Sequence 685 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enterococcus
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Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                 13-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antisense;
                                                                                                                                                                                                                                                                                                                                                                                                            AAU35203;
                                                                                                                                                                                                                                                                                                                                    412
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                                                             Query Match
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                                                                                 Matches.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical furgs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
                                         140
                                                                                 165
                                                                                                                                       LSRFKQEYSQEASVLVGDIKVL---LMDSQDKYFEATQTVYEWCGVVTQL---LSAYILL 100
              ---KNERDSTIQNIFFHYNLGNVPSTPFSTEVVLNLTNRIKSRLGELEMDLLDKKKSNET 421
                                                                                                                           -----GAAAGIVAGPFGLIISY 196
                                                                                                                                                                  SI-----AAGVIEGKLIP-----ELNDRLKAVQNFFTSLSVTVKQANKDIDAAKLKLA 244
                                                                                                                                                                              542 RIDECKDRIRGVLKGRLPPEKDMKREIVQALRSIEREYDDLSLKSREAEKEVNMLQMKIQ 601
                                                                                                                                                                                                           245 TEIAAIGEIKTETETTRFYVDYD------DLMLSLLKGAAKKMINTCNEYQQRHG 293
                                                                                                                                                                                                                        :: : :||: :||: :| :: EVNNSLFKHNKDTESRKRYIESKLQALKQESVTIDAYPKILESAKDKRDDRKREYNMANG 661
                                                                                                     422 ALSTAWDCYMDANDRWKSIEAQKRAKDEIKWGISKRIEEKEIERDSFEFEISTVDVKQTD 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                         ----DILIRILDDGVNKLNEAQKSLLGSSQS---
                                                                                                                                                                                                                                                                                                                                                                                                            developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure, SEQ ID NO 18846; 21pp + Sequence Listing; English.
                                                                                 ---LTNDFSEKSSY-
                                                                                                                                                                                                                                                                                                                                                                                       Orosophila melanogaster polypeptide SEQ ID NO 18846.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Myers EW;
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                                         FDEYNEKKASAQK------
                                                                                 ------FINNASGKLLALDSQ-
                                                                                                                                                                                                                                                                                                                          ABB64018 standard; protein; 685
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-656860/75.
                                                                                                                                                                                                                                                     294 KKTLLE 299
                                                                                                                                                                                                                                                                       MRQMFE 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ABL08121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        interactions.
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                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila;
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                                         101
 47
                    305
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ABB64018
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                                                                                                                                                                                                                                                                                                                                                          62 VGDIKVLLMDSQDKYFEATQTVYEWC---GVVTQLLSAYILLFDEYNEKKASAQKDILIR 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            237 VVMKIKEEQLQHIMKLNESRGECTNDKPPLNNYEVKLLKTKADM---LGLAAKYFAAQKE 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                354 LREQIE-QIRLELDAGAKQLENHDLKLG-SVKQVYGDINSSINRIQQDWVQLSQIKEKIL 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89 EQALKQL------ETFYGMCDDGNAVNNLAEAKQRLWDQMRSTFADIPNSLLLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----IEGKLIPELNDRLKAVQNFFTSLSVTVKQANKDIDAAKLKLATEIAAIGEIKTETE
ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                           4 IFAEQTVEVVKSAIETADGALDFYNKYLDQVIPWK--TFDETIKELSRFKQEYSQEASVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 ILD-----DGVNKLNEAQKSLLGSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3
                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prokaryotic cellular proliferation protein; antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---VDRIRKEAYA--GAAAGIVAGPFGLIISYSIAAGV-----
                                                                                                                                                                                                         64;
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                                                                                                                                                      Length 685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotides for the identification and development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           faecalis cellular proliferation protein #490
                                                                                                                                                                                                      51; Mismatches 143; Indels
                                                                                                                                                         4;
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                                                                                                                                                    6.9%; Score 104; DB 20.9%; Pred. No. 8.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTRFYVD--YDDLMLSLLKGAAKKMI 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FSRNMMKNLLDDMQAATQKQNAKSQL 437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    722 AA
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26-MAY-2000; 2000US-0207727P.
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27-NOV-2000; 2000US-0253625P.
22-DEC-2000; 2000US-0257931P.
16-FEB-2001; 2001US-0269308P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibacterial; drug design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                         68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ohlsen KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Snterococcus faecalis
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291 NAQGDYVGIDVDLVKRAAELQGFTVEFKFIGFSSAVQAVE----SGQADGMVAG-
                                                                                                                                                                            16 AIETADGALDFYNKYLDQVIPWKTFDETIKELSRFKQEY
                                                                                                                                                                                                                                                                                                   243 LATEIA-AIGEIKTETETTRFYVDYDDLMLSLLK 275
                                                                                                                                                                                                                                                                                                          SEQ ID NO 10796; 511pp; English
                                                                                                                            ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                 Acinetobacter baumannii protein #158.
                                                                                                                                                                                                                                                                                                                                             ADA32997 standard; protein; 815 AA
                                                                                                                                                                                                                                                                                                                                                                      (first entry
                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               Acinetobacter baumannii
                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                   plant biocontrol
                                                                                                                                         Sequence 722 AA;
                                                                                                                                                                                                                                                                                                                                                                                              Acinetobacter
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                                                                                                                                                                                                                                                                                        341
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epidermidis; open reading frame; ORF; bacterial infection; gene therapy.
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                                                                                                                                                                                                                                        New Acinetobacter baumanii proteins and nucleic acids, useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for
                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to isolated Acinetobacter baumannii nucleic acids. The A. baumannii nucleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. baumannii and other Acinecobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agents for baumannii present sequence represents the amino acid sequence of an A. baumannii protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDE--YNEKKASAQKDILIRI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --RKEAYAGAAAGIVAGPFGL----IISYSIAAGVIEG--KLIPELNDRLKAVQNFFTSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---LDDGVNKLNEAQKSLLGSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDRI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 TVEVVKSAIETADGALDFYNKYLDQVIPWKTFDETIKELSRFKO--EYSQEASVLVGDIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------FDDAVYAEKRPGGGYRVVVAIADVSH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 6; Length 815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.9%; Score 104; DB 6; Length 815
22.0%; Pred. No. 10;
tive 47; Mismatches 123; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         281 MINTC-----NEYQORHGKKTLLEV 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    470 LIEECMLLANVAAAEYALEHDIPMLYRV 497
                                                                                                                                                                                                                                                                                                                                                                Example; SEQ ID NO 4284; 328pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABP39975 standard; protein; 1211 AA.
                                                                                        (GENO-) GENOME THERAPEUTICS CORP.
99US-00328352.
                                             98US-0088701P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              426 YQILKNLRVDRHA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 22.0° nes 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    280 LVTIDGEDARD----
                                                                                                                                                                                      WPI; 2003-576092/54.
                                                                                                                                        Bush D;
                                                                                                                                                                                                           N-PSDB; ADA28871.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 815 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus
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  04-JUN-1999;
                                               09-JUN-1998;
                                                                                                                                        Breton G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABP39975;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                           The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, pseudomonas actuginosa and Enterococcus facedils. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain proteins capable of binding to the express these proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein. Note: The sequence data for this parent did not form part of the printed specification, but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89 VVTQLLSAYILLFDEYNEKKASAQKDILIRILDDGVNKLNEAQKSLLGSSQS-----FN 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     242 TYDKILNNYLATGDETNTQDAGEQ-------MKKITPKKEKYVIASDSTFAPFEFQ 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NASGKILALDSQLTNDFSEKSSY-----FQSQVDRIRKEAYAGAAAGIVAGPFGLII 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------MIIIDDRKKAPDFSVPYPDSGIQIAVKKGNDKIKSYDDLKGKKVGVK 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 ADAIVDDYPVLGYAVKNGQKLQLVGDKETGSSYGFAVKKGONPELIKKFNAGLKNLKDNG 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 AVKKGNDKIKSYDDLKGKTVAAKVGTESANFLEKNKEKYDYTIKNFDDATGLYKALENGE 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         195 SYSIAAGVIEGKLIPELNDRLKA----VQNFFTSLSVTVKQAN---KDIDAAK----LK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASVLVGDIKVL-----KYFEATQTVYEWCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        baumannii; bacterial disease; antibacterial; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.9%; Score 104; DB 4; Length 722;
19.8%; Pred. No. 8.9;
vative 51; Mismatches 109; Indels 1
       antibiotics, comprise sequences of antisense nucleic acids
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Gaps

hyperalgesia; surgery; analgesic; chronic pain; ERK;

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ellular signal regulated kinase; withdrawal; pain sensitisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABP29330 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                  (TEXA ) UNIV TEXAS SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                 WPI; 2002-608414/65.
                                    MEK1; human; enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 60; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2334 AA;
                                                                                                                                                                                                                                             N-PSDB; ABK90804.
                                                                                   WO200258687-A2
            Extracellular
                                                                                                                                                                                                                                                                                                           kinase (ERK).
                                                             sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-JUL-2002
                                                                                                         01-AUG-2002
                                                                                                                                                                                                          Gutstein HB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABP29330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                      opioid
                                                             Homo
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                                                                                                                                                                                                                                                                   ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences qiven in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | :: | : | : | : | : | : | : EESAGVLKYKKRKAESIQKLDHTEDNLNRVEDILYDLEGRVEPLKEEAAIAKEYKQLSKE 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - KGKRQQN-----DYDIEKLN---YELVKATENYEQLSGKLNVLBERKKNQSETNARYE 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               217 AVQNPFTSLSVTVKQANKDIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDLMLSLLKG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              382 EVOELESILYISDEOHDEKLEEIKNSYYTLMSEQSVVNNDIRFLEHTINENEAKKSRLDS 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----GVVTQLLSAYILLFDEYNE 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 EQTVEVVK-----SAIETADGALDFYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KKASAQKDILIRILDDGVNKLNEAQKSLLGSSQSFNNASGKLLALDSQLTND-----FS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNDRL----K
                                                                                                                                                                                                          Novel isolated nucleic acid encoding a Staphylococcus epidermis polypeptide, useful for diagnosing and treating bacterial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          82;
                                                                                                                                                                                                                                                                                                                                                                                                                                6.9%; Score 104; DB 5; Length 1211;
18.0%; Pred. No. 17;
ive 60; Mismatches 131; Indels 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----RHGKKTLLEV 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RLVEAFNOLKDIQQNITQTQKEYQSSKKSMEKV 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LVGDIKVLLMDSQDKYFEATQTVYEWC-----
                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 4820; 267pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein; 2334 AA
                                                                                                                       (GENO-) GENOME THERAPEUTICS CORP.
                                                             98US-00134001
                                                                                     97US-0055779P
                                                                                                97US-0064964P
                                                                                                                                                                                                                                                                                                                                                                                                                                                          60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAKKMINTCNEYQQ-
                                                                                                                                                                       2002-381255/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
                                                                                                                                                 Doucette-Stamm LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human kinase, MEK1
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1211 AA;
                                                                                                                                                                                   N-PSDB; ABN92520
                                                             13-AUG-1998;
                                                                                     14-AUG-1997;
             US6380370-B1
                                                                                                08-NOV-1997;
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                                    30-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 EATQTV-YEWCGVVTQLLSAYILLFDEYNEKK-ASAQKDILIRILD---DGVNKLNEAQK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                      Reducing or reversing tolerance, physical dependence, hyperalgesia, withdrawal symptoms, or pain sensitization in patients on analgesics for chronic pain, comprises inhibition of the extracellular signal-regulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a method of reducing or reversing tolerance, reducing the risk of physical dependence or hyperalgesia, reducing the symptoms of opioid withdrawal or inhibiting pain sensitiation in a patient taking analgesics. The method comprises administering an analgesic and an extracellular signal-regulated kinase (ERK) inhibitor comprised in a formulation to reduce or reverse tolerance, risk of physical dependence, hyperalgesia, symptoms of opioid withdrawal, or inhibiting pain sensitisation in patients taking analgesics for chronic pain or those undergoing surgery. The present sequence represents the amino acid sequence of human MEKI (not defined)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133 SLLGSS----QSFNN--ASGKLLALDSQLTNDFS---EKSSY-FQSQVDRIRKEAYAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGIVAGPFGL-IISYSIAAGVIEGKLIPELNDRLKAVQNFFTSLSVTVKQANKDIDAAKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 KLATEIAAIGEIKTETTRFYVDYDDLMLSLLKGAAKKMINTC-NEYQQRHGK 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.9%; Score 104; DB 25.6%; Pred. No. 41; ive 39; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus polypeptide SEQ ID NO 7836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, Page 156-161; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1322 SGVLSGSKALEVLSQSTSAGTDHG----
25-JAN-2002; 2002WO-US002128.
                                                                           25-JAN-2001; 2001US-0264336P.
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The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus pyogenes), comprising one of 5483 sequences (81), given in the specification. The proteins have antibacterial and antinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and the specification. The proteins have antibacterial and antinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a bindingical sample. (I) is used to determine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used to recombinantly produce (I) and may be seed encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135
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Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FYORYADK----EKIDLSEARKRASELDISAYOKKAKELVAKAEKLRREGKIVTRDDFTH 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSSQSFNNASGKLLALDSQLTNDF--SEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLI 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      222 JARDIRREFDVSAŠYAKRLAITĖHARVOMEVGRLSMAENGFAMFDILPEPKACDVCKDIA 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---LKLATEIAAIGEIKTETETTRFYUDYD-----DLMLSL--- 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   105 QENADMSIYN-LAMKTNALELLRINIDLEMQELANGEHKLTKKFIDEGYRKETEFQAGIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                194 I-----SYSIAAGVIEGKLIPELNDRLKAVQNFFTSLSVTVKQANKDI--DAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FYNKYLDQVIPWKTFD--ETIKELSRFK-QEYSQEASVLVG-----DIKVLLMDSQDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 YFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRILDDGVNKLNEAQKSLL
                                                                                                                                                                                                                                                                                                                                                                                                               Fraser C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 6.9%; Score 103.5; DB 5; Length 541; Best Local Similarity 21.6%; Pred. No. 6.7; Matches 71; Conservative 51; Mismatches 142; Indels 65;
                      group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                             Masignani V, Margarit Y RosI, Grandi G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 3916; 4525pp; English.
                                                                                                                                                                                                                                                         27-OCT-2000; 2000GB-00026333.
24-NOV-2000; 2000GB-00028727.
07-MAR-2001; 2001GB-00005640.
                                                                                                                                                                                                               29-OCT-2001; 2001WO-GB004789
                                                                                                                                                                                                                                                                                                                                            (CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC RES
                                                                                       Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2002-352536/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ABN69961.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 541 AA;
                                                                                                                               WO200234771-A2.
                                                                                                                                                                         02-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                          Telford J,
Tettelin H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26
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282 KHGPYHLDKWRIGENSPPFHPYCRCAIVGVDESGVATDR-QLDYNRNMNNIDLMAKTQSF 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            215 DOLIKDLER--ONISYEA-VLTNAGEVIKASSEAGIKLGOALOSIVD-AGDOSO---AAV 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotide for treating Chlamydia infections encodes a polynucleotides containing an immunogenic portion of a Chlamydia antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 DETIKELSRFKQEYSQEASVLVGDIKVLLMDSQD--KYFEATQTVYEWCGVVTQLLSAXI 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to isolated polynucleotide encoding at least a partial Chlamydia protein which is an antigenic fragment, or the complements, fragments, homologues and variants, and antibodies raised against the antigenic proteins (or fragments). The nucleic acids, proteins and antibodies are used to diagnose and treat Chlamydia infections (e.g. a sexually transmitted disease, pelvic inflammatory disease (PID), acute respiratory tract infection, trachoma, atherosclerosis and coronary heart disease) in a patient, and in the treatment of male infertility. The compounds of the invention are also useful for detecting the presence of Chlamydia in a patient, and stimulating and/or expanding T cells specific for a Chlamydia protein. The present sequence represents a Chlamydia antigen. (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   155 EEVNNIKKALEAQKDTIDKLNKLVTLQNQNKSLTEVLKTTDSADQIPAINSQLEINKNSA
                                                                                                                                                                                                                                                                                                                                       Chlamydia; sexually transmitted disease; PID; antibacterial; pelvic inflammatory disease; antigen; trachoma; gynecological; acute respiratory tract infection; atherosclerosis; male infertility; coronary heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.9%; Score 103.5; DB 4; Length
21.7%; Pred. No. 8.7;
ve 48; Mismatches 119; Indels
                                                          341 IINKDVRVSAKKVVGTRYDFWAQDNTKKI 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 QTVEVVKSAIETADGALDFYNKYL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Page 205-207; 208pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stromberg EJ;
                                                                                                                                                                    AAU38921 standard; protein; 660 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                     Chlamydia trachomatis; serovar E.
                                                                                                                                                                                                                                                                                                    C. trachomatis CT875 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-APR-2001; 2001WO-US013081.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-APR-2000; 2000US-0198853P.
20-JUL-2000; 2000US-0219752P.
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                                                                                                                                                                                                                                             (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bhatia A, Probst P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-616771/71.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAS56995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 660 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200181379-A2.
                                                                                                                                                                                                                                               11-SEP-2003
16-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-2001.
                                                                                                                                                                                                          AAU38921;
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                                                                                                                                 RESULT 28
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pelvic inflammatory disease (which results in tubal obstruction and infertility in women), male infertility, ocular infection (which may cause blindness), acute respiratory tract infections, atherosclerosis, coronary heart disease. The present sequence is used in the exemplification of the present invention.

Sequence 660 AA;

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The present invention describes compounds and methods for diagnosing and treating Chlamydial infection. Chlamydia polynucleotide and protein sequences have antibiotic, antiinflammatory, antiinfertility, cardiant, antiarteriosclerotic and ophthalmological activities, and can be used in vaccines, and in gene therapy. The Chlamydia polynucleotides, proteins, compositions or methods from the present invention can be used for the serodiagnosis or treatment of Chlamydial infections, particularly in humans. The polynucleotides, proteins or compositions are particularly useful for stimulating an immune response in a patient, or for stimulating an immune response in a patient, or for stimulating an immune response in compositions are useful as specifically, the polynucleotides, proteins or compositions are useful as vaccines for treating or preventing Chlamydial infections including
LLFDEYNEKKASAQKDILIRILDDGVNKLNEAQKSLLGSSQSFNNASGKLLALDSQLTND 158
                                                                      210
                                                                                                        367
                                                                                                                                                              -----TDSPLVKK 311
                                                                                                                                         LNDRLKAV-----QNFFTSLSVTVKQANKDIDAAKLKLATE----IAAIGBIKTETETTR 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New DNA and proteins comprising a portion of a Chlamydia antigen, useful for diagnosing or treating Chlamydial infections, particularly as vaccines for treating or preventing Chlamydial infections, e.g. pelvic
                                                                      FSEKSSYFQSQVDRIRKEAYAGAAGIVAGPFGLIISYSIAAGVIEGK-----LIPE
                                                                                                    312 AEEQISQAQKDIQEIKP---SGSDIPIV-GPSGSAASAGSAAGALKSSNNSGRISLLLDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antiinfertility; cardiant; antiarteriosclerotic; ophthalmological; vaccine; gene therapy; immune response; pelvic inflammatory disease; tubal obstruction; infertility; male infertility; ocular infection; blindness; acute respiratory tract infection; atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      infection; Chlamydia; antibiotic; antiinflammatory;
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                  Chlamydia trachomatis antigen protein SEQ ID NO:139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 4; SEQ ID NO 139; 275pp; English.
                                                                                                                                                                                                                                                                                                                                         ADD42726 standard; protein; 660 AA
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05-DEC-2001; 2001US-00007693.
15-JUL-2002; 2002US-00197220.
                                                                                                                                                                                                                FYVDYDDLMLSLLK 275
                                                                                                                                                                                                                                                   -----DALAQALK 435
                                                                                                                                                                                                                                                                                                                                                                                                               15-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Guderian J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             coronary heart disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inflammatory disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chlamydial
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Probst P;
                                   268
                                                                                                                                                                            368
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                                                                                                                                                                                                                                                                                                                                                                            ADD42726;
66
                                                                    159
                                                                                                                                         211
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ADD42726
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                                                                                                                                                                                                                                                                                       368 VDNEMAAIALQGFRSMIEQFNVNNPATAKELQAMEAQLTAMSDQLVGADGELPAEIQAIK 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to
                                                                                                                                                              LLFDEYNEKKASAQKDILIRILDDGVNKLNEAQKSLLGSSQSFNNASGKLLALDSQLTND 158
                                                      40
                                                                                                         86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                              215 DQIIKDLBR--QNISYBA-VLTNAGBVIKASSBAGIKLGQALQSIVD-AGDQSQ--AAV
                                                                                                                                                                                         268 LQAQQNNSPDNIAATKELIDAAETKVNELKQEHTGL-------TDSPLVKK
                                                                                                                                                                                                                                                                        211 LNDRLKAV----QNFFTSLSVTVKQANKDIDAAKLKLATE----IAAIGEIKTETETR
                                                                              155 EEVNNIKKALEAQKDTIDKLNKLVTLQNQNKSLTEVLKTTDSADQIPAINSQLEINKNSA
                                                                                                                                                                                                                  159 FSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGK-----LIPE
                                                                                                                                                                                                                                   DETIKELSRFKQEYSQEASVLVGDIKVLLMDSQD--KYFEATQTVYEWCGVVTQLLSAYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zyskind JW;
Xu HH;
                            Gaps
                         161
 Length 660;
                                                     8 QTVEVVKSAIETADGALDFYNKYL---------DQV---
6.9%; Score 103.5; DB 7; Length 21.7%; Pred. No. 8.7; ive 48; Mismatches 119; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ohlsen Forsyth F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein encoded by Prokaryotic essential gene #15619.
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Yamamoto R,
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Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-PEB-2002; 2002US-00072851.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2002US-0362699P
                                                                                                                                                                                                                                                                                                                            262 FYVDYDDLMLSLLK 275
                                                                                                                                                                                                                                                                                                                                                     -----DALAQALK 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ELIT-) ELITRA PHARM INC.
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Trawick JD,
            Similarity
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N-PSDB; ACA33962.
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                         68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-JUN-2003
                                                                                                                                                              66
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 Query Match
Best Local 8
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Wall D,
                            Matches
                                                                                                                                                                                                                                                                                                                                                                                               RESULT 30
                                                                                                                                                                                                                                                                                                                                                                                                          ABU30092
                                                                                                                                                                                                                                                                                                                                                                                                                                     74X38X11X3XX8X838X6X6X6X8X8X6X6X6X
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19-JUN-2003 (first entry)

The invention relates to an isolated mucleic acid comprising any one of the foll antisense sequences given in the specification where expression of the mucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the mucleic acid concluded are: (2) a host cell containing the vector; (3) an isolated concluded are polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for conjuded for proliferation, or that inhibits cellular proliferation; (8) identifying a gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the extent or compound's activity; (11) a culture computaing strains in which the extent or which each of the strains is present in a culture or collection of strains; or (13) identifying proteins or screening for homologue nucleic acids are useful for confideration or solve an organism. The antisense nucleic acids are useful for for cellular proliferation to solate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences isolate candidate molecules for rational drug discovery programs Claim 25; SEQ ID NO 58016; 1766pp; English

Zyskind JW; Xu HH;

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Ohlsen Forsyth

Sequence 1020 AA;

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217
                                                                                                                  FKQEYSQ-EASVLVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKK 108
                                                                                                                                                                            ASAQKDILIRILDDGVNKLNEA---QKSLLGSSQSFNNASGKLLALDSQLTNDFSEKSSY 165
                                                                                                                                                                                             246 AQLAKFNL-----ELGKLSESIQEQESILAKQRKENAQADRLIEKNQQVLLDLSEKLKQ 299
                                                                                                                                                                                                                                     166 FQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNDRLKAVQNFFTSL 225
                                                                                                                                                                                                                                                                                                                :: | ||:| ||:|
---HFEKLQESLMKAAAEKETEIQ 354
                                                                                                                                                                                                                                                                   -----VLOERTKHTOKSSOEY 321
                                                         4
                                                                                                                                       226 SVTVKQANKDIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDIMLSLLKGAAKK----
                                                         GIFAEQTVEVVK-----SAIETADG---ALDFYNKYLDQVIPWKTFDETIKELSR
                                                                                     GIF-BEAAGVLKYKQRKKKKAEQKLFETEDNLSRVQDIIHELEEQLTPLAAQSEAAKEFLR
                             Indels 133; Gaps
   Length 1020;
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9
                               90;
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DB
6.9%; Score 103.5; D
19.8%; Pred. No. 15;
ative 41; Mismatches
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                               Conservative
            Local Similarity
es 65; Conserv
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   Query Match
                                Matches
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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the mucleic acid inhibites proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid concluded are:

(2) a vector comprising a promoter operably linked to the nucleic acid concluded whose expression is inhibited by the antisense concluded or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding compoundation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway required for that has an activity against a biological pathway or equired for proliferation, or that that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product in the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the test compound that inhibits proliferation of an organism activity; (11) a culture comprising strains in which the strains is present in a culture or collection of the which each of the strains is present in a culture or collection of strains; or (13) identifying the target compound that inhibits the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is encoded by one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   K. pneumoniae or P. aeruginosa. The present sequence is encoded by one can target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                              Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                         Protein encoded by Prokaryotic essential gene #9467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 25; SEQ ID NO 51864; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                           ; 2001US-00948993.
; 2001US-0342923P.
; 2002US-00072851.
; 2002US-0362699P.
                                                                                                                                                                                                                                                             21-MAR-2002; 2002WO-US009107
                                                                                                                             Clostridium acetobutylicum
                                                                                                                                                                                                                                                                                                                                                                                                                                             (ELIT-) ELITRA PHARM INC
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Trawick JD,
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                                                                                                                                                                           40200277183-A2
                                                                                                                                                                                                                                                                                                                              06-SEP-2001;
25-OCT-2001;
08-FEB-2002;
                                                                                                                                                                                                                                                                                                         21-MAR-2001;
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Wall D,
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ABU23940 standard; protein; 1163 AA
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14; 48 1 MTGIFAEQTVEVVKSALETADG----ALDFYNKYLDQVIPWKTFDETIK------ELS Gaps 95; DB 6; Length 1163; Indels 142; 6.9%; Score 103.5; 21.7%; Pred. No. 18; ive 55; Mismatches 81; Conservative Best Loca Matches

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ABU23940;

RESULT 31
ABU23940
ID ABU23
XX
AC ABU23

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(GEHO ) GEN HOSPITAL CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1976 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2003016475-A2
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derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence
                                                                                                                                                       92 QLLSAYILLFDEYNEKKASAQKDILI----RILDDGVNKLNE----AQKSLLGSSQS--- 140
                                                                                                                                                                                     BASKEYLKAEEEYNEGKEVWGLQIEIEEKNRVRKDLMEKKDEIDLKEKRARLGESSSKVK 289
                                                                                                                                                                                                                                                                                                                                    183 AGIVAGPFGLIISYSIAAGVIEGKLIPELNDRLKAVQNFFTSLSV-----TVKQANKD 235
                                                                                              ----FINNASGKLLALDSQLTN------DFSEKSSYFQSQVDRIRKEAYAGAA 182
                                                                                                                                                                                                                                                                                        290 PYIDNYENTLKQIDILKEQILSRENTMKAISLEKEDMEKKLSIAKDNKEK----- 339
                                                                                                                                                                                                                                                                                                                                                                             340 ----ALPKFMIKHHIILDAIKEKDLLDNIKLEKKRLQGKIEKLSLEASNKEELIKQNIKD 395
                                                                                                                                                                                                                                                                                                                                                                                                                         236 IDAAKLKLATEIAAIGEIKTETETTRFYVDYDDLMLSLLKGAAKKMIN-----TCNEYQ 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment,
                                                                     ----VLVGDIKVLLMDSQDKYFEATQTVYEWCGVVT 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Costigan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADE63514 standard; protein; 1976 AA.
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                                                                     RF--KQEYSQEAS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page; 1017pp; English
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26-NOV-2001; 2001US-033347P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-268312/26.
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                                                                     49
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that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more of pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that moulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at (tp. wipo.int/pub/published_pot_sequences).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1338 --IRQLEEEKNSLOEQQEE---EEEARKONLEKQVLALOSQLADT-----KKKVDD-- 1382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---LEEAKKKLLK 1399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nerve injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 VEVVKSAIETADGALDFYNKYLDQV----IPWKTFDETIKEL-----SRFKQEYSQE
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chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . Match 6.9%; Score 103.5; Local Similarity 21.9%; Pred. No. 37; les 61; Conservative 43; Mismatches
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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Bone marrow; diagnostic; therapeutic; gene therapy; antigenic; haematopoiesis; myeloid; lymph cell disorder; tissue regeneration; wound healing; nutritional supplement; immune disorder;

Novel bone marrow polypeptide #2.

severe combined immunodeficiency; SCID

WO200157187-A2.

Homo sapiens

Costigan M;

Befort K,

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New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                                             frp.wipo.int/pub/published_pct_sequences.
                                             Claim 1; Page; 1017pp; English.
          D'urso D,
                    WPI; 2003-268312/26
(FARB ) BAYER AG.
          Woolf C,
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Xue AJ;

Sequence 1976 AA;

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---LEEAKKKLLK 1399
                                                                                                  LEKNKOGLETDNKELACEVKVLOQVKAESEHKRKKLDAQVQELHAKVSEGDRLRVELAEK 1281
                                                                                                                                                                                                    115 ILLRILDDGVNKLNEAQKSLLGSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDRIR 174
                                                                                                                                  58 ASVL---VGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKD 114
                                                                                                                                                                                                                                                                      175 KEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNDRLKAVQNFFTSLSVTVKQANK 234
                                                                   57
                                                                10 VEVVKSAIETADGALDFYNKYLDQV----IPWKTFDETIKEL-----SRFKQEYSQE
                                   79; Gaps
6.9%; Score 103.5; DB 7; Length 1976; 21.9%; Pred. No. 37; tive 43; Mismatches 96; Indels 79;
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                                   61; Conservative
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Best Local Similarity
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(first entry)

24-OCT-2001 AAU14603;

RESULT 34 AAU14603

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Gaps

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AAU14602-AAU14794 represent novel bone marrow polypeptides of the invention. The proteins and corresponding coding sequences may be used in the prevention, diagnosis and treatment of diseases associated with the proteins and treatment of diseases associated with decreased expression. For example, to treat disorders associated with decreased expression by rectifying mutations or disorders associated with decreased expression by rectifying mutations or polypeptides by expressing inactive proteins or to supplement the colypeptides by expressing inactive proteins or to supplement the conjugation of the polypeptide. Additionally, the nucleic acids may be used to produce the polypeptides, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. The nucleic acid and its complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acid sequences in samples, and therefore which patients can seasys to identify medulators of their expression and activity. The antiposes in the protein antibodies against bone marrow proteins and confined samples and antiposes in the protein antibodies and antagonists may also be used to down regulate expression and activity. The antipodies may also be used as the antipose and antipodies and antagonists may also be used to can assays to identify medulators of their expression and activity. The artichodies may also be used to the activity and consequently in the presence of the protein in samples of e.g. by enzyme linked immunoschant assay (ELISA)). The proteins may be used to regulate haematopoiesis activity, and consequently in the cused to require hammatopoiesis activity, and consequently in the cused to require hammatopoiesis activity, and consequently in the protein as wound healing, as a nutritional supplement; and in treatment of immune disorders such as severe combined immunodeficiency (SCID)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1424 DIEKAILEQOVLSEELTTKKEQVSEAIKTSQIFLAKHG-HKLSEKEKKQI--SEQLNALN 1480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1369 KYISDAL--RRLEBEBEKVVEBEKÖEHVEKVKELLGWVSTLARNTOCK---ÄTSSETKEST 1423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89 VVTQLLSAYILLFDEYNEKK---ASAQKDILIRILDDGVNKLNEAQKSLLGSSQSFN--- 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding bone marrow polypeptides, useful in diagnostic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29 KYLDQVIPWKTPDETIKELSRFKQEYSQEASVLVGDIKVLLMDSQDKYFBATQTVYEWCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.9%; Score 103.5; DB 4; Length 5373; 23.0%; Pred. No. 1.4e+02; tive 49; Mismatches 106; Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Asundi V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 10; Page 198-208; 392pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-JUN-2000; 2000US-00598075.
19-JUL-2000; 2000US-00620325.
30-NOV-2000; 2000US-0250683P.
                                                                                                                                                                                                                                                                                                                                                                                                                                               05-FEB-2001; 2001WO-US003782.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-FEB-2000; 2000US-00496914.
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nes 56; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-488875/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ford JE, Boyle BJ,
Ren F, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5373 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAS22908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                        09-AUG-2001.
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Matches
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                                                                                                                                                                                                                                                                                                                                               The invention discloses a composition comprising two or more isolated rate or human polynuclectides or a polynuclectide which represents a fragment, or human polynuclectides or a polynuclectide which represents a fragment, contains a vector comprising the movel polynuclectide, a host cell comprising the vector, a method for identifying a nuclectide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynuclectide sequence that increases or decreases the expression of the polynuclectide sequence subjected to pain, a method for identifying a compound which regulates the expression of a polynuclectide sequence which is differentially a compound that regulates the activity of one or more of the composition, a compound that regulates the activity of one or more of the composition, a method for identifying a compound useful that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating the pain and a method for identifying a compound useful in treating a pain and a method for identifying a compound useful in treating a pain and a method for identifying a compound useful in treating an animal of one or more of the polypeptides given in the pain and a method for identifying a compound useful in treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pain and a pharmaceutical composition comprising the one or more poin and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (chung), chronic constriction injury (CCI) and spared nerve injury (chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU14603 standard; protein; 5373
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This invention relates to novel mitochondrial targets that can be used for therapeutic intervention in treating a disease associated with a letter discondrial function. Specifically, it refers to a method for identifying proteins of the human heart mitochondrial proteome that are useful for drug screening assays, as well as therapeutic targets. The present invention describes a method for identifying such proteins that can be used in the treatment of various diseases associated with altered mitochondrial function including diabetes mellitus, Huntington's disease, osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial concephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy ragged red fibre syndrome (MERRP) or cancer. Accordingly, these compositions have neuroprotective, nootropic, antidiabetic, anticonvulsant, antiarthritic, osteopathic, ophthalmological and cytostatic activities. This polypeptide sequence is a human heart mitochondrial protein of the invention.
                                                                                         248
-----NASGKLLALDSQLTNDFSEKSSYFQSQVDRIRKE----AYAGAAAGIVAGP 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leber's hereditary optic neuropathy; LHON, mitochondrial encephalopathy lactic acidosis and stroke; MELAS; mycolonic epilepsy ragged red fibre syndrome; MERRF; cancer; neuroparotective; nootropic; antidiabetic; anticonvulsant; antiarthritic; osteopathic; ophthalmological; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying a mitochondrial target for drug screening assays and for treating diseases associated with altered mitochondrial function, comprises detecting a modified polypeptide in a sample and correlating with the disease.
                     190 FGLIISYSIAAGVIEGKLIPELNDRLKAVQNFFTSLSVTVKQANKDIDAAKLKLA-TEIA
                                                                                                                                                                                                                                                                                                                                                                                     Human heat mitochondrial protein as a therapeutic target SeqID741.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glenn GM;
                                                                                                                                                                                                                                                                                                                                                                                                                         mitochondrial; human; screening assay; diabetes mellitus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gibson BW, Taylor SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 741; 180pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Huntington's disease; osteoarthritis;
                                                                                                                                                                                                                                                                        ADJ68935 standard; protein; 5373 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhang B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-APR-2002; 2002US-0372843P.
17-JUN-2002; 2002US-0389987P.
20-SEP-2002; 2002US-0412418P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-APR-2003; 2003WO-US010870
                                                                                                                                                                                                                                                                                                                                              06-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MITO-) MITOKOR.
(BUCK-) BUCK INST AGE RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fahy ED,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-845369/78.
                                                                                                                                                                                1596 ALRE 1599
                                                                                                                                             249 AIGE 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2003087768-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-OCT-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Warnock DE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SS,
                                                                                                                                                                                                                                                                                                              ADJ68935;
143
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ADJ68935
ID ADJ68
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                                                                                                                                                                                                                                        1481 KAYHDLCDGSANQLQQQLQSQLAHQTEQKT--LQKQQNTCHQQLEDLCSWVGQAERALAGH 1538
                                                                                                                                                                                                                                                                              248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to Enterococcus faecalis polynucleotides and polypeptides. The invention also relates to a recombinant expression vector comprising a polynucleotide operably linked to a transcription regulatory element, a cell comprising a recombinant vector, a method for producing an E. faecalis polypeptide, an isolated nucleic acid comprising a sequence not given in the specification, a recombinant vector comprising the nucleic acid and a cell comprising the recombinant vector. The polynucleotides can be used to detect the presence of E. faecalis in
                                                                                                  88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid comprising a sequence encoding an Enterococcus fecalis polypeptide, useful for preparing a composition for diagnosing or treating E. fecalis infection.
                                                                                                  29 KYLDQVIPWKTFDETIKELSRFKQEYSQEASVLVGDIKVLLMDSQDKYFEATQTVYEWCG
                                                                                                                                                                                                                    -----NASGKLLALDSQLTNDFSEKSSYFQSQVDRIRKE----AYAGAAAGIVAGP
                                                                                                                                                                                                                                                                              190 FGLIISYSIAAGVIEGKLIPELNDRLKAVQNFFTSLSVTVKQANKDIDAAKLKLA-TEIA
                                                                                                                                                           89 VVTQLLSAYILLFDEYNEKK---ASAQKDILIRILDDGVNKLNEAQKSLLGSSQSFN---
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enterococcus faecalis infection; transcription regulatory element;
                                                                      33;
                                         Length 5373;
                                                                     Indels
                                           DB 7;
                                         6.9%; Score 103.5; DB 7;
23.0%; Pred. No. 1.4e+02;
ive 49; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 3594; 193pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    faecalis polypeptide #189.
                                                                                                                                                                                                                                                                                                                                                                                                                                             ADH85709 standard; protein; 284 AA.
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                                   Query Match
Best Local Similarity 23.04
Matches 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enterococcus faecalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-895394/82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Joucette-Stamm LA,
                                                                                                                                                                                                                                                                                                                                                                      1596 ALRE 1599
                                                                                                                                                                                                                                                                                                                                         249 AIGE 252
             Sequence 5373 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ADH82304.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BUSH D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antibacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US6617156-B1
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                                                                                                                                                                                                                                                                                                   206 TITDDRKKAFDFSVPYFDSGIQIAVKKGNDKIKSYDDLKGKKVGVKIGTESADFLEKNKK 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    £
                                                                                                                                                                       119
                                                                                                                                                                                           EYNEKKASAQKDILIRILDDGVNKLNEAQKSLLGSSQS-----FNNASGKLLALDSQLT 156
                                                                                                                                                                                                         157 NDFSEKSSY-----FQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLI 208
                                                                                                                                                                                                                                                                               PELNDRLKA----VQNFFTSLSVTVKQAN---KDIDAAK----LKLATEIA-AIGEIKT 255
                                                                                                                                                  -----LMDSQD-----KYFEATQTVYEWCGVVTQLLSAYILLFD 102
                                                                                                         68
                                                                                                                           6 AVKVGGEGANFLEKNKEK-----YDYTİKNFDDATGLYKALENGEADAIVDDYPVLGYA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. and (II) can have antibacterial activity and therefore can be used in
                                                                                                                                                                      60 VKNGQKLQLVGDKETGSSYGFAVKKGQNPELIKKFNAGLKNLKDNGTYDKILNNYLATGD
a sample. The sequences are useful for preparing a composition for diagnosing or treating Enterococcus faecalis infection. This sequence represents an E. faecalis polypeptide of the invention.
                                                                                                        16 AIETADGALDFYNKYLDQVIPWKTFDETIKEL----SRFKQEYSQEASVLVGDIKVL---
                                                               Match 6.8%; Score 103; DB 7; Length 284; Local Similarity 21.0%; Pred. No. 3.2; es 67; Conservative 46; Mismatches 106; Indels 100; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                S. epidermidis open reading frame protein sequence SEQ ID NO:1660.
                                                                                                                                                                                                                                                         KRAAELQGFTVEFKFIGFSSAVQAVE----SGQADGMVAG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 18; Page 462; 2188pp; English
                                                                                                                                                                                                                                                                                                                                                                                                      AAG82283 standard; protein; 885 AA
                                                                                                                                                                                                                                                                                                                            ETETTRFYVDYDDLMLSLL 274
                                                                                                                                                                                                                                                                                                                                           KYDYSIKYLDTTDALYSAL 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-NOV-2000; 2000WO-US030782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0164258P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus epidermidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GLAX ) GLAXO GROUP LTD
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N-PSDB; AAH53133.
                                              Sequence 284 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200134809-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   endocarditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kimmerly WJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-MAY-2001
                                                                                                                                                                                              103
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                                                                                                                                                     69
                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                  RESULT 37
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vaccination. The nucleic acids (I) may be used to produce the S.
epidermidis polypeptides (II) via the production of vectors containing
them which are used to produce hosts cells which express the
collapseptides. The polypeptides (II) (and/or nucleic acids) may then be
used to vaccinate subjects and to raise antibodies against the bacteria.
The polypeptides may also be used to assay for other inhibitors of their
activity and herefore identify compounds that may be used for the
treatment of S. epidermidis infections, eg. endocarditis. AAH53971 to
AAH55090 represent specifically claimed S. epidermidis genomic DNA
copressor specifically claimed S. epidermidis genomic DNA
cepresent oligonucleotide sequences and primers which are used in the
exemplification of the present invention. N.B. The present invention
specifically claims all the polymucleotide sequences given in the
cequence listing of the present specification, however the sequence
listing only goes up to SEQ ID NO:4454 so even though sequences are given
in the disclosure for SEQ ID NO:4455 to 4472, no sequences are present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 AQINQLLQXY------KGKRQQN-----DYDIEKLN---YELVKATENYEQLSGK 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148 LLALDSQLTND-----PSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | :|| : :|| | : :| EPLKEEAAIAKEYKQLSKEMEQSDVIVTVSDIDHYTEDNQRLDERLMHLKSQQAEKEGQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202 VIEGKLIPELNDRL----KAVONFFTSLSVTVKQANKDIDAAKLKLATEIAAIGEIKTET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88 GVVTQLLSAYILLFDEYNEKKASAQKDILIRILDDGVNKLNEAQKSLLGSSQSFNNASGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42 ETIKELSRFKQEYSQEASVLVGDIKVLLMDSQDKYFEATQTVYBWC------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 staged assembly; nanostructure; peptide nucleic acid; PNA; structural reinforcement; aerogel; paper; plastic; cement; tensile strength; identification marker; anti-counterfeiting marker; enzyme support; catalyst support; assembly scaffold; nanowire; nanocircuit; molecular sieve; molecular filter; biosensor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   258 ETTRFYVDYDDLMLSLLKGAAKKMINTCNEYQQ------RHGKKTLLEV 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              199 RFLEHTINENEAKKSKLDSRLVEAFNQLKDIQQNITQTQKEYQSSKKSMEKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.8%; Score 103; DB 4; Length 885; 18.2%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   General vesicular transport factor p115 SEQ ID NO:155.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADB67135 standard; protein; 961 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-FEB-2002; 2002US-00080608.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-FEB-2003; 2003WO-US005390.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for SEQ ID NO:4455 to 4464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NANO-) NANOFRAMES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2003072829-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 885 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-SEP-2003.
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peptide nucleic acid; PNA; nanostructure.

21-FEB-2003; 2003US-00370685. 21-FEB-2002; 2002US-00080608.

JS2003215903-A1

Synthetic.

0-NOV-2003.

Goldberg EB;

Hyman PL,

HYMAN P L. GOLDBERG E

(HYMA/) (GOLD/)

Nanostructure assembly protein #57

(first entry)

20-MAY-2004

ADL99406;

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The present invention describes a meturo (MI) tot the staget abserming to contacture using peptide nucleic acids (PMAs). MI comprises: (a) contacting a nanostructure intermediate (NSI) having at least one unbound contacting a nanostructure intermediate (NSI) having at least one unbound different JE where: (i) none of these JE can interact with itself or content JE where: (i) none of these JE can interact with itself or content JE where: (i) none of these JE can interact with itself or complementary, so that AU becomes non-covalently linked to NSI to produce a new NSI for us in subsequent cycles; (b) removing unbound AU; and (c) cyclic repetition of (a) and (b) to form a nanostructure. The new feature CG is that the complementary JE in at least one cycle are PNAs. Also described are nanostructures formed from many AU, comprising different JE, where at least one AU includes PNA. MI is useful for producing nanostructural reinforcements (for aeroge), paper; plastics or cement.

CG nanostructural reinforcements (for aeroge), paper; plastics or cement, particularly as long fibres to improve tensile strength); identification (anti-counterfeiting) markers; enzyme or catalyst supports; assembly caffor construction of nanowires on anostructures for construction and elivering specific molecules; in high-counter menories; as artificial zeolite for absorbing ions from water and for construction of new materials, including use in biosensors.

CG by a se more homogeneous than inorganic nanoparticiles generally used to construction of new materials, including use in biosensors.

CG by a ser more homogeneous than inorganic nanoparticiles generally used to construction of new materials, including use in biosensors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           form nanostructures, so will produce structures with predictable geometry and stoichiometry. The present sequence represents a protein containing colled coil dimerisation sequences that can be used for structural elements of assembly units, given in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a method (M1) for the staged assembly of
                                                                                                                                                                                                                                         Staged assembly of nanostructures, useful e.g. in biosensors or as catalyst supports, using assembly units derived from peptide nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 58; 118pp; English
Goldberg EB;
Hyman PL,
                                                                                                                                                                                                                                                                                                                                                              acids
EXEXER ELXEX SOCIOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COOLO COO
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Sequence 961 AA;

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14;
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                                                                                                                                                                                                                     743
                                                                                                                                                                                                                                                                109 AS-----AQKDILIRILDDGVNK--LNEAQKSLLGSSQSFNNASGKLLALDSQLTND 158
                                                                                                                                                                                                                                                                                                                                                   FSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKL-----IPELN 212
                                                                                                                                                                                                                                                                                                                                                                                            803 QSVEITKLÓTEKQELLQKTEÁFÁKSAPVPGESETVIATKTTD--VEGRĽSALLQETKELK 860
                                                                                                                                                                                                                                                                                                                                                                                                                                       DRIKAVONFFTSLSVTVKQANKDIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDLMLS 272
                                                                                                                              EEVKKTLEQHDSIVTHYKNMIREQDLQLEELKQQISTLKCQNEQLQTAVTQQVSQIQQHK 698
                                                                                                                                                                           52 QEYSQEASVLVGDIKVLL-MDSQDK--YFEATQTVYEWCGVVTQLLSAYILLFDEYNEKK 108
                                                                                                                                                                                                                                                                                                      744 SNRELLOSOLAEKOSLIENLKSSOLSPGTNEOSSATAGDSEOIAELKOELATLKSOL-NS 802
                                                                                                                                                                                                                     699 DQYNL-----LKVQLGKDSQHQGPYTDGAQ----MNGVQPEEISR---LREEIEELK
                                                                                       EVVKSAIETADGALDFYNKYL------DQVIPWKTFDE-----TIKELSRFK
                                                 66; Gaps
6.8%; Score 103; DB 7; Length 961; 22.0%; Pred. No. 16; tive 53; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NEIKALSEERTAIKEQLDSSNSTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLKGAAKKMINTCNEYQQ 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       || :|: |: :
LLADQDQKIFSLKNKLKE 928
  Query Match
Best Local Similarity 22.0%
Matches 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 861
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ADL99406 standard; protein; 961 AA.

RESULT 39 ADL99406 ID ADL99

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unbound joining element with an assembly unit comprising different unbound joining elements (b) removing unbound assembly units; and (c) repeating steps (a)-(b) for a sufficient number of sycles to form a nanostructure, where the assembly unit in at least one cycle comprises a peptide nucleic acid. A single joining element of the different joining element and a cide. A single joining element of the different joining element and a cide unbound joining element of the different joining element of the manostructure intermediate are complementary joining element of complementary joining element of complementary joining element of complementary joining element of complementary joining elements of complementary joining elements of a nanostructure further comprises: (i) capping the nanostructure with at least one capping unit; and (ii) post-assembly conversion of specific concovalent interactions of complementary joining element to covalent concovalent interactions of complementary joining element covalent comprises a surface bound initiator assembly unit used in at least one cycle comprises at least one cycle comprises at least one cycle comprises at least one cycle comprises at least one cycle comprises at least one cycle comprises at least one cycle comprises at least one cycle comprises at least one cycle comprises at least one cycle comprises at least one cycle comprises at least one cycle comprises at least one cycle comprises at least one cycle comprises at least one cycle comprises at least one cycle comprises at least one cycle comprises at least one cycle comprises at least one cycle comprises at least one cycle comprises at least one cycle comprises at least one cycle comprises at least one cycle comprises at least one cycle comprises at least one cycle comprises at least one cycle comprises at least one cycle comprises at least one cycle comprises at least one cycle comprises and least one cycle comprises at least one cycle comprises and least one cycle comprises and least one cycle cycle cycle cycle cycle 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staged assembly of a nanostructure containing peptide nucleic acid assembly units comprises contacting a nanostructure intermediate with an assembly unit comprising different joining elements, and removing unbound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          539 EEVKKTLEQHDSIVTHYKNMIREQDLQLEELKQQISTLKCQNEQLQTAVTQQVSQIQQHK 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52 QEYSQEASVLVGDIKVLL-MDSQDK--YFEATQTVYEWCGVVTQLLSAYILLFDEYNEKK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to staged assembly of a nanostructure comprising: (a) contacting a nanostructure intermediate comprising at least one unbound joining element with an assembly unit comprising different
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 EVVKSAIETADGALDFYNKYL------DQVIPWKTFDE-----TIKELSRFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        can be used as a structural element in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 8; Length 961;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.8%; Score 103; DB 8; Length 961
22.0%; Pred. No. 16;
tive 53; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 43-44; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-021840/02.
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les 70; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 961 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    assembly units.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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16;

Gaps

64

152

121

us-09-993-292b-24.rag

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osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy ragged red fibre syndrome (MERRF) or cancer. Accordingly, these compositions have neuroprotective, nootropic, antidiabetic, anticonvulsant, antiarthritis, osteopathic, ophthalmological and cytostatic activities. This polypeptide sequence is a human heart mitochondrial protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           698 NIAFQRDEKVLELEKEIKCLQEESVVQCEELKSLLRDYEQEKVLLRKELEEIQSEKEALQ 757
                                                                                                                                                                                                                                        EQTIQ------YNSELEQKVNELTGGLEETLKE----KDQNDQKLEKLMVO
                                                                                                                                                                                                                                                                                                 7 BQTVEVVKSAIETADGALDFYNKYLDQVIPWKT--FDETIKELSRFKQEYSQEASVLVGD
                                                                                                                                                                                                                                                                                65 IKVILMDSQDKYFRATQTVYEWCGVVTQLLSAYI-LLFDEYNEKKASAQKDILIRILD--
                                                                                                                                                                                                                                                                                                                                                                       611 LSQKEDVILKEHITQLEKKLQLMVEEQDNLNKLLENEQVQKLFVKTQLY----GFLKEMG
                                                                                                                                                                                                                                                                                                                                                                                                   SQLTNDFSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKL----
                                                                                                                                                                                                                                                                                                                                          -----DGVNKL--NEAOKSLLGSSOSFNNASGKLLALD
                                                                                                                                                                                                                                                                                                                                                                                                                                   ----VVNVLQAVGESLAKINEEKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----IPELNDRLKAVQNFFTSLSVTVKQANKDIDAAKLKLATEIAAIG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                          89; Indels 150;
                                                                                                                                                         6.8%; Score.103; DB 7; Length 1583;
19.9%; Pred. No. 30;
tive 55; Mismatches 89; Indels 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----EIKTETETTRFYVDYDDLMLSLLKGAAKKMINTCNEYQQRHGK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster polypeptide SEQ ID NO 4824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Myers EW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB59344 standard; protein; 2056 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-2001; 2001WO-US009231
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                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEVSEDSEEKD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-656860/75.
N-PSDB; ABL03447.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        297 LLEVPDI 303
                                                                                                                                                                 Query Match
Best Local Similarity
Matches 73; Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLEOKEL 817
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                                                                                                                                   Seguence 1583 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208
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                 8888888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention relates to novel mitochondrial targets that can be used for therapeutic intervention in treating a disease associated with altered mitochondrial function. Specifically, it refers to a method for identifying proteins of the human heart mitochondrial proteome that are useful for drug screening assays, as well as therapeutic targets. The present invention describes a method for identifying such proteins that can be used in the treatment of various diseases associated with altered mitochondrial function including diabetes mellitus, Huntington's disease,
                                                                                          802
                                                                                                                                                                                 DRLKAVQNFFTSLSVTVKQANKDIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDLMLS 272
                                                                                                                                                                                                    AS-----AQKDILIRILDDGVNK--LNEAQKSLLGSSQSFNNASGKLLALDSQLTND 158
                                                                                                                      FSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKL-----IPELN 212
                                                                                                                                                 QSVEITKLOTEKQELLOKTEAFAKSAPVPGESETVIATKTTD--VEGRLSALLOETKELK 860
               Hunchington's disease; osteoarthritis;
Hunchington's disease; osteoarthritis;
Leber's hereditary optic neuropathy; LHON;
mitochodrial encephalopathy lactic acidosis and stroke; MELAS;
mycolonic epilepsy ragged red fibre syndrome; MERRF; cancer;
neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying a mitochondrial target for drug screening assays and for treating diseases associated with altered mitochondrial function, comprises detecting a modified polypeptide in a sample and correlating
                                                                                        SNRELLQSQLAEKDSLİENLKSSQLSPGTNEQSSATAGDSEQIAELKQELATLKSQL-NS
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human heat mitochondrial protein as a therapeutic target SegID1635.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glenn GM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mitochondrial; human; screening assay; diabetes mellitus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Taylor SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gibson BW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  osteopathic; ophthalmological; cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            claim 1; SEQ ID NO 1635; 180pp; English.
                                                                                                                                                                                                                                                                                                                                                       Ą
                                                                                                                                                                                                                  NEIKALSEERTAIKEOLDSSNSTI
                                                                                                                                                                                                                                                                                                                                                       ADJ69829 standard; protein; 1583
                                                                                                                                                                                                                                                LLKGAAKKMINTCNEYQQ 290
                                                                                                                                                                                                                                                                 || :|: |: ELADODOKIFSLKNKLKE 928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhang B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-APR-2002; 2002US-0372843P.
17-JUN-2002; 2002US-0389987P.
20-SEP-2002; 2002US-0412418P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-APR-2003; 2003WO-US010870.
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                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-845369/78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2003087768-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MITO-) MITOKOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                  06-MAY-2004
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                                                                                              744
                                                                                                                                                           803
                                                                                                                                                                                                                     861
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                                    669
                                                                  109
                                                                                                                             159
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                                                                                                                                                                                                                                                                              911
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ADJ69829
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------DLAKELEEĞK--KRİNKDIEALER------QVKE 1493
                                                                                                           The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NKINEAQKSL-----LGSSQSFNNASGKLLALDSQLTNDFSEKSSY-----FQSQVD 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNDRLKAVQNFFTSLSVTVKQ 231
                                                                                                                                                                                                                                                                                                                                                                                                      64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antisense; prokaryotic essential gene; cell proliferation; drug design.
             detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                    8 QTVEVVKSAIETADGALDFYNKYLDQVIPWKTFDETIKELS-RFKQEYSQ--EASVLVGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRILDDGV
                                                                                                                                                                                                                                                                                                                                                                     62;
                                                                              Disclosure; SEQ ID NO 4824; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                6.8%; Score 103; DB 4; Length 2056; 23.8%; Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                   44; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein encoded by Prokaryotic essential gene #12886.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1494 LIAQNDRLDKSKKKIQSELED-ATIELEAQRTK 1525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---ANKDIDAAKLKLATEIAAIGEIKTETETTR 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABU27359 standard; protein; 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-03072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-MAR-2002; 2002WO-US009107.
               New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EIKKKAEEDA
                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 65, Conserv
                                                                                                                                                                                                                                                                                                   Sequence 2056 AA;
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                                                interactions.
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the 613 antisense sequences given in the specification where expression of the aucleic acid inhibits proliferation of a cell. Also included are:

(1) a westor comprising a promoter operably linked to the mucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation or the activity of against a biological pathway consideration or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation or the proliferation or the decrease of a gene on which the test compound that inhibits cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound, a activity; (11) a culture comprising strains in which the gene or which each of the strains an antibiotic; (10) profiling a compound activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains of strains in which each of the strains or screening for homologous nucleic acids are useful for proliferation to isolate candidate molecules for rational dentifying proteins or screening for homologous nucleic acids are useful for the target prokaryotic essential genes. Note: The sequence data for this patent did not format directly from INPO aureus, S. typhimurium, K. pneumonias or P. aeruginosa. The present sequence is encoded by one of patent did not format directly from MIPO accellulation, but was obtained in electronic format directly from MIPO accellulation of the proper sequences.
                                                                                                                                                New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -DGVNKINBAQKSILGSSQSFNNA----SGKLLALDSQLTNDF----SEKSSYFQSQVD 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      140 RDVTTALDDAQNLLFRISQTTNFAPYVLVSDKLKGLSSTKDKSFLLALQERQEAFQASSH 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIRKEAYAGAAAGIV-----AGPFGLIISYSIAAGVIEGKLIPELNDRLKAVQNF-- 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 QDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNE-----KKASAQKDILIRILD-- 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----FTSLSVTVKQ-----ANKDIDAAKLKLATEIA-----AIGEIKTETETTR 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----ELSRFKQEYSQEASVLVGDIKVLLMDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48 DFY--FLEHRIIFRVLQDAFKSDRPMDPHLTGEELKR------RDQLNVIGGASYLI---
Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                invention relates to an isolated nucleic acid comprising any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.8%; Score 102.5; DB 6; Length 4
23.1%; Pred. No. 6.8;
iive 42; Mismatches 105; Indels
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Ohlsen I
Forsyth I
Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                  Claim 25; SEQ ID NO 55283; 1766pp; English.
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  Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 23.13
Matches 74; Conservative
  Zamudio C,
Trawick JD,
                                                                          WPI; 2003-029926/02
                                                                                                       N-PSDB; ACA31229
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       Wang L,
Wall D,
     유
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                             18-JUN-1999;
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02-AUG-1999;
02-AUG-1999;
 Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                          Arabidopsis thaliana protein fragment SEQ ID NO: 59165.
                              AAG46982 standard; protein; 746 AA
                                                                                                                                                                               9905-0121825P.
9905-0123180P.
9905-012578BP.
9905-012678FP.
9905-0126785P.
9905-0126785P.
9905-0126748P.
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                                                           18-OCT-2000 (first entry)
                                                                                                                      Arabidopsis thaliana
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                                             AAG46982;
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222 LEDLKKQLQAVEERKQIA-VTELSAKHQKNLEGLEAQVVDALSERDKAAET-ISSLQVLL 279
                        ---IRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNDRLKAVQNFFTSLSVTV 229
 162 LERTROGANEALKAMDAERQOLRSANNKLRDTIEELRGSLOPKENKIETLQQSLLDKDQI 221
                                                                                                                                                                                                                                                           Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                    Arabidopsis thaliana protein fragment SEQ ID NO: 59164.
                                                                                      : : | | : | : | 280 AEKESKIAEMEAAATGEAARLRAAAETLKGELAHLKSENE 319
                                                                        230 KQANKDI------DAAKLKLATEI--AAIGEIKTETE 258
                                                                                                                                                              AAG46981 standard; protein; 788 AA
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990S-0127462P.
990S-0128734P.
990S-0128714P.
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99US-0136021P.
99US-0136392P.
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99US-0137724P.
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                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | | | : : | | | : : | | | : : | | 113 --DAKFTRIHKR-----AKQRIQE----IQKEKDDLDARFREVNETAERASSQHSSMQQE 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 IDDGVNKINEAQKSILGSSQSFNNASGKILALDSQLTNDFSEKSSYF----QSQVDR--- 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGIFAEQTVEVVKSAIETADGALDFYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 6.8%; Score 102.5; DB 3; Length 746;
Best Local Similarity 22.5%; Pred. No. 12;
Matches 63; Conservative 51; Mismatches 121; Indels 45; Gaps
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9908-0149722P

9908-0149723P

9908-0149923P

9908-0149930P

9908-0150864P

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9908-0151066P

9908-0151066P

9908-0151060P

9908-0151303P

9908-0151303P

9908-0151303P

9908-0151308P

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9908-015303P

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9908-015473P

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99US-0162142P
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990S-0138540P.
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990S-013962P.
990S-014287P.
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99US-0145276P.
99US-0145913P.
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99US-0147303P.
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99US-0146386P
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US-0147935P US-0148171P US-01481319P US-0148341P US-0148341P US-0149175P US-0149175P US-014972P US-014972P US-014992P US-014992P US-014992P US-0149902P	US-01508499 US-01510659 US-01510669 US-01510809 US-01513039 US-01513309 US-01513309 US-01513309 US-01513309 US-0151309 US-0151309 US-01540189 US-01540189 US-01540189 US-01565918 US-0156	0159299 0159299 0159299 0159333 0159333 0159333 0159333 0159333 016074
-AUG-1999; -AUG-1999; -AUG-1999; -AUG-1999; -AUG-1999; -AUG-1999; -AUG-1999; -AUG-1999; -AUG-1999; -AUG-1999; -AUG-1999; -AUG-1999; -AUG-1999; -AUG-1999;	ANG-1999; -ANG-1999; -ANG-1999; -ANG-1999; -ANG-1999; -ANG-1999; -SEP-1999; -SEP-1999; -SEP-1999; -SEP-1999; -SEP-1999; -SEP-1999; -OCT-1999; -OCT-1999; -OCT-1999;	0001-1999; 0001-1999;
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Query Match 6.8%; Score 102.5; DB 3; Length 788; Best Local Similarity 22.5%; Pred. No. 13; Matches 63; Conservative 51; Mismatches 121; Indels 45; Gaps

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Heterologous expression for the expression of two or more Neisserial
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29-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE10039;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU14602-AAU14794 represent novel bone marrow polypeptides of the invention. The proteins and corresponding coding sequences may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate bone marrow polypeptide expression. For example, to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of the polypeptides by expressing inactive proteins or to supplement the patient's own production of the polypeptide. Additionally, the nucleic acids may be used to produce the polypeptides, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. The nucleic acids and its complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of
                                                                                                                                 ---IRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNDRLKAVONFFTSLSVTV 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding bone marrow polypeptides, useful in diagnostic and
             154
                                    VGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNE--KKASAQKDILIRI 119
                                                            203
                                                                                  LDDGVNKLNEAQKSLLGSSQSFNNASGKLLALDSQLTNDFSEKSSYF----QSQVDR--- 172
                                                                                                        LERTROQANBALKAMDAERQQLRSANNKLRDTIEELRGSLQPKENKIETLQQSLLDKDQI 263
                                                                                                                                               264 LEDLKKOLOAVEERKOIA-VTELSAKHOKNLEGLEAQVVDALSERDKAAET-ISSLOVLL 321
                                                  | : ||| :| :: | || :: |: || TRVAAEQALEHIREAYSEADAKSQEYSSKFSQV--EQKLDQEIKERD---EKYADL---
                                                                                                                                                                                                                                                                                                                                                               Bone marrow; diagnostic; therapeutic; gene therapy; antigenic; haematopoiesis; myeloid; lymph cell disorder; tissue regeneration; wound healing; nutritional supplement; immune disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                     severe combined immunodeficiency; SCID
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                                                                                                                                                                                                                                                                  AAU14697 standard; protein; 5447 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-FEB-2001; 2001WO-US003782.
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20-JUN-2000; 2000US-00598075.
19-JUL-2000; 2000US-005050325.
30-NOV-2000; 2000US-0250683P.
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Drmanac RT;
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may be in need of restorative therapy. The proteins may also be used as antigens in the production of antibodies against bone marrow proteins and in assays to identify modulators of their expression and activity. The anti-bone marrow protein antibodies and antagonists may also be used to diagnostic agents for detecting the presence of the protein in samples (e.g. by enzyme linked immunosorbant assay (ELISA)). The proteins may be used to regulate haematopoiesis activity, and consequently in the succeeding the presence of the proteins may be used to regulate haematopoiesis activity, and consequently in the succeeding of my antibodies in thissue regeneration, such as wound healing, as a untritional supplement; and in treatment of immuno disorders such as severe combined immunodeficiency (SCID)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190 FGLIISYSIAAGVIEGKLIPELNDRLKAVQNFFTSLSVTVKQANKDIDAAKLKLA-TEIA 248
nucleic acid sequences in samples, and therefore which patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1533 KAYHDLCDGSANQLQQLQSQLAHQTEQKT--LQKQQNTCHQQLEDLCSWVGQAERALAGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29 KYLDQVIPWKTFDETIKELSRFKQEYSQEASVLVGDIKVLLMDSQDKYFEATQTVYEWCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 -----AYAGALLALDSQLTNDFSEKSSYFQSQVDRIRKE----AYAGAAAGIVAGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heterologous expression, Neisserial protein; 961c-741 fusion protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 5447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.8%; Score 102.5; DB 4; Length 23.0%; Pred. No. 1.7e+02; tive 49; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N. meningitidis strain 2996 961c-741 fusion protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Galeotti C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE10039 standard; protein; 590 AA.
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13-NOV-2000; 2000GB-00027675.
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The present invention relates to a method for simultaneous heterologous expression of two or more Neisserial proteins which are in a fused state. The method is useful for simultaneous heterologous expression of two or more Neisserial proteins. A protein that may be unstable or poorly expressed on its own is assisted by adding a suitable hybrid partner and commercial manufacture is simplified-only one expression and purification need to be employed in order to produce two separately- useful proteins. The present sequence is Neisseria meningitidis (serogroup B, strain 2996) 961c-741 fusion protein. (Updated on 11-SEP-2003 to standardise OS field) 111 AQXDILIR-----ILDDGVNKLNEAQKSLLGSSQ-SFNNASGKLLALDSQLTNDFSEK 162 303 163 SSYFQSQVDRIRKEAYAG-----AAAGI-----VAGPFGLIISYSIAAGVIEGKLIPELN 212 262 353 HKDKGLQ-----SLTLDQSVRKNE--KLKLAAQGAEKTYGNGDSLNTGKLKND-KVSRF 403 EASVLVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYI-----LLFDEYNEKKAS 110 352 :|| | :: | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | :: | | :: | :: | | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | : FAEQTV -----EVVKSAIETADGALDFYNKYLDQVIPWKT-FDETIKELSRFKQEYSQ DRLKAVONFFTSLSVTVKQANKDIDAAKLKLATEIAA------IGEIKTETETTRF Score 102; DB 4; Length 590; Pred. No. 10; 2; Mismatches 129; Indels ---YVDYDDLMLSLLKGAAKKMINTCNEYQQRHGKKTLLEVPDI 303 DFIRQIEVDGQLITLESGEFQ-----VYKQSHSALTAFQTEQ1 441 6.8%; Scor 21.4%; Predative 62; Local Similarity 21.49 Sequence 590 AA; 304 404 57 Query Match g g 셤 g ò ઠે 8 ò g ò ઠે

Masignani V, Guiliani MM; Neisseria gonorrhoeae; leader peptide; fusion protein; ORF46.1; Neisserial protein. Neisseria meningitidis fusion protein 961c-741. Galeotti C, Ż AAU27604 standard; protein; 590 28-FEB+2000; 2000GB-00004695. 13-NOV-2000; 2000GB-00027675. 28-FEB-2001; 2001WO-IB000452 (first entry) Comanducci M, Neisseria meningitidis. (CHIR-) CHIRON SPA WO200164922-A2. 18-DEC-2001 07-SEP-2001 Arico MB, AAU27604;

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                                                                                 Producing heterologous proteins from Neisseria meningitidis and
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Best Local Similarity 21.4<sup>‡</sup>
Matches 74<sup>‡</sup>, Conservative
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Heterologous expression; Neisserial protein; 961cL-741 fusion.protein. N. meningitidis strain 2996 961cL-741 fusion protein. Neisseria meningitidis; 2996 (revised)
(first entry) WO200164920-A2 11-SEP-2003 29-NOV-2001 07-SEP-2001 AAE10042;

28-FEB-2001; 2001WO-IB000420

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AAE10042 standard; protein; 612

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                                                                                                                                                                                           present invention relates to a method for simultaneous heterologous
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                                                                                                                                 Heterologous expression for the expression of two or more Neisserial
                                                           Giuliani MM;
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                                                           Masignani V,
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                                                           Galeotti C,
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                                                                                                                                                                                                                                                                                    Galeotti C, Masignani V, Guiliani MM;
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21.4%; Pred. No. 11;
Live 62; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 23; Page 75; 119pp; English.
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                                                              8-FEB-2001; 2001WO-IB000452.
                                                                                                                             28-FEB-2000; 2000GB-00004695
13-NOV-2000; 2000GB-00027675
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                                                                                                                                                                                                                                                                                                                                                                                    2001-582163/65
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07-SEP-2001
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Pizza M;
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The present invention relates to the genomic sequence of Pyrococcus abyssi (see AAF86431 and AAH41223-7) and P. abyssi proteins. P. abyssi is a hyperthermophilic archaeon, which is isolated from deeps sea hydrochermal vents. The present sequence is one such P. abyssi protein. The proteins of the present invention have various potential industrial uses, since the proteins are stable at very high temperatures, some up to 110 degrees centigrade. Note: This patent is in the same patent family as WO200065062, which contains additional sequences as shown in AAB99132-AAB99143, AAH75903-AAH75920 and AAG66436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QLINDFSEKSSY----FQSQVDRIR---KEAYAGAAAGI-VAGPFGLIISYSIAAGVIEG 205
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Putative sensory transduction histidine kinase and response regulator #3
                                                                                                                                                                                                                                                                                                                                                                                                      nucleotide sequences isolated from Pyrococcus abyssi encode proteins
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                                                                                                                                                                                                                                                                                                                 Lecompte 0;
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                                    Hyperthermophilic archaeon; hyperthermophilic protein
                                                                                                                                                                                                                                                                                                               Thierry JC, Prieur D, Dietrich J,
Weissenbach J, Saurin W, Heilig R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              266 YDDLMLSLLKGAAKKMINTCNEYQQRHGK 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 7; Page 1203-1205; 1657pp; French.
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                                                                            Pyrococcus abyssi
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Querellou J,
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Search completed: January 28, 2005, 19:12:41 Job time : 165 secs

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GenCore version 5.1.6
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- protein search, using sw model

OM protein

January 28, 2005, 19:07:04; Search time 41 Seconds (without alignments) 711.065 Million cell updates/sec Run on:

US-09-993-292B-24 1510 1 MTGIFAEQTVEVVKSAIETA.....TCNEYQQRHGKKTLLEVPDI 303 Title: Perfect score: Sequence:

283416 segs, 96216763 residues Gapop 10.0 , Gapext 0.5 Searched:

BLOSUM62

Scoring table:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB E Maximum DB E

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 100 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	haemolysin HlyE [i	hemolysin E - Esch	ш	probable pore form	myosin heavy chain	hypothetical prote	щ	1	hetical	tail protein [bact	hetical		recombination prot	hypothetical prote	٠	hypothetical prote	m		ď	VSG expression sit		•~	aBB	protein J - Yersin	phage lambda-relat	myosin heavy chain	myosin heavy chain	pro	10
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hemolysin B [imported] - Escherichia coli (strain 0157:H7, substrain RIMD 0509952)
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                            A,Gene: hlyE, hpr
C,Function:
A,Description: hemolytic activity
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R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, t., T.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A; Ahuthors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Aththors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica servo A; Reference number: AB0502; MUID:21534947; PMID:11677608
A; Accession: AB0673
A; Accession: AB0673
A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-305 APM: A; Residues: 1-3
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Molecule type: DNA
Residues: 1-305 «PAR»
(Cross-references: GB:AL513382; PIDN:CAD01758.1; PID:g16502606; GSPDB:GN00176
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                                                                                                                                                                                                                                  C:Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MTGIFAEQTVEVVKSAIETADGALDLYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASV
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                                                                                                                                                                                             - Salmonella enterica subsp.
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Pred. No. 5.3e-91;
2; Mismatches 6
        ALIGNMENTS
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C,Superfamily: Escherichia coli hemolysin E
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hemolysin E - Escherichia coli
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C)Accession: C64864
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: C64864
A;Accession: C64864
A;Accession: A;Accession: A64720; MUID:97426617; PMID:91787410; DIDN:AAC74266.1; PID:91787430;
A;Residues: 1-305 cBLAT>
A;Escidues: 1-305 cBLAT>
A;Experimental source: strain K-12, substrain MG1655
N'Altérnate names: hemolysin-inducing protein
C;Species: Escherichia coli
C;Date: 12-5ep-1997 #sequence_revision 17-5ep-1997 #text_change 01-Mar-2002
C;Accession: C64664
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; F
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240 180 DGITKLNEAQKSLLVSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDKIRKEAYAG 182 9 62 AAAGIVAGPFGLIISYSIAAGVIEGKLIPELNDRLKAVQNFFTSLSVTVKQANKDIDAAK 243 LKLTTEIAAIGEIKTETETTRFYVDYDDLMLSLLKEAAKKMINICNEYQKRHGKKTLFEV 61 LVGDIKVILMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRIL DDGVNKLNEAQKSLLGSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDRIRKEAYAG LKLATEIAAIGEIKTETETTRFYVDYDDLMLSLLKGAAKKMINTCNEYQQRHGKKTLLEV 1 MTGIFAEQTVEVVKSAIBTADGALDFYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASV Gaps ö transmembrane protein Length 305; Indels A,Note: pore formation C;Superfamily: Escherichia coli hemolysin E C;Keywords: cytolysis; cytotoxin; hemolysis; transmembr: F;181-197/Domain: transmembrane #status predicted <TMM> F;123/Active site: Asp #status predicted ; Score 1381; DB 2; ; Pred. No. 6.2e-85; 18; Mismatches 13; 91.5%; 89.8%; Query Match Best Local Similarity 89.89 Matches 272; Conservative PDI 303 PEV 305 121 123 181 241 301 303

A;Gross-references: UNIPROT:09REB3; GB:BA000007; PIDN:BAB35100.1; PID:913361141; GSPDB:GRA;Experimental source: strain O157:H7, substrain RIMD 0509952 C;Species: Escherichia coli C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004 C;Accession: E30638 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, (gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001 A;Fitle: Complete ganome sequence of enterohemorrhagic Escherichia coli 0157:H7 and (A;Reference number: A99629; MUID:21156231; PMID:11258796 1-305 <HAY> A,Accession: E90838 A,Status: preliminary A,Molecule type: DNA

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ö 61 LVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRIL 120 63 LVGNIKTLLAMDSQDKYFBATQTVYEWGGVATQLLAAYILLEDEYNEKKASAQKDILIKVL 122 62 3 MTEIVADKTVEVVKQAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASV MTGI PAEQTVEVVKSAI ETADGALDFYNKYLDQVI PWKTFDETI KELSRFKQEYSQEASV Gaps ö Length 305 14; Indels 90.5%; Score 1366; DB 2; 88.8%; Pred. No. 6.2e-84; ive 20; Mismatches 14; Local Similarity 88.8 ses 269; Conservative Query Match Best Loca Matches à d 8

121 DDGVNKLNEAQKSLLGSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDRIRKEAYAG 180

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submitted to the EMBL Data Library, February 1997
A;Reference number: Z18865
A;Accessor 178296
A;Status: Piralianary; translated from GB/EMBL/DDBJ
A;Status: preliminary;
A;Molecule type: DNA
A;Residues: 1-2139 cGUI>
A;Cross-references: UNIPROT:Q07569; EMBL:L03534; NID:g1850912; PID:g1850913; PIDN:AAB4806
C;Genetics:
A;Gene: mACo
A;Gene: mACo
C;Superfamily: myosin heavy chain; myosin motor domain homology
F;91-780/Domain: myosin motor domain homology cMMO>
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C;Species: Bacillus subtilis phage SPBc2
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T12818; F66913
Submitted to the EMBL Data Library, August 1997
A;Description: The complete nucleotide sequence of the Bacillus subtilis SPbetac2 prophage A;Reference number: 217583
A;Accession: T12818
A;Accession: t12818
A;Accession: translated from GB/EMBL/DDBJ
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A;Cross-references: UNIPROT:O64067; EWBL:AF020713; NID:g3025478; FID:g3025532; FIDN:AAC1:
B;Kunst, F: Ogasawara, N.; Moszer, I: Albertini, A.M.; Alloni, G:; Azevedo, V:; Berterc
C:; Bron, S.; Brouillet, S.; Bruechi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
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A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallerc
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Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maucel,
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle,
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Scenor,
A;Authors: Schleich, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Togato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
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C;Species: Entamoeba histolytica
C;bate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18296
R;Guillen, N.
                                                                                                                                                        AAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNKLKSVQSFFTTLSNTVKQANKDIDAAK
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C;Genetics:
A;Gene: hlyE
C;Superfamily: Escherichia coli hemolysin E
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PEV 305
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ein, E.; Yoshikawa, H.; Danch ence of the Gram-positive bac 98044033; PMID:9384377 lot shown; translation not shc ::AL009126; NID:g2634478; PIDN	Qy 171 DRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNDELKAVQNFFTSLSVTVK 230 Db 414 SRLKNHELE 435 Qy 231 QANKDIDAAKLKIAT-BIAAIGBIKTETETTRFVVDYDDLMLSLLKGAAKKMINT 284 i
Query Match 7.7%; Score 116.5; DB 2; Length 478; Best Local Similarity 23.0%; Pred. No. 2.3; Matches 58; Conservative 39; Mismatches 74; Indels 81; Gaps 12;	RESULT 8 LEECA
QY 25 DFYNKY-LDQVIPWKTFDETIKELSRFKQEYSQEASVLVGDIKVLLMDSQDKYFEATQTV 83	hemolysin A - Escherichia coli C;Species: Escherichia coli C;Date: 30-52p-198 Heequence_revision 30-Sep-1988 #text_change 09-Jul-2004.
Qy 84 YEWCGVVTQLLSAXILLFDEYNEKKASAQKDILIRILDDGVNKLNEAQKSLLGSSQSFNN 143	Rifelnies, T.; Pellett, S.; Welch, R.A. J. Bacteriol. 163, 94-105, 1985 A;Title: Nucleotide sequence of an Escherichia coli chromosomal hemolysin. A;Reference number: A24433; MUID:85234404; PMID:3891743
Qy 144 ASGKLIALDSQLINDFSEKSSYFQSQVDRIRKEAYAGAAAGIVAG 188	A, Accession: A24433 A, Molecule type: DNA A, Residues: 1-1023 <fel> A, Cross-references: UNIPROT: P09983; GB:M10133; GB:M12863; NID:g146377; PIDN:AAA23975.1; E</fel>
Qy 189 PFGLIISYSIAAGVIEGKLIPELNDRLKAVQNFFTSLSVTVKQANKDIDAAKLKLATEIA 248 :	A;Experimental gource: strain J96, O4 serotype R;Stanley, P.; Packman, L.C.; Koronakis, V.; Hughes, C. S;chanley, P.; Packman, L.C.; Koronakis, V.; Hughes, C. S;chance 266, 1992-1996, 1999, 1996, 1996, 1996, 1997-1996, 1997-1996, 1997-1996, 1997-1996, 1996, 1997-1
Qy 249 AIGEIKTETET 260 bb 443 DLVSVPTETNT 454	A; Reference number: A55387; MUID:95099325; PMID:7801126 A; Contents: annotation; lysine palmitoylation A; Note: lysine modification is performed by the hlyC gene product B; Hacte: lysine modification is performed by the hlyC gene product B; Hactilein M: Schiess!, S.; Manner, W.; Rdest, U.; Kreft, J.; Goebel, W.
	J. Cell Biol. 22, 87-97, 1983 A;Title: Transport of hemolysin by Escherichia coli. A;Reference number: 141280
etical protein pXO1-90 - Bacillus anthracis virulence plasmid pXO1 ies: Bacillus anthracis :: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 09-Jul-2004	A;Accession: 141280 A;Status: translated from GB/EMBL/DDBJ A;Actus: trype: DNA A;Residues: 1.'T', 3.'V',5,'T',7-44 <res></res>
	Ajfross references: GB:M29173; NID:g146337; PIDN:AAA23957.1; PID:g146338 CjGenetics: AjGene: hlyA
	C; Function: A; Description: attacks blood cell membranes and causes cell lysis C; Superfamily: hemolysin A; hemolysin A homology C; Keywords: calcium binding; cytolysis; exotoxin; hemolysis; lipoprotein; tandem repeat; F; 246-791 (Domain; hemolysin A homology < HLYA>
A;Residues: 1-652 <0XL> A;Cross-references: UNIPROT:Q9X360; GB:AF065404; NID:g4894216; PIDN:AAD32394.1; PID:g489 A;Experimental source: strain Sterne A;Experimental source: strain Sterne A;Experimental source: protein; PFB0765w (980 aa); Plasmodium falciparum (AE001	F;723-851/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIYF]-X) F;563,689/Binding site: palmitate (Lys) (covalent) #status experimental Onery Match
cs: pxo1-9(:: plast	Pred. No. 6.7; 99; Mismatches 112; Indels 98; Gaps
Query Match 7.7%; Score 116.5; DB 2; Length 652; Best Local Similarity 19.0%; Pred. No. 3.4; Matches 59; Conservative 65; Mismatches 106; Indels 81; Gaps 10;	QY 2 TGIFAEQTVEVVKSAIETADGALDFYNKYLDQVIPWKTFDETIKELSRFKQE 53 : : :: :: :: :: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
25 DFYNKYLDQVIPWKTFDE : : : 237 DVINQKIDEFDKLNS	QY 54 YSOEASULVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILL-FDEY 104
QY 79 ATQTVYEWGGVVTQLLSAYILLFDEYNEKKASAQKDILIRILDDGVNK 126 1	QY 105 NEKKASAQKDILIRILDDGVNKLNEAQKSLLGSSQSFNNASGKLLALDSQLTNDFSE 161
127	Qy 162 KSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNDRLKA 217

OY 218 VONFFISLSVTVKOANKDIDAAKLKLATEIAAIGEIKTETFTRFYVDYDDLMLSLLKGA 277	A;Title: Comparative genomics of Listeria species. A;Reference number: AB1077; MUID:21537279; PMID:11679669 A;Accession: AC1753 A;Actus: preliminary A;Molecule type: DNA A;Residues: 1-1093 <gla> A;Residues: 1-1093 <gla> A;Residues: UNIPROT:Q928G7; GB:AL592022; PIDN:CAC97795.1; PID:g16415090; GSPDB:GN A;Experimental source: strain Clip11262 C;Genetics: A;Gene: lin2568</gla></gla>
A44462 hypothetical protein MJ1322 - Methanococcus jannaschii C;Species: Methanococcus jannaschii C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004	Query Match 7.6%; Score 115; DB 2; Length 1093; Best Local Similarity 22.6%; Pred. No. 8.5; Matches 71; Conservative 40; Mismatches 127; Indels 76; Gaps
C;Accession: A64465 R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R.Bult, C.J.; White, O.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996 A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.A.; Tile: Complete genome sequence of the methanoqenic archaeon, Methanococcus jannaschii	OY 2 TOTFABOTVEVYKSAIETADGALDFYNKYL
A; Reference number: A64300; MUID: 96337999; PMID: 8688087 A; Accession: A64465 A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA A; Residues: 1-1005 < BUL> A; Residues: 1-1005 < BUL> A; Cooss.references: UNIPROT: Q58718; GB: U67572; GB: L77117; NID: 91591958; PIDN: AAB99331.1;	QY 87 CGVVTQLLSAYILLFDEYN-EKKASAQKDILIRILDDGVNKLNBAQKSLLG 136
Cjeshelles: A;Map position: REV1273394-1270377 C;Superfamily: hypothetical protein MJ1322	446
Query Match 7.6%; Score 115; DB 2; Length 1005; Best Local Similarity 19.4%; Pred. No. 7.6; Matches 59; Conservative 54; Mismatches 93; Indels 98; Gaps 11; Qy 7.EQTVEVVKSAIETADGALDFYNKYLDQVIPWKTFDETIKELSRPKQEYSO 56	ISISIARGVIEGALIFELINICAGOVIEGAS STATUS AND LIMANIELALIA IB NTVKVLTAMGDINGELGAVQGKYDDVKGASEKLTETNSKQDLTKOMHELQTA IAAIGEIKTETETT 260 :
605 DEILEDIKSQLNKFKNFYNQYLSAVSYLNSVDEGGIRNRIKEIENIVSGWNKEKCRE 57 RASVLVGDIKVLLMDSQDKYPEATQTVYEWCGVVTQLLSAYILLFDEYNEKKAS	Db 549 LAPIGEYLLELANT 562 RESULT 11
Db 662 BLNKLREDEREINRLKOKLNELKNKEKELIEIENRRSLKFÖKYKEYLGL 710 Qy 1111 AQKDILIRILDDGVNKLNEAQKSLLGSSQSFNNASGKLLALD	cal proteir te names: b : Saccharon 2-Jul-1996 on: S67087
Oy 153SQLTNDFSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLI 208 1:	Ridghes, B.; Pohl, T.M. aubmitted to the Protein Sequence Database, July 1996 A;Reference number: S66685 A;Accession: S67087 A;Molecule type: DNA
Qy 209 PELNDRLKAVQNFFTSLSVTVKQANKDIDAAKLKLATEIAAIGEIKTETETTRFYV 264 bb 793 KELYENKRQELDNVREQKTEIETGIEYLKKDVESLKARLKEMSNLEKEKEKLTKFV 848 Cy 265 DYDD 268 c) 1 (1) c) 265 EYLD 852	A; Residues: 1-821 <- HUG> A; Residues: 1-821 <- HUG> A; Cross-references: UNIPROT: Q08581; EMBL: Z75103; NID: g1420464; PID: e252389; PID: g1420465; A; Cross-references: UNIPROT: Q08581; EMBL: Z75103; NID: g1420464; PID: e252389; PID: g1420465; A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: Ge
AC1753 AC1753 AC1753 AC1753 AC1753 AC1753 AC1754 AC1755 AC1755 AC1755 AC1755 AC1755 AC1755 AC1755 AC1755 AC1755 C.Species: Listeria innocua C.Species: Listeria innocua C.Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004 C.ACCEBSION: AC1753 B.Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker C.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001 A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitcournam, A.; Ma Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,	Query Match Best Local Similarity 20.8%; Pred. No. 6.3; Matches 70; Conservative 52; Mismatches 115; Indels 99; Gaps 12; Atches 70; Conservative 52; Mismatches 115; Indels 99; Gaps 12; Atches 70; Conservative 52; Mismatches 115; Indels 99; Gaps 12; Atches 70; Conservative 52; Mismatches 115; Indels 99; Gaps 12; Atches 70; Conservative 52; Mismatches 115; Indels 99; Gaps 12; Atches 70; Conservative 52; Mismatches 115; Indels 99; Gaps 12; Atches 70; Conservative 52; Mismatches 115; Indels 99; Gaps 12; Atches 70; Conservative 68 Atches 70; Conservative 68 Atches 70; Conservative 70; Indels 99; Gaps 12; Atches 70; Mismatches 70; Indels 99; Gaps 12; Atches 70; Mismatches 70; Mismatches 70; Indels 99; Gaps 12; Atches 70; Mismatches 70; Mismatches 70; Indels 99; Gaps 12; Atches 70; Mismatches 70; M

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Appointational protein - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803
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                                                                                                 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-520 <AQF> A;Residues: 1-520 <AQF> A;Residues: 1-520 <AQF> A;Residues: 1-520 <AQF> A;Residues: 1-520 <AQF> A;Residues: 1-520 <AQF> A;Residues: 1-520 <AQF> A;Residues: C;Genetics: Strain VF5 C;Genetics:
       A,Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: F70350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             160 SEKSSYFQSQYDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELN-DRLKAV 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 -VGDIKVILMDSQDKYFEATQTVYEWCGVVTQLLS---AYILLFDEYNEKKASAQKDI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              195 NLEKVKKAVGESLYKLLEGENSVXEILGEIRKNLAKVESYSGKFSELIEKIANLEEEVYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----LIRILDDGVNKLNBAQKSLLGSSQSFNNASGKLL----ALDSQLTN----DF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   255 LYNSLKEEMPEISEBEVNEINEKLFRIQRLEEKYKKSFPEILKEVEEIKEELSNLNSVOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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A;Accession: S75986
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.5%; Score 112.5; Local Similarity 20.1%; Pred. No. 4.7; see 59; Conservative 70; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   315 KEEE--LREEVEKLREE-----
                                                                                                                                                                                                                                                                                                                                                                                                       C; Superfamily: recN protein
392, 353-358, 1998
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Best Local S:
Matches 76
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C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: F70350
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
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C;Genetics:
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BPS2 protein homolog (bps2) [imported] - Sulfolobus solfataricus

C;Species: Sulfolobus solfataricus

C;Species: Sulfolobus solfataricus

C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004

C;Accession: A90194

R;She, Q; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan Jong, I.; Jefffites, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.

arrett, R.A.; Ragan, April 2001

A;Description: Sulfolobus solfataricus complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14;
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                                                                                                                     AYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELM-DRLKAVQNFFTSLSVTVKQANKD
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           LKSKENELDNLKLSLKETLSISKDFNDSD-----LIGQINELISTKNNLQQKNDD----
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1 Similarity 19.5%; Pred. No. 4.7;
64; Conservative 68; Mismatches 109;
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                                                                                                                                                                                                                                                                                 236 IDAAKL---KLATEIAA-----IGEIKTET
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A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-587 <KUR>
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Best Local S
Matches 64
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A,Gene: bps2
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Vugt, B.

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Directin T22A3.8 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: F87908; E87908
R;Anchymous, The C. elegans Sequencing Consortium.
S;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_elegans/ abiNote: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: F87908
                                                                                                                                                                                A;Status: preliminary; nucleic acid sequence not shown; translation not shown.
A;Molecule type: DNA
A;Rosidues: 1-1098 «KLES.
A;Cross-references: UNIPROT:O50733; GB:AE000786; NID:g2690008; PIDN:AAC66075.1; PID:g2690
A;Experimental source: strain B31
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A;Molecule type: DNA
A;Residus: 1-2823 <STO>
A;Crossine Eerences: UNIPROT:045614; GB:chr_I; PIDN:CAA15432.1; PID:g3924779; GSPDB:GN0001
A;Accession: E87908
A;Status: preliminary
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A;Residues: 1-2823 <ST2>
A;Cross-references: GB:chr_I; PIDN:CAB03385.1; PID:g3924881; GSPDB:GN00019; CESP:T22A3.8
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, I Nature 390, 580-586, 1997
A; Muthors: Smith, H.O.; Venter, J.C.
A; Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi. A; Reference number: A70100; MUID:98065943; PMID:9403685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       133 -----SLLGSSQSFNNA----SGKLLALDS-----QLTNDFSEKSSYFQSQV 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           171 DRIRKEAYAG-----AAAGIVAGPFGLIISYSIAA-----GVIEGKLIPELNDRLKAV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TQLLSAYILLFDEYNEKKASAQKDILIRI------LDD---GVNKLNEAQK------ 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    219 ONFFISLSVTVKQANKDIDAAKLKLATEIAAI-----GEIKTETETTRFYVDYDDLMLSL 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 720 KAQDITKSLYDSMIDGLNVFKNAFMKDIAGKFLNKDTGESIGEEFHNLINGKDVNWGEGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -FKQEYSQEASVLVGDIK--VLLMDSQDKYFEATQ------TVYEWCGVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------KDOVIPWKTFDETIKELSR
                                                                                                                                                                                                                                                                                                                                                                                                       7.5%; Score 112.5; DB 2; Length 1098; ilarity 20.6%; Pred. No. 13; Conservative 60; Mismatches 122; Indels 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | | | | : |:|:| | :|
886 LKQAQSKGQISGEEFQKRLHDVQT 909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VEVVKSAIETADGALDFYNKY----
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 7.5%;
Best Local Similarity 20.6%;
Matches 79; Conservative 6
                                                                                                                                                                                                                                                                                                                                                        A;Genome: plasmid
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R;Hess, J.; Wels, W.; Vogel, M.; Goebel, W.
FEMS Microbiol. Lett. 34, 1-11, 1986
A;Title: Vucleotide sequence of a plasmid-encoded hemolysin determinant and its comparis A;Reference number: S07209
A;Accession: S10056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | : : | :: | :: | | :: | | :: | | 1.55 TALSSMKIDELIKKOKSGGNVSSSELAKASIELINQLVDTVASLN-----nnvnsfsQQ 208
           LLQE-----KDLLVEDNGAQCVFLDGFTNKDGDRLPLIVQKSDGGYNYATTDLAAL 325
                                                                                             210 ELNDRLKAVQNFFTSLSVTVKQANKDID-----AAKLKLATEIA---AIGEIK---T 255
                                                                                                                                                                                                 303
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                                                            DSQLTNDFSEKSSYF -- QSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIP 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54 YSQEASVL------VGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILL-FDEY 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105 NEKKASAQKDILIRILDD---GVNKLNEAQKSLLGSSQSFNNASGKLLALDSQLTNDFSE 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162 KSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIIS----YSIAAGVIEGKLIPELNDRLKA 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    218 VONFFISLSVTVKQANKDIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDLMLSLLKGA 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hyporhetical protein BBG10 - Lyme disease spirochete plasmid G/lp28-2
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                            nemolysin A - Escherichia coli plasmid pHly152
C;Species: Escherichia coli
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 04-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 TGIFAEQTVEVVK-----SAIETADGALDFYNKYLDQVIPWKTFDETIKELSRFKQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: hemolygin A; hemolygin A homology
C;Keywords: lipoprocein
F;547-79//Domain: hemolysin A homology <HLYA>
F;564,690/Binding site: palmitate (Lys) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 7.5%; Score 112.5; DB 2; Best Local Similarity 20.5%; Pred. No. 11; Matches 69; Conservative 55; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      256 ETETTRFYVDYDDLMLSLLKGAAKKMI 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-1024 <HES>
A;Cross-references: EMBL:M14107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome: plasmid pHly152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Status: preliminary
Molecule type: DNA
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           275
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C; Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like H Query Match Best Local Similarity 19.9%; Score 112.5; DB 2; Length 2823; Best Local Similarity 19.9%; Pred. No. 44%; Best Local Similarity 19.9%; Pred. No. 44%; Best Local Similarity 19.9%; Pred. No. 44%; Best Local Similarity 19.9%; Pred. No. 44%; Best Local Similarity 19.9%; Pred. No. 44%; Best Local Similarity 19.9%; Pred. No. 44%; Best Local Similarity 19.9%; Pred. No. 44%; Best Local Similarity 19.9%; Pred. No. 44%; Best Local Similarity 19.9%; Pred. No. 44%; Best Local Similarity 19.9%; Pred. No. 44%; Pre	60 v 1916 I 1916 I 1976 I 129 · 2032 I 174 I 2090 J 2132 291 2
OY 174 RKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPBIANDRLKAVQNFFTSLSVTVKQ 231	4 4 9 9 1 4
Pypothetical protein T22A3.8 - Caenorhabditis elegans (fragment) hypothetical protein T22A3.8 - Caenorhabditis elegans (fragment) hypothetical protein T22A3.8 - Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C; Accession: T23064; T25096 R; Barlow, K, the EMBL Data Library, October 1997 A; Reference number: 219669 A; Accession: T23064 A; Reference number: 219669 A; Accession: T23084 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Status: preliminary; A; Molecule type: DNA A; Residues: 1-283 < WILb A; Residues: 1-283 < WILb A; Residues: 1-283 < WILb A; Residues: 1-283 < WILb A; Residues: 1-283 < WILb A; Residues: 1-282	A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Cross-references: UNIPROT: 045614; EMBL: AF074902; PIDN: AAC26793.1 A; Genetics: C; Genetics: A; Map position: 1 A; Map position: 1 A; Map position: 1 A; Match C; Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like hc A; Mote: lama1/2 C; Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like hc C; Genetics: 7: Score 112.5; DB 2; Length 3102; C; Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like hc C; Genetics: 7: Score 112.5; DB 2; Length 3102; C; Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like hc C; Genetics: 7: Score 112.5; DB 2; Length 3102; C; Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like hc C; Genetics: 7: Score 112.5; DB 2; Length 3102; C; Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like hc C; Genetics: 7: Score 112.5; DB 2; Length 3102; C; Superfamily: laminin-type EGF-like hc C; Superfamily: laminin-type EGF-like hc C; Superfamily: laminin-type EGF-like hc C; Superfamily: laminin-type EGF-like hc C; Superfamily: laminin-type EGF-like hc C; Superfamily: laminin-type EGF-like hc C; Superfamily: laminin-type EGF-like hc C; Superfamily: laminin-type EGF-like hc C; Superfamily: laminin-type EGF-like hc C; Superfamily: laminin-type EGF-like hc C; Superfamily: laminin-type EGF-like hc C; Superfamily: laminin-type EGF-like hc C; Superfamily: laminin-type EGF-like hc C; Superfamily: laminin-type EGF-like hc C; Superfamily: laminin-type EGF-like hc C; Superfamily: laminin-type laminin-type EGF-like hc C; Superfamily: laminin-type l
R;McMurray, A. Submitted to the EMBL Data Library, October 1996 Squbmitted to the EMBL Data Library, October 1996 A;Reference number: Z1980 A;Reference number: Z1980 A;Reference number: Z1980 A;Reference preliminary; translated from GB/EMBL/DDBJ A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2> A;Residues: 1-2823 <wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2></wi2>	IEKAR HAEKU LLALI II S II S IKLI PI KELI PI KELI PI KELI PI KELI PI KELI PI KELI PI KELI PI KELI PI KELI PI KELI PI KELI PI KEKKU

Oy 291 RHGKKT 296 Db 2174 SEGIKT 2179	: :: ::
RESULT 20	Qy 62 VGDIKVLLMDSQDKYFBATQTVYEWCGVVTQLLSAYILLFDEYNBKKASAQKD1 115
VMU121 VSG expression site-associated protein 221a precursor - Trypanosoma brucei N;Alternate names: BSAG protein C;Species: Trypanosoma brucei	Qy 116 LIRILDDGVNKLNBAQKSLLGSS
	Qy 148 -LLALDSQLTNDFSEKSSYFQSQVDRIRKEAYAGAAGIVAGPFGLIISYSIAAGVIEGK 206
A;Title: Coordinate transcription of variant surface glycoprotein genes and an expressic A;Reference number: A90868; MUID:85254917; PMID:2861910 A;Accession: A03395 A;Molecule type: mRNNA A;Decidine: 1,129 cmr.	Qy 207 LIPELNDRLKAVQNFFTSLSVTVKQANKDIDAAKLKLATEIAAIG 251
A,Cross-references: UNIPROT: P04478, GB:M11452; NID:g162072; PIDN:AAA30191.1, PID:g162073 C; Comment: The function of the ESAG proteins is not known but may be related to activating C; Superfamily: VSG expression-site associated protein	Qy 252 BIXTETETTR 261 : : Db 970 SAQHSTETSR 979
Circymotas: 91yvoptorum F;1-23/Domain: signal sequence #status predicted <sig> F;24-329/Product: VSG expression site-associated protein 221a #status predicted <mat> F;73,294,308/Binding site: carbohydrate (Asn) (covalent) #status predicted</mat></sig>	RESULT 22 B72420
Query Match Best Local Similarity 22.9%; Pred. No. 3.2; Matches 48; Conservative 33; Mismatches 63; Indels 66; Gaps 9;	hypothetical protein TM0088 - Thermotoga maritima (Btrain MSBB) C;Species: Thermotoga maritima C;Species: Thermotoga maritima C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004 C;Accession: B72420
Qy 92 QLLSAYILLPDEYNEKKASAQKDILIRILDDGVNKL-NEAQKS 133	
Qy 134 LLGSSQSFNNASGKLLALDSQLTNDFSEKSSYPQSQVDRIRKEAYAGAAAGIV 186	A;Title: Bvidence for lateral gene transfer between Archaea and Bacteria from genome seg. A;Reference number: A72200; MUID:99287316; PMID:10360571 A;Accession: B72420 A;Status: preliminary
QY 187 AGPFGLIISYSIAAGVIEGKLIPELNDRLKAVQNFFTSLSVTVKQA 232	A;Molecule type: DNA A;Residues: 1-1285 <arn> A;Cross-references: UNIPROT:Q9WXU3; GB:AE001695; GB:AE000512; NID:g4980569; PIDN:AAD3518; A;Experimental source: strain MSB8</arn>
Qy 233 NKDIDAAKUKLATEIAAIGEIKTE 256	C;Genetics: A;Gene: TM0088 Query Match 7.3%; Score 110; DB 2; Length 1285; Best Local Similarity 19.5%; Pred, No. 23;
RESULT 21 T24587 hypothetical protein T06E4.1 - Caenorhabditis elegans	1 MTGIFAEQTVEVVKSAIETADGALDFYNKYLDQVIPWKTFDETIKELSRF 5
C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 09-Jul-2004 C;Accession: T24587 R;Lloyd, C. R;Lloyd, C.	51 -KQEYSQEASVLVGDIKVLIAMDSQDKYFEATQTVYEWGGVVTQLLSAYILLFDEYNEK-K
AlReference number: 219910 AlReference number: 219910 AlAccession: T24587 AlStatus: preliminary; translated from GB/EMBL/DDBJ AlAccession: DNA	109 ASAQUILIRILDDGVNKINEAQKSLLGSSQSFNNASGKILALDSQLTNDFSEKSSY 101 ASAQUILIRILDDGVNKINEAQKSLLGSSQSFNNASGKILALDSQLTNDFSEKSSY 102 ASAQUILIRILDDGVNKINEAQKSLLGSSQSFNNASG
	Qy 166 FQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNDRLKAVQNFFT 223
A;Gene: CESP:T0684.1 A;Map position: 5 A;Introns: 17/3; 218/2; 385/3; 481/3; 946/3; 1034/3; 1222/2	QY 224 SLSVTVKQANKDIDAAKLKLATEIAALGEIKTETETTRF
Query Match 7.4%; Score 111; DB 2; Length 1295; Best Local Similarity 21.0%; Pred. No. 20; Matches 65; Conservative 58; Mismatches 93; Indels 94; Gaps 13; On.	265 DYDDLMLSLLKGAAKKMINTCNEYQQRHGKKTLLEVP 301
6 AEÇIVEVVASAIBIADGALDFINAILDÜVIFWANFEDEIIKELSKFAÇEISÇEASVD	

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Similarity 20.79 S9; Conservative
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Matches 59;
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CySpecies: Yersinia pestis
CySpecies: Yersinia pestis
CySpecies: Yersinia pestis
CyDate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
CyDate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
CyDate: 20-Sep-1999 #sequence_revision: Tu4652
CyDate: Yersinia Data Library, March 1998
AyDescription: Structural organization of virulence determinants in three Yersinia pestin AyDescription: Structural organization of virulence determinants in three Yersinia pestin AyDecession: Tu4652
AyStatus: preliminary; translated from GB/EMBL/DDBJ
AyMolecule type: DNA
AyBesiques: 1-1492 < HUPP-
AyCoss-references: UNIPROT: 068724; EMBL: AF053947; NID: g2996286; PID: g2996342; PIDN: AACT
                                             C. Species: Clostridium acetobutylicum C. Species: Clostridium acetobutylicum (C. Species: Clostridium acetobutylicum C. Species: Clostridium acetobutylicum C. Species: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004 (C. Jace: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004 (C. Jaces) (C. Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004 (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (C. Jaces) (
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A;Molecule type: DNA
A;Residues: 1-573 «KUR»
A;Cross-references: UNIPROT:Q97DG6; GB:AE001437; PIDN:AAK81437.1; PID:g15026604; GSPDB:
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 109; DB 2; Length 57; Pred. No. 9.1; 66; Mismatches 122; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -IAAIGEIKTETETTRFYVDYDDLMLSLLKGAAKKMINTCNEYQQR
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20.7%; Pred. No. 3;
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Best Local Similarity 18.5%;
Matches 64; Conservative 6
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Best Local &
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Cispecies: Yerainia pestis
Cispecies: Yerainia pestis
Cispecies: Verainia pestis
Cispecies: O-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
Cispate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
Cispate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
Rinindler, L.E.; Plano, G.V.; Burland, V.; Mayhew, G.F.; Blattner, F.R.
Infect. Immun. 66, 5731-5742, 1998
A,Title: Complete DNA sequence and detailed analysis of the Yersinia pestis KIMS plasmid A,Reference number: Z18268; MUID:99043898; PMID:9826348
A,Accession: T14966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Reaidues: 1-1545 <LLN>
A;Reaidues: 1-1545 <LLN>
A;Cross-references: UNIPROT: Q9ZH03; EMBL: AF074611; NID: g3883003; PID: g3883049; PIDN: AAC82
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Myosin heavy chain, nonmuscle - chicken
N;Contains: myosin Arpase (BC 3.6.4.1)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Datession: A33977; S06116; A43422
R;Shohet, R.V.; Conti, M.A.; Kawamoto, S.; Preston, Y.A.; Brill, D.A.; Adelstein, R.S. Proc. Natl. Acad. Sci. U.S.A. 86, 7726-7730, 1989
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969 REARVEGDKANAKQIEAMKSSVDDSVAAVEEMKKTVAEVERASAEASTNIEALAKTNIDL
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                                                                              --- SAYILLFDE 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----DSQLTND-----FSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLII
Gaps
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                                                                                                                                                                                     104 YNEK----KASA-QKDILIRILDDGVNKLNEAQKSLLGSSQSFNNASGKLLAL-
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                                                                                                                                                                                                                                                                                                                                                                                                                                     97; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                      195 SYSIAAGVIEGKLIPELNDRLKAVQNFFTSLSVTVKQANKDIDAA
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                                                                                         KVLLMDSQDKYFEATQTVYEWCGVVTQLL-
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A; Molecule type: mRNA
A; Residues: 1-1999 & SUNA
A; Cross-references: UNIPROT:Q63731; EMBL:X62659
R; Sun, W.; Chancler, P.D.
Biochem. Biophys. Res. Commun. 175, 244-249, 1991
A; Title: A unique cellular myosin II exhibiting differential expression in the cerebral c
A; Reference number: PN0013; MUID:91151356; PMID:19998509
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1914-1998, I' <SU2>
A;Residues: 1914-1998, I' <SU2>
A;Residues: 1914-1998, I' <SU2>
A;Experimental source: brain
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Reywords: actin binding; ATP; coiled coil; hydrolase; methylated amino acid; nucleotide
C;Reywords: actin binding motor domain homology <AMOT>
F;144-763/Domain: myosin motor domain pomology <AMOT>
F;141-575/Region: actin binding #status predicted
F;836-1999/Domain: coiled coil #status predicted
F;836-1276/Region: S2
N;Alternate names: myosin II
N;Contains: myosin APPase (EC 3.6.4.1)
C;Opecies: Rattus norvegicus (Norway rat)
C;Opecies: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: $21801; PNO013; $18134
R;Sun, W.; Chancler, P.D.
J. Mol. Biol. 224, 1185-1193, 1992
A;Title: Cloning of the cDNA encoding a neuronal myosin heavy chain from mammalian brain A;Reference number: $21801; MUID:92235856; PMID:1569576
A;Reference number: $21801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66; Conservative
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                                                                            A;Molecule type: mRNA
A;Residues: 1-1959 <SHO>
A;Crose_references: UNIPROT:P14105; GB:M26510; NID:g212382; PIDN:AAA48974.1; PID:g212383
R;Katsuragawa, Y.; Yanagisawa, M.; Inoue, A.; Masaki, T.
Eur. J. Biochem. 184, 611-616, 1989
A;Title: Two distinct nonmuscle myosin-heavy-chain mRNAs are differentially expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Title: Cloning of the cDNA encoding the myosin heavy chain of a vertebrate cellular my 
Reference number: A33977; MUID:90046668; PMID:2813355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of a vertebrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Status: nucleic acid sequence not shown; not compared with conceptual translation :Molecule type: mRNA .Residues: 1900-1959 <HOD>
                                                                                                                                                                                                                                                                                                                                            A;Residues: 716-1008 «KAT»
A;Cross-references: GB:XI7589
A;Note: this translation is not annotated in GenBank entry GGMHCFMHA, release 114
R;Hodge, T. P.; Cross, R.; Kendrick-Jones, J.
Cell Biol. 118, 1085-1095, 1992
A;Title: Role of the COOH-terminal nonhelical tailpiece in the assembly of a verte A;Reference number: A43422; MUID:92381096; PMID:1512291
A;Accession: A43422
A;Status: nucleic acid sequence not shown; not compared with concentual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----EHKRKKVDAQLQE 1256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1357 KQISVLQQQAVEARKKMDDGLGCLEIAEEAKKKLQKDLESLTQRYEEKIAAYD--KLEKT 1414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56 QEASVLVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDI 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 L-----IRILDDGVNKLNEAQKSLLGSSQSFNNASGKLLALDS---QLTNDFSEKSSY 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------AKDIDAAKLKLATEIAAIGEIKTETE
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                                                                                                                                                                                                                                                             A;Reference number: S06116; MUID:90032648; PMID:2806244
A;Accession: S06116
A;Steatus: not compared with conceptual translation
A;Molecule type: mRNA
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F;1937-1959/Domain: carboxyl-terminal <CBT>
F;125/Modified site: N6,N6,N6,Trimethyllysine (L
F;180/Binding site: ATP (Lys) #status predicted
F;694,704/Active site: Cys #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.2%; Score 108.5;
11.0%; Pred. No. 50;
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| SERAELSNEVKVLLQGKGDA-----
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                                                         Accession: A33977
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 RILDDGVNKLNEAQKSLLGSSQSFNNASGKLLALD---SQLTNDFS------- 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein F55C5.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                           58 ASVLVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----EKSSYFOSOVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGV
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                                                                                                                                                                                                                                                                                                     Gapa
F;1277-1999/Region: light meromyosin
F;125/Modified site: N6,N6,N6-trimethyllysine (Lys) #status predicted
F;180/Binding site: ATP (Lys) #status predicted
F;693,703/Active site: Cys #status predicted
F;1916/Binding site: phosphate (Ser) (covalent) #status predicted
F;1916/Binding site: phosphate (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                     95;
                                                                                                                                                                                                                                    7.2%; Score 108.5; DB 1; Length 19.5%; Pred. No. 51; tive 53; Mismatches 124; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: T22716
R;Harris, B.
submitted to the EMBL Data Library, August 1996
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myosin heavy chain, neuronal [similarity] - rat
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A,Gene: myo-1; CESP:R06C7.10
A,Map position: 1
A,Map position: 1
A,Map position: 1
A,Marcons: 23/3; 114/3; 229/1; 264/1; 320/1; 857/3; 1745/3; 1814/1; 1892/3
A,Introns: 23/3; 114/3; 229/1; 264/1; 320/1; 857/3; 1775/3; 1814/1; 1892/3
C,Superfamily: myosin heavy chain; myosin metor domain homology
C,Superfamily: myosin motor domain homology <MMOT>
F,87-773/Domain: myosin motor domain homology <MMOT>
F,177-184/Region: nucleotide-binding motif A (P-loop)
F,660-682/Region: actin binding #status predicted
F;764-778/Region: actin binding #status predicted
F;764-778/Region: actin binding #status predicted
F;846-1160/Region: S2.
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A,Recession: T23973
A,Status: T23973
A,Status: translated from GB/EMBL/DDBJ
A,Status: translated from GB/EMBL/DDBJ
A,Status: translated from GB/EMBL/DDBJ
A,Residues: 1-1938 *MI2>
A,FCOSS-references: EMBL:Z71266; PIDN:CAA95848.1; GSPDB:GN00019; CESP:R06C7.10
A,Reperimental source: clone R06C7
A,Experimental source: clone R06C7
B,Dibb, N.J.; Maruyama, I.N.; Krause, M.; Karn, J.
A,Mol. Biol. 205, 603-613, 1989
A,FITLE: Sequence analysis of the complete Caenorhabditis elegans myosin heavy chain gene A,Reference number: S02771; MUD:89178677; PMID:2926820
A,Accession: S02772
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A;Residues: 24-93,'E',95-97,'R',99-376,'V',378-388,'GDV',392-407,'N',409-473,'G',475-576,
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Residues: 1-1938 <WIL>
A,Cross_references: UNIPROT:P02567; EMBL:Z71261; PIDN:CAA95806.1; GSPDB:GN00019; CESP:R06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Karn, J.; Brenner, S.; Barnett, L. Pros. 1983 Proc. Natl. Acad. Sci. U.S.A. 80, 4253-4257, 1983 A;Title: Protein structural domains in the Caenorhabditis elegans unc-54 myosin heavy A;Reference number: A3958; MUID:83273600; PMID:6576334
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                                                                                                                                                                                                                                                                                                                      revision 19-May-2000 #text_change 09-Jul-2004
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A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1-376,'V',378-390,'V',392-576,'D',578-680,'I',682-1938 <DIB>
A,Cross-references: EMBL:X08065; NID:g6785; PIDN:CAA30854.1; PID:g6786
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F;128/Modified site: N6,N6,N6.trimethyllysine (Lys) #status predicted
F;183/Binding site: ATP (Lys) #status predicted
F;700,710/Active site: Cys #status predicted
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tive 63; Mismatches 112;
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--DALMRANKYYTAIAEVVRTVWDDVKAVE 163
                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, April 1996 A;Reference number: Z19388 A;Accession: T21193 A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                            myosin heavy chain D [similarity] - Caenorhe N;Alternate names: myosin heavy chain I N;Contains: myosin ATPase (EC 3.6.4.1) C;Spacies: Caenorhabditis elegans C;Date: 28-Feb-1986 #sequence revision 19-Ms C;Accession: T21193; T23973; S02772; A02993 R;McMurray, A.
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Best Local Similarity 17.3
Matches 52; Conservative
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               136
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Variant Surface glycoprotein UIEC - Trypanosoma brucei gambiense (fragment)

Variant surface glycoprotein UIEC - Trypanosoma brucei gambiense (fragment)

C,5pecdession: A45522

C,5pecdession: A45522

C,5Accession: A45522

Mol. Biochem. Parasitol. 41, 101-114, 1990

A,7title: Bloodstream and metacyclic variant surface glycoprotein gene expression sites of A,7teference number: A45522; MUID:90348709; PMID:2385264

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                                                                                                                                         A, Molecule type: DNA
A, Residues: 1-622 <WILL>
A, Cross-references: UNIPROT: Q20822; EMBL: Z78198; PIDN: CAB01573.1; GSPDB: GN00023; CESP: F5
A, Experimental source: clone F55C5
C, Genetics:
A, Gene. CSPS: F55C5.8
A, Map position: 5
A, Introns: 24/3; 44/2; 147/3; 251/3; 561/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 AAAGIVAGPFGLIISYSIAAGVI-----EGKLIPELNDRLKAVQNFFTSLSVTVK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            418 FRCFYMASSYSALHKYSEAAALFDRTVSRVQDAEGKL----KKLKSSSFITNETQSSLN 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     231 QANKDIDAAK--LKLATEIAAIGEIKTETETTRFYVDYDDLMLSLLKGAAKKMINTCNEY 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L'UDDYYGKNLH-ESVCYLRCLSNALN'KLYSEGEKKLLATEEVYANAS---LILD-DMEGR 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361 LAI---IDNIKSEKKŠKPQDLLRLYDSVIEIYKEVAEIPGADHDKNLIQAFEVKVEYYRA 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98 --ILLFDEYNEKKASAQKDILIRILDDGVNKLNE-AQKSLLGSSQSF-----NNASGKL 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : | | :: | | :: | | :: | | : | | 305 EKWALF----EKATADTRDAIDRISDIIRRKSSENADTTVLQSIKAYLEFLKWNGTASRY 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -QVDRIRKEAYAG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.2%; Score 108; DB 2; Length 62 20.6%; Pred. No. 12; Live 54; Mismatches 111; Indels
                      A;Reference number: 219604
A;Accession: T22716
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LALDSQLTNDFSEKSSYFQS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       520 RÓWDVRNSLKDKKTIP 535
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QY 105 NEKKASAQKDILIRILDDGVNKLNEAQKSLLGSSQSFNNASGKLLALD 152 Db 1433 EDARSDVDRHLTVIASLEKKQRAFDKIVDDWKRKVDDIQKEIDATTRDSRNTSTEVFKLR 1492 QY 153 SQLTNDFSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELN 212 Db 1493 SSMDNLSEQIETLRRE	Qy 140 -SFNNASGKLLALDSQLTNDFSEKSSYFQSQVDRIRKEAVAGAAAGIV 186 Db 768 TELNLLTEKIRKVEIEFERIKKDNQELEDHERTARDDLKQETNRNHLLAKELEEARADIV 827 Qy 187 AGPFGLISYSIAAGVIBGKLIPELNDRL-KAVQNFFTSLSVTVKQANKDIDAAK 240 Db 828 A
RESULT 31 T43214 ovt1 protein - nematode (Onchocerca volvulus) NyAlternate names: myosin-like antigen C;Species: Onchocerca volvulus C;Species: Onchocerca volvulus C;Species: Onchocerca volvulus C;Date: 11-Jan-2000 #sequence revision 11-Jan-2000 #text_change 09-Jul-2004 C;Accession: T43214; A44939; Ā54513; S27825 R;Triteerappapab, S.: Richie, T.L.; Tuan, R.S.; Shepley, K.J.; Dinman, J.D.; Neubert, T. Mol. Biochem. Parasitol. 69, 16-171, 1995 A;Title: Molecular cloning of a gene expressed during early embryonic development in Onc A;Reference number: 222341; MUID:95287898; PMID:7770081 A;Accession: T43314 A;Accession: T43314 A;Residues: 1-2022 cTRL> A;Cross-references: UNIRROT:P21249; EMBL:U12681; NID:9530824; PID:9530825; PIDN:AAA80009 A;Residues: Donelson, J.E. Mol. Biochem. Parasitol. 40, 213-224, 1990 A;Title: Characterization of a myosin-like antigen from Onchocerca volvulus. A;Accession: A44939; MUID:90301142; PMID:2194123	RESULT 32 T22976 T22976 T22976 T22976 T22976 T22976 T22976 T22976 T22976 T22976 T22976 T22976 T22976 T22976 T22976 T22976 T23157
A; Molecule type: mRNA A; Residues: 733-874, E', 876-916, S', 918-1038,1040-1047, S', 1049-1283, E', 1285-1363 < ERO> A; Residues: 733-874, E', 876-916, S', 918-1038,1040-1047, S', 1049-1283, E', 1285-1363 < ERO> A; Residues: 733-874, E', 876-916, S', 918-1038,1040-1047, S', 1049-1283, E', 1285-1363 < ERO> A; Robersences: GB: M30398 A; Note: the sequence is revised in GenBank entry ONGANTML, release 115, (PIDN:AA29413.1 R; Donelson, J.E.; Duke, B.O.L.; Moser, D.; Zeng, W.; Erondu, N.E.; Lucius, R.; Renz, A.; MOL. Biochem. Parasaitol. 31, 241-250, 1988 A; Title: Construction of Onchocerca volvulus cDNA libraries and partial characterization A; Reference number: A55513; MUID:89127417; PMID:2464764 A; Accession: A5413 A; Molecule type: mRNA A; Residues: 733-866 < DON> A; Residues: 733-866 < DON> B; NGOSI E: REACHAN R: DONELSON J R: PROPISE RESIDENT R: PROPISE REACHAN R: RESIDENT R: REACHAN R: R: REACHAN R: R: REACHAN R: R: REACHAN R: R: REACHAN R: R: REACHAN R: R: R: R: R: R: R: R: R: R: R: R: R:	738/3; 795 2; Gaps WCGVTQ IQGELEESK
Lto the EMBL Date Library, April 1990 tion: Characterization of a myosin-like antigen from Onchocerca volucion: Characterization of a myosin-like antigen from Onchocerca voluce number: \$27825 en : \$27825 et rype: mRNA s: 733-874, E', 876-916, 'S', 918-1038,1040-1047, 'S', 1049-1283, 'E', 128 eferences: EMBL:M30398; NID:g159876; PIDN:AAA29413.1; PID:g159877 s: s: let. ls: leucine zipper latch 7.1%; Score 106.5; DB 2; Length 2022; hotal Similarity 22.3%; Pred. No. 71;	Oy 93 -LLSAVILLFDEYNEKKASAQKDILIRILDDGVNKLNBAQKSLLGSSQSFNNASGKLLAL 151 Db 17 KVLESEKQAFENEKGGEREGQLAKAMEKLNSEQNILDEVTKKLEQSEEEVLAARGAIQEL 156 QY 152 DSQLTNDPSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPEL 211
6; Conservative S: DOVIPWKTFDETIKELSRF ::	249 SULT 33 5837 Species: Rat Species: Rat Accession: J

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A;Accession: T41342
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1115 <LYN>
A;Cross-references: UNIRROT:094488; EMBL:AL035076; PIDN:CAA22653.1; GSPDB:GN00066; SPDB:£
A;Experimental source: strain 972h-; cosmid C417
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                                                                          1903 ASANIFAROVGVEKEKVNAENAAAQVEAEKCAVIAK------EVSEKQASCEKDLA 1902
                                                                                                                                                                                                             1903 AAEPLVAEAMAALETVTKKDLGEAKSLKKPPPGVDDITAVVIILLENNPKDKSWQAAQKL 1962
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                                                                                                                                                                                                                                                                                 --IRKEAY---AGAAAGIVAGPF 190
                                                                                                                                                                                                                                                                                                                                                                                                                    191 GLIISYSIAAGV-----KQANKD 235
                 --ATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDIL 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       236 IDAA-----KLKLATEIAAIGEIKTETETTRFYVD-----YDDLMLSLLKGAA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable coiled-coil protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Dete: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 VLLMDS---QDKYFEATQTVYEWCGVVTQLLSAYILLFDE---YNEKKASAQKDILIRIL
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KiLyna, M.; Rajandream, M.A.; Barrell, B.G.; Volckaert,
Submitted to the EMBL Data Library, January 1999
A;Reference number: Z21970
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                                                                                                                                                     IR--ILDDGVNKLNEAQKSLLGSSQSF---
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Gene: SPDB:SPCC417.07c
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Best Local S
Matches 66
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dynein alpha heavy chain - Chlamydomonas reinhardtii (fragment)
C;Species: Chlamydomonas reinhardtii
C;Species: Chlamydomonas reinhardtii
C;Species: Chlamydomonas reinhardtii
C;Species: Chlamydomonas reinhardtii
C;Species: 21.May-1999 #sequence_revision 21-May-1999 #text_change 02-Feb-2001
C;Accession: T08164
R;Mitchell, D.R; Brown, K.S.
J. Cell Sci. 107, 635-644, 1994
A;Title: Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes.
A;Recession: T08164
A;Title: Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes.
A;Accession: T08164
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-2405 *MIT>
A;Residues: 1-2405 *MIT>
A;Residues: 1-2405 *MIT>
A;Cross-references: EMBL:L26049; NID:g415679; PIDN:AA57316.1; PID:g603079
A;Cross-references: Expain 21gr
C;Genetics:
C;Genetics:
A;Gene: ODA11
A;Note: Intron positions not resolved (incomplete sequence)
C;Superfamily: dynein heavy chain, ciliary
C;Keywords: nucleotide binding; P-loop
E;575-582/Region: nucleotide-binding motif A (P-loop)
RiToki, C.; Fujiwara, T.; Sohda, M.; Hong, H.S.; Misumi, Y.; Ikehara, Y.
Cell Struct. Funct. 22, 565-577, 1997
A, Title: Identification and characterization of rat 364-kDa Golgi-associated protein rec
A, Reference number: JCS837; MUID:98093490; PMID:9431462
A, Recession: JCS837
A, Rolecule type: mRNA
A, Residues: nucleic acid sequence not shown
A, Rolecule type: mRNA
A, Residues: 1-3187 - TOKS
A, Comment: This protein plays a role in the formation and maintenance of the characteris
C, Comment: This glantin
F, 4549-549, 624-1176, 1238-1707, 1763-3114/Domain: coiled-coil leucine zipper #status predict
F, 3165-3187/Domain: membrane anchor #status predicted <MAD>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 AQKDILIRILDDGVNKLNEAQKSLLGSSQSFNNASGKLLALDSQLTN-----DFSEKSS 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      165 YF---QSQVD-RIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNDRLKAVQ- 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 AEQTV--EVVKSAIETADGALDFYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVLVG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----NFFTSLSVTVK------QANKDIDAAKLKLATEI-----AAIGEIK----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 3187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
7.0%; Score 106; DB 2; Length 318;
Best Local Similarity 22.2%; Pred. No. 1.46+02;
Matches 78; Conservative 53; Mismatches 134; Indels
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hypothetical protein E - slime mold (Physarum polycephalum) mitochondrion integrated plass c) Species: mitochondrion Physarum polycephalum c) Date: 23-Apr-1999 #text_change 09-Jul-2004 c) Accession: T03754 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004 c) Accession: T03754 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004 c) Arabagawa, C.C.; Jones, E.P.; Miller, D.L. Curr. Genet. 33, 178-187, 1998 A/Fille: Mitochondrial DNA rearrangements associated with mF plasmid integration and plass A, Reference number: Z15055; MUID:98177147; PMID:9508792
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                                                                                                                                                                                                                                                                                          1166 BQBVTHLKKTLEDBARTHEGQIQEIRQKHSQAV--EELSEQLEQTKRLKGNLEKAKQALE 1223
                                                                                                                                                                                                                                                                                                                                                                                                                                 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1354 NLCKQISTLQSQMTDMKKKMDENVGSLETVEELKKKLQKDLEAVNQRFEEKAAAYD--KL 1411
                                                                                                                                                                                                                                                                                                                                                                                   56 QEASVLVGDIKVLLMDSQDKYPEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQ-KD 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115 ILIRI-----LDDGVNKLN---EAQKSLLGSSQSFNNASGKLLALDSQLTNDFSEK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174 RKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNDRLKAVQNFFTSLSVTVKQAN 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163 SSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGK---LIPELNDRLKAVQ 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69
                                                                                                                                                                                                                                       7 EQTVEVVKSAIE----TADGALDFYNKYLDQVIPWKTFDETIKE-----LSRFKQEYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----TV----KQANKDIDAAKLKLATEIAAIGEIKT
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                                                                                                                                                              47; Mismatches 103; Indels 105;
                                                                                     Length 1964;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 640;
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1 Similarity 22.5%; Pred. No. 23;
61; Conservative 40; Mismatches 104; Indels
                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182 LDIMSYASRTAD --- OLYNNYIOSLVNLNTLPTT----
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A;Molecule type: DNA
A;Residues: 1-640 <NAK>
                   8;84-764/Domain: myosin motor domain homology <MMO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     380 NDLS----KLANSILNLENQIKEIAAQRVTT 406
                                                                                        Score 104.5;
Pred. No. 93;
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C, Keywords: mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1412 EKTKTRLQOELDDISVDL 1429
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                                                                                     Query Match 6.9%;
Best Local Similarity 19.8%;
Matches 63; Conservative 4
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Best Local S:
Matches 61
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Modecule type: DNA
A,Residues: 1-1292 (STO>
A,Cross-references: UNIPROT:Q9SL02; GB:AE002093; NID:g4263721; PIDN:AAD15407.1; GSPDB:GN
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A;Molecule type: mRNA
A;Residues: 1-1964 eBHA>
A;Cross.references: UNIPROT:093522; GB:AF055895; NID:93660671; PIDN:AAC83556.1; PID:9366
                                                                                                Rilin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A64420; MUID:20083487; PMID:10617197
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R;Bhati.Dey, N.; Taira, M.; Conti, M.A.; Nooruddin, H.; Adelstein, R.S.
R;Bhati.Dey, N.; Taira, M.; Conti, M.A.; Nooruddin, H.; Adelstein, R.S.
A;Title: Differential expression of non-muscle myosin heavy chain genes during Xenopus A;Reference number: A59282; MUID:99077683; PMID:9858676
A;Reference number: A59282
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.Species: Arabidopsis thaliana (mouse-ear cress)
:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
:Accession: D84727
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C,Species: Xenopus laevis (African clawed frog)
C,Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 6.9%; Score 104.5; DB 2; Length 1292; Best Local Similarity 15.0%; Pred. No. 53; Matches 64; Conservative 93; Mismatches 132; Indels 137; Gaps
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C;Superfamily: myosin heavy chain; myosin motor domain homology
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C, Superfamily: RAD50 protein
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A;Status: preliminary
A;Status: preliminary
A;Residues: preliminary
A;Residues: 1-1163 «KUR»
A;Cross-references: UNIPROT:Q97FK1; GB:AE001437; PIDN:AAK80682.1; PID:g15025772; GSPDB:GR
A;Cross-references: UNIPROT:Q97FK1; GB:AE001437; PIDN:AAK80682.1; PID:g15025772; GSPDB:GR
A;Cross-references: UNIPROT:Q97FK1; GB:AE001437; PIDN:AAK80682.1; PID:g15025772; GSPDB:GR
A;Coss-references: UNIPROT:Q97FK1; GB:AE001437; PIDN:AAK80682.1; PID:g15025772; GSPDB:GR
A;Coss-references: UNIPROT:Q97FK1; GB:AE001437; PIDN:AAK80682.1; PID:g15025772; GSPDB:GR
A;Gene: CAC2736
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A;Gene: wapA; N17G
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hypothetical protein F20D10.190 - Arabidopsis thaliana (5) Species: Arabidopsis thaliana (mouse-ear cress) (5) Species: Arabidopsis thaliana (mouse-ear cress) (5) Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004 (5) Accession: T05634 (Startant M.) Wambutt, R.) Bancroft, I.) Mewes, H.W.; Mayer, submitted to the Protein Sequence Database, February 1999 A; Reference number: Z15420 A; Mayer, Pa.M.) A. Accession: T05634
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EWBEEKSKILDEIYSLQTKIDSVTRISEDLQKKLQMCNGALTQ------EETRRKHL 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110 SAQKDILIRILDDGVNKLNEAQKSLLGSSQSFNNASGKLLALDSQLTNDFSBKSSYFQ-- 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               221 FFTSLSVT-----TTRFYV 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    363 IHKNCSANLRSKEAEWSSQVEKNVEBINDYKLQLQSKEAALKEVELENCRSSTAKMIL 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  153 İEABKTVKGMKENRGRDDVVVYMEBEEKSQVEEKLKWKKEQFKHLEBAYEKLKNLFKDSKK 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 IFAEQTVEVVKSAIETADGA--LDFYNKYLDQVIPWKT-----FDETIKELSRF----KQ 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----SQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEG----KLIPELNDRLKAVQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-1496 <BEV>
A;Cross-references: UNIPROT:Q9SZK7; EMBL:AL035538
A;Experimental source: cultivar Columbia; BAC clone F20D10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 104; DB 2; Lu; Pred. No. 70; 67; Mismatches 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Map position: 4
A,Introns: 1042/2; 1212/2; 1232/1; 1263/3; 1349/3
A,Note: F20D10.190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DYDDLMLSLLKGAAKKMINTCNEYQQR 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             317 KYENGKLEQENRELLGSLK-----
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Matches 62; Conservative
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1203 KATESYQYDKDGNVTSVKDAYGTETYEYNKONDVTKNKDTEGNVTDIAYDGLDAVSETDQ 1262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 AGIVAGPFGL-IISYGIAAGVIEGKLIPELNDRLKAVQNFFTSLSVTVKQANKDIDAAKL 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78 EATOTV-YEWCGVYTOLLSAYILLFDEYNEKK-ASAQKDILIRILD---DGVNKLNEAOK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSATOTV----EL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242 KLATEIAAIGEIKTETETTRFYVDYDDLMLSLLKGAAKKMINTC-NEYQORHGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 2334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.9%; Score 104; DB 2;
Local Similarity 25.6%; Pred. No. 1.3e+02;
Local Go, Conservative 39; Mismatches 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C, Superfamily: cell wall-associated protein wapA
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14; Gaps 95; Length 1163; Indels DB 2; 142; Query Match 6.9%; Score 103.5; 1 Best Local Similarity 21.7%; Pred. No. 54; Matches 81; Conservative 55; Mismatches

Qy 1 MTGIFAEQTVEVVKSAIETADGALDFYNKYLDQVIPWKTFDETIKELS 48	154 QLTNDFSBKSSYPQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELND
QY 49 RFKQEYSQEASVLVGDIKVLLMDSQDKYFEATQTVYEWGGVVT 91	
QY 92 QLLSAYILLFDEYNEKKASAQKDILIRILDDGVNKLNEAQKSLLGSSQS 140 230 EASKEYLKABEEYNEGKEVWGLQIEIEEKNRVRKDLMEKKDEIDLKEKRARLGESSSKVK 289	1404 DILALQLYKFDAQINBVVEVASKEAKIEKKLKMIETAWLKQIFEFEDYKETKVFLPLDN 270 MLSLKRGAAKKMINTCNEYQQRHGKKTLLEV
Qy 141FNNASGKLLALDSQLTNDFSEKSSYFQSQVDRIRKEAYAGAA 182 : : : 0.50 PXIDNYENTLKOJILSREDMEKKLSJAKDNKRK 339	Db 1464 MEMLDQHSLDLMGMKGQGKYVEFFYNTVEDWREKLGRVDSVVGEWLKVQKNWKTLVNI 1521 RESULT 43
183 AGIVAGPFGLIISYSIAAGVIEGKLIPELNDRLKAVQNFFTSLSVTVKQANKD 235	A36014 myosin heavy chain, nonmuscle - fruit fly (Drosophila melanogaster) NyContains: myosin ATPase (EC 3.6.4.1) C.Snecies: Drosophila melanogaster
236 IDAAKLKLATEIAAIGEIKTETETTRFYUDYDDLMLSLLKGAAKKMINTCNEYQ 289	C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004 C;Accession: A36014; B36014 R;Ketchum, A.S.; Stewart, C.T.; Stewart, M.; Kiehart, D.P.
290QRHGKKTLL 298	A,Title: Complete sequence of the Drosophila nommuscle myosin heavy-chain transcript: cor A, Reference number: A36014; MUID:90349606; PMID:2117279
Db 452 VDFEKAKSKKEML 464	A;Accession: Assula: acid sequence not shown A;Status: nucleic acid sequence not shown A;Molecule type: mRNA
	A; Residues: 1-2017 < KET> A; Cross-references: UNIPROT: Q99323; GB: M35012
-	C;Generics: A;Gene: FlyBase:zip A;Cross-references: FlyBase:FBgn0005634 C;Superfamily: myosin heavy chain; myosin motor domain homology C;Keywords: actin binding; alternative splicing; ATP; coiled coil; hydrolase; methylated
al a	F;1-2017/Product: myosin heavy chain, form I #status predicted <ma1> F;46-2017/Product: myosin heavy chain, form II #status predicted <ma2> F;135-815/Domain: myosin motor domain homology <mmot> F;225-232/Region: nucleotide-binding motif A (P-loop)</mmot></ma2></ma1>
	F;598-631/Region: actin binding #status predicted F;705-727/Region: actin binding #status predicted F;888-2017/Domain: coiled coil #status predicted <coi></coi>
A; Residues: 1-4588 «KAN» A; Cross-references: UNIPROT: Q94709; EMBL: U19464; NID: g625089; PID: g625090; PIDN: AAA61680 A; Cross-references: UNIPROT: Q94709; EMBL: U19464; NID: g625089; PID: g625090; PIDN: AAA61680 B; Asai, D.J.; Beckwith, S.M.; Kandl, K.A.; Keating, H.H.; Tjandra, H.; Forney, J.D. J. Cell Sci. 107, 839-847, 1994 A; Title: The dynein genes of Paramecium tetraurelia: Sequences adjacent to the catalytic	F;888-1328/Region: S2 F;1329-2017/Region: light meromyosin F;176/Modified site: N6,N6,N6.reimethyllysine (Lys) #status predicted F;21/Binding site: ATP (Lys) #status predicted F;745,755/Active site: Cys #status predicted
	Query Match 6.8%; Score 103; DB 1; Length 2017; Best Local Similarity 23.8%; Pred. No. 1.2e+02; Matches 65; Conservative 44; Mismatches 102; Indels 62; Gaps 13;
C;Genetics: A;Introns: 43/2; 113/3; 171/3; 4490/1 C;Superfamily: dynein heavy chain, ciliary	Qy 8 QTVEVVKSAIETADGALDFYNKYLDQVIPWKTFDETIKELS-RFKQEYSQEASVLVGD 64 :
C;Keywords: nuclectide binding; P-loop F;1886-1893/Region: nuclectide-binding motif A (P-loop)	Qy 65 IKVILMDSQDKXFEATQTVZEWGGVVTQLLSAYILLFDBYNEKKASAQKDILIRILDDGV 124
Query Match 6.9%; Score 103.5; DB 2; Length 4588; Best Local Similarity 19.3%; Pred. No. 3.3e+02; Matches 69; Conservative 67; Mismatches 115; Indels 107; Gaps 15;	Db 1315 IERARSELĢEKCTKLQQEAENITNQLEEAELKASAAVKSASNME 1358 Qy 125 NKLNBAQKSLLGSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVD 171
Qy 7 EQTVEVVKSAIETADGALDFYNKYLDQVI-PWKTFDETIKELSRFKQ 52 ::	Db 1359 SQLTEAQQLLEEETRQKLGLSSKLRQIESEKEALQEQLEEDDEAKRNYERKLAEVTTQMQ 1418 Ov 172 RIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNDRLKAVQNPFTSLSVTVKQ 231
53 EYSQEASVLVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFD 102	1419
DD 1267 EAADYNQEKLPELEKSGYKQLRETNVDLKSLKIMWDAISMVNY 1310 QY 103 EYNEKKASAQKDILIRILDDGVNKINBAQKSLIGSSQSFNNASGKLLALDS 153	QY 232ANKIDDAMAKLARIENETIN 201 Db 1455 LIAQNDRLDKSKKKIQSELED-ATIELEAQRTK 1486

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1479 KPUVEEYATIGREAAEKIVSAAQQSAELLSQSNSGMVGMVEGAISDYAAAGTDAASKLVA 1538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        161 -EKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIIS------YSIAAGVIEG 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 AQKDILIRILDDGVNKLNBAQKSLLGSSQSFNNASGKLLALDSQLTNDFS------ 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Gene: AGR C 2490
A,Map position: circular chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Guery Match
Best Local Similarity 20.29
Matches 71; Conservative
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Conserved hypothetical protein Atul348 [imported] - Agrobacterium tumefaciens (strain CS conserved hypothetical protein Atul348 [imported] - Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Date: 11-Jan-2002
R;Maco, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, Y.; Woo, I R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Morgins, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell, S; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: FlyBase:FBgn0005634
A;Cross-references: 10/3; 162/3; 215/1; 255/3; 263/3; 303/3; 334/3; 1248/1; 1349/3; 1526/3; A;Introns: 10/3; 90/3; 162/3; 215/1; 255/3; 263/3; 303/3; 334/3; 1248/1; 1349/3; 1526/3; C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Reywords: alternative splicing; ATP; nucleotide binding; P-loop
C;Reywords: myosin motor domain homology <MMOT>
F;135-855/Domain: myosin motor domain potif A (P-loop)
                                                                                                                                                                                     encode
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A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A,Reference number: AB2577; MUID:21608550; PMID:11743193

A,Accession: AD2742

A,Statuus prelimnary

A,Holecule type: DNA

A,Residues: 1-2155 <KUR>
myosin II heavy chain, non-muscle - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 19-101-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Date: 19-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: S61477; S65349
R;Mansfield, S.G.; Al-Shirawi, D.Y.; Ketchum, A.S.; Newbern, E.C.; Kiehart, D.P.
J; Mol. Biol. 255, 98-109, 1996
A;Title: Molecular organization and alternative splicing in zipper, the gene that & A;Reference number: S61477; MUID:96144835; PMID:8568878
                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-2057 <MAN>
A; Residues: 1-2057 <MAN>
A; Residues: 1-2057 <MAN>
A; Cross-references: UNIPROT: 19987; EMBL: U35816
R; Analsfield, S. G.; Al-Shirawi, D.Y.; Ketchum, A.S.; Newbern, E.C.; Kiehart, D.P. Submitted to the EMBL Data Library, September 1995
A; Reference number: 863349
A; Recession: 863349
A; Residues: 1-1908; ML', 1911-2057 <MAN>
A; Residues: 1-1908, ML', 1911-2057 <MAN>
A; Cross-references: EMBL: U35816; NID: 91141789; PIDN: AAB09049.1; PID: 91572481
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1355 IERARSELOEK---CTKLOOEAENITNOL-----EEAELKASA----AVKSASNME 1398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NKINBAQKSL-----FGSSQSFNNASGKLLALDSQLTNDFSEKSSY-----FQSQVD 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172 RIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNDRLKAVQNFFTSLSVTVKQ 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     232 ---ANKDIDAAKLKLATEIAAIGEIKTETTR 261
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A;Cross-references: UNIPROT:QBUFP9; GB:AE008688; PIDN:AAL42354.1; PID:g17739760; GSPDB:GP.Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atul348
A;Map position: circular chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 SVLVGDIKVLLMDSQDKYFEATQTVYE-----WCGVVTQLLSAYILLFDEYNEKKAS 110
                                                                                                                                                                                                                                                          1479 KPVVEBYATIGRBAABKIVSAAQQSABLLSQSNSGMVGMVEQAISDYAAAGTDAASKLVA 1538
                                                                                                                                                                                                                                                                                                                  206 KLIPBINDRIK------AVQNFTSLSVTVKQANKDIDAAKLKLATEIAAIGEIK 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 GIFAEQTVEVVKSAI----ETADGALDFYNKYLDQVIPWKTFDETIKELSRFKQEYSQEA
                                                                                                                                                                                                                                                                                                                                                          161 -EKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIIS------YSIAAGVIEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.8%; Score 103; DB 2; Length 2155;
20.2%; Pred. No. 1.3e+02;
tive 64; Mismatches 116; Indels 100; Gaps
                                                                                                                                                                                      SVLVGDIKVLLMDSQDKYFEATQTVYE-----WCGVVTQLLSAYILLFDEYNEKKAS
                                                                                                                                                                3 GIFAEQIVEVVKSAI----ETADGALDFYNKYLDQVIPWKTFDETIKELSRFKQEYSQEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 AQKDILIRILDDGVNKLNEAQKSLLGSSQSFNNASGKLLALDSQLTNDFS----
                                                                                                   Query Match
6.8%; Score 103; DB 2; Length 2155;
Best Local Similarity 20.2%; Pred. No. 1.38+02;
Matches 71; Conservative 64; Mismatches 116; Indels 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        255 TETETTREYVDYDDLMLSLLKGAAKK-------MINTCNEYQQR
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Db 1599 EQSATNFNAAVERAAQGFGAADEALNASATRFSESASQAADMVSSSSRLLEG 1650 Qy 206 KLIPELNDRLKAVONFFTSLSVTVKOANKDIDAAKLKLATEIAAIGEIK 254	C;Genetics: A;Gene: TC0784 C;Suverfamily: phage P22 gene 12 protein
	6.8%; 23.1%; ative
1700ERQDALRSLSVGLVKRSEEIETAMRNVVGVVENTLNEA	Qy 25 DFYNKYLDQVIPWKTFDETIKELSRFKQBYSQEASVLVGDIKVLLMDS 72
RESULT 47 D97198 methyl-accepting chemotaxis protein [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text change 09-Jul-2004	73 QDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNBKKASAQKDILIRILD
	Qy 122 -DGVNKLNBAQKSLLGSSQSFNNASGKLIALDSQLTNDFSEKSSYFQSQVD 171
A, Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld A; Reference number: A96900; MUID:21359325; PMID:21359325 A; Accession: D97198	Qy 172 RIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNDRLKAVQNF 221
A. Molecule type: DNA A. Residues: 1-379 <kur> A. Cross-references: UNIPROT: Q97GE7; GB: AE001437; PIDN: AAK80375.1; PID: g15025436; GSPDB:G</kur>	QY 222FTSLSVTVKQANKDIDAAKLKLATEIAAIGEIKTETETTR 261
Ajscherimental Bource: Clostridium acetobutylicum AfcC824 CjGenetics: AjGene: CAC2420	OY 262 FYUDYDDLMLSLLKGAAKKM 281
Query Match 6.8%; Score 102.5; DB 2; Length 379; Best Local Similarity 21.2%; Pred. No. 14; Matches 58; Conservative 40; Mismatches 83; Indels 93; Gaps 13;	DD 312 LIDDYPGLK1TDLKARARRM 331 RESULT 49
.Qy 72 SQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDI 115 :	144825 hypothetical protein wzc [imported] - Acinetobacter lwoffii N;Alternate names: protein tyrosine kinase C;Species: Acinetobacter lwoffii
Qy 116 -LIRILDDGVNKLNEAQKSLLGSSQSFNNASGK 147 ::: :	99-Jul-2004
Qy 148LLALDSQLTNDPSEKSSYFQSQVDRIRKEAYAGAAAGIVA 187 Db 167 ITEQMLNIENRV-NSLSEVISKLKTHCDNINNYSNVISDIAEETNLLSLNANIEAARA 223	A; Description: Genomic organization of the wce region of Acinetobacter lwoffil RAG-1 req. A; Reference number: 222856 A; Accession: T44825 A; Status: preliminary; translated from GB/EMBL/DDBJ
Qy 188 GPFGLIISYSIAAGVIEGKLIPELN-DRLKAVQNFFTSLSV 227	A;Molecule type: DNA A;Residues: 1-726 <nak> A;Cross-references: UNIPROT:Q9RMD9; EMBL:AJ2431; PIDN:CAB57193.1 A;Experimental source: strain RAG-1</nak>
Qy 228 TVKQANKDIDAAKLKLATEIAAIGEIKTETETTR 261 	ģ
RESULT 48 H81665 replicative DNA helicase TC0784 [imported] - Chlamydia muridarum (strain Nigg) C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn C;Dates: Al-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004 C;Accession: H81665 R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, M.C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, M.C.; All, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg,	0 /; CONBELVALIVE '48; MISMACCHEB '5; INGLE LOS; CAPS 8 QTVEVVKSAIETADGALDFYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASV 173 KTDEIVLTAPLNKLNQLKNQFGTWKVAIFTNDTFDANYFVQKNSLPAAVQAILS 2 61LVGDIKVLLMDSQDKYFFATQTVYEWCGVYTQLLSAYILLFDEXNEKKASA 1 7
Aritle: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39. A; Reference number: A81500; MUID:20150255; PMID:10684935 A; Status: preliminary A; Status: preliminary	QY 112 QKDILIRILDDGVNKLMBAQKSLLGSSQSFNNASGKLLALDSQLTNDFSEKSSYFQ 167 :: :: ::: ::: ::: ::: ::: :::
A;Molecule type: DNA A;Residues: 1-472 <tet> A;Cross-references: UNIPROT:Q9PJP4; GB:AE002346; GB:AE002160; NID:g7190805; PIDN:AAF3958 A;Experimental source: strain Nigg (MoPn)</tet>	Qy 168 SQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNDRLKAVQNF 221 :

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methyl-accepting chemotaxis protein (tlpc) PAB1336 - Pyrococcus abyssi (strain Orsay)

C; Species: Pyrococcus abyssi
C; Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C; Accession: H75001
R; anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A; Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A; Reference number: A75001
A; Reference number: A75001
A; Residues: preliminary
A; Molecule type: DNA
A; Residues: 1-739 < KAW>
A; Kesidues: 1-739 < KAW>
A; Cross-references: UNIPROT:Q9UYF8; GB:AJ248288; GB:AL096836; NID:g5458960; PIDN:CAB5045
A; Experimental source: strain Orsay
C; Genetics:
A; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                206 KLIPELNDRLKAVONFFTSLSVTVKQANKDIDAAKLKLATEIAAIGEIKTETETTRFYVD 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 SVLVGDIKVLLMDSQDKYFFATQTVYFWCGVVTQLLSAYILLFDFYNFKKASAQKDI--- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            483 NEITDGMRLVAQTSE----ESVRAMEEFSGAVTEVVS----IANEGSQKGDEALKRIEDI 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 --LIRILDDGVNKLNE------AQKSLLGSSQSFNNA----SGKLLALDS 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              365 ITQLNSTLKQL-PDIQRQYLQLFREV---EVKTQ------LYTALL----- 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MIGIFAEQTVEVVKSA--IETADGALDFYNKYLDOVIPWKTFDETIKELSRFKQEYSQEA 58
222 FTSLSVTVKGANKDIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDLMLSLLKGAAKKM 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 6.8%; Score 102; DB 2; Length 739;
Best Local Similarity 19.3%; Pred. No. 37;
Matches 64; Conservative 73; Mismatches 140; Indels 52; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: January 28, 2005, 19:16:48
Job time : 46 secs
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Q58718 methanococc Q92897 listeria in Q08581 acacharomyc Q97wh8 sulfolobus Q77dzQ plasmodium Q65486 synechocyst G6cgc3 yarrowia li O50733 borrelia bu Q6c359 yarrowia li O6c359 yarrowia li O6c359 yarrowia li O6gne7 xenopus lae Q77fq7 plasmodium Q81ff plasmodium Q81ff plasmodium Q8478 trypanosoma
                                                                                                                                                                                                                                                                                                                                           Q7xeh4 oryza sativ
Q77;32 plasmodium
Q00799 plasmodium
Q8d3e6 wiggleswort
Q7xnh1 plasmodium
Q9xxu3 thermotoga
Q9xxu3 thermotoga
Q9xxu3 escherichia
Q8g3v4 escherichia
Q8g40 escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O77E93 plasmodium

O7886 oryza sativ

Cae01868 oryza sativ

Cae01868 cloetridium

O70249 fusobacteri

08744 podospora a

08744 potospora a

08744 potospora a

08724 yersinia pe

Aas8642 yersinia pe

Aas8642 yersinia pe

08754 plasmodium

08754 plasmodium

08755 bacillus ce

Aas3419 bacillus ce

Aas3419 bacillus ce

Aas3419 bacillus ce

Aas3419 bacillus co

08xnw clostridium

09b10 caenorhabdi

06109 mesoplasma

06109 mesoplasma

06109 oryza sativ

077zf8 placobacter

06109 mesoplasma

06466 paramecium

077zf8 neurospora

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Q26749 trypanosoma
Q7rd3 plasmodium
061851 caenorhabdi
Q74ja0 lactobacil
Aas09030 lactobacil
P02567 caenorhabdi
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Q73aj3 bacillus ce
Aas40708 bacillus
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                                                                                                                                                                                                                                                                                                                  Q8cpiO staphylococ
Q22257 caenorhabdi
                                                                                                                                                                                                                                                                                                     Aas41161 bacillus
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RBP2 PLAVB
Q8D3E6
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SR68 CAEEL
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Q7235 escherichia
Q9228 escherichia
Q9228 escherichia
Q9127 escherichia
Q9127 overa sativ
P71497 mycoplasma
Q7266 plasmodium
Q6mc03 mycoplasma
Q77155 mycoplasma
Q77155 parcohala
Q77152 plasmodium
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Q77152 plasmodium
Q77151 plasmodium
Q77154 neurospora
Q7716 plasmodium
Q7716 plasmodium
Q7717 helicobacte
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P09983 escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27rm79 plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       293rr6 salmonella
                                                                                                ; Search time 198 Seconds
(without alignments)
880.498 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                    .....TCNEYQQRHGKKTLLEVPDI
                version 5.1.6 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                     1825181 segs, 575374646 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                                                                                                                         Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HLYE SALPA
HLYE SALTI
HLYE ECOLI
HLYE ECOS7
QYZSB
HLEL SHIFL
HLEL ECOL6
Q9LIW7
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HLY1_ECOLI
                                                                       using sw model
                                                                                                 January 28, 2005, 19:06:39
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CAE77235
Q7N5U5
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AAT28865
Q7RM79
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Q7RQB6
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                    1 MTGIFAEQTVEVVKSAIETA.
                GenCore (c) 1993 -
                                                                                                                                                                                                                                                                                                                                                                                                                 UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                                                                                                                                                                                 seq length: 0
seq length: 200000000
                                                                                                                                                        US-09-993-292B-24
1510
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Match Length
                                                                       protein search,
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713
577
1521
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693
693
555
2139
                             Copyright
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                                                                                                                                                                                                               Scoring table:
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382
136.5
132
130
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128.5
126.5
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124.5
122.5
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Perfect score:
                                                                       OM protein
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Maximum DB
                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                           Searched:
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11144 11164 1164

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Nature 413:848-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                NCBI_TaxID=601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity)
                                                           DI 303
                                                                                       301 Di 302
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                                                                                                                                              HLYE_SALTI
                                                                                                                                 RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 VGDIKVLAMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILLRILD 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRILD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DGVNKINEAQKSLIGSSQSFNNASGKLIALDSQLTNDFSEKSSYFQSQVDRIRKEAYAGA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGIFAEQTVEVVKSAIETADGALDFYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                            STRAIN=SMI S3068/99;
MEDLINE=22212112; PubMed=12228306;
Oscarsson J., Westermark M., Loefdahl S., Olsen B., Palmgren H.,
Oscarsson J., Westermark M., Loefdahl S., Olsen B., Palmgren H.,
Mizunce Y., Wai S.N., Uhlin B.E.;
Mizunce Y., Wai S.N., Uhlin B.E.;
Mizunce Y., Wai S.N., Uhlin B.E.;
Infect acterization of a pore-forming cytotoxin expressed by Salmonella enterica servoras typhi and paratyphi A.";
Infect Immun. 70:5759-5769(2002).
Infect Immun. 70:5759-5769(2002).
Infect Immun cells. Acts by forming a pore-like structure upon contact with mammalian cells (By similarity).
Is SUBNIT: Monomer and oligomer: In periplasm, it is present as a monomer, while in outer membrane vesicles, it oligomerizes to form a pore structure that is active. Probably forms an octamer (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGIFAEQTVEVVKSAIETADGALDFYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  similarity).

PTM: In periplasm, it forms a disulfide bond, which prevents the oligomerization. In outer membrane vesicles, the redox status prevents formation of the disulfide bond, leading to oligomerization and pore formation (By similarity).

SIMILARITY: Belongs to the hemolysin E family.
                                                                                                                                                                                                                                                                                                                                                          similarity).
SUBCELLULAR LOCATION: Secreted. Exported from the cell by outer
membrane vesicles. Also found in the periplasmic space (By
                                                                            Name-nlyE; Synonyms-clyA, sheA;
Salmonella paratyphi-a.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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Potential.
In monomeric form (By similarity)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22DB9112B763A061 CRC64;
                                    29-WAR-2004 (Rel. 43, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Hemolysin E (Cytotoxin clyA) (Silent hemolysin sheA).
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Pfam; PF06109; H1yE; 1.
Cytolysis; Hemolysis; Toxin; Transmembrane.
INIT MER.
By similarity.
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302 AA
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                          (Rel. 43, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.0
Matches 302; Conservative
STANDARD;
                                                                                                                                    NCBI_TaxID=54388;
                                                                                                                                                                 SEQUENCE FROM N.A
                           29-MAR-2004
  HLYE SALPA
Q93RR6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INIT MET
TRANSMEM
DISULFID
SEQUENCE
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240
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-i. FUNCTION: Toxin, which has some hemolytic activity towards mammalian cells. Acts by forming a pore-like structure upon contact with mammalian cells (By similarity).

-i. SUBDUT: Monomer and oligomer. In periplasm, it is present as a monomer, while in outer membrane vesicles, it oligomerizes to form a pore structure that is active. Probably forms an octamer (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=TY2 / AICC 700931;
MEDLINE=22531367; PubMed=12644504;
MEDLINE=22531367; PubMed G III, Mayhew G.F., Rose D.J.,
Deng W., Liou S.-R., Plunkett G III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-CT18;
MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
MEDLINE=21534947; PubMed=11677608, DOI=10.1038/35101607;
Marcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davies R.M., Dowd L., White N., Farrar J., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K., Mohitehead S., Barrell B.G.;
Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=TY21a, and SMI S2369/96;
STRAIN=TY21a, and SMI S2369/96;
STRAIN=TY21a, and SMI S2369/96;
MEDLINE=2221571D: PubMed=12228306;
OSCATESON J., Westermark M., Loefdahl S., Olsen B., Palmgren H.,
Mizunce Y., Wai S.N., Uhlin B.E.;
"Characterization of a pore-forming cytotoxin expressed by Salmonella enterica serovars typhi and paratyphi A.";
Infect. Immun. 70:5759-5769(2002).
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PTM: In periplasm, it forms a disulfide bond, which prevents the oligomerization. In outer membrane vesicles, the redox status prevents formation of the disulfide bond, leading to oligomerization and pore formation (By similarity).
SUBCELLULÂR LOCATION: Secreted. Exported from the cell by outer membrane vesicles. Also found in the periplasmic space (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HIVE SALTI STANDARD; PRT; 302 AA.

082727; 0934C4;
29-MAR-2004 (Rel. 43, Last sequence update)
29-MAR-2004 (Rel. 45, Last annotation update)
01-0CT-2004 (Rel. 45, Last annotation update)
Hemolysin E (Cytotoxin clyA) (Silent hemolysin sheA).
Hame-lhyE; Synonyms=clyA, sheA; OrderedLocusNames=STY1498, t1477;
Salmonella typhi.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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STRAIN=K12 / AB1157;
Woodgate R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=K12 / MG1655;
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=3030-2;
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                                                                                                                                                                    INDUCTION.
STRAIN=K12;
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             This SWISS-RROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182 AAGIVAGPFGLIISYSIAAGVIEGKLIPELNDRLKAVQNFFTSLSVTVKQANKDIDAAKL 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 KLATEIAAIGEIKTETETTRFYUDYDDLMLSLLKGAAKKMINTCNEYQQRHGKKTLLEVP 301
241 KLATEIAAIGEIKTETETTRFYUDYDDLMLSLLKGAAKKMINTCNEYQQRHGKKTLFEVP 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 VGDIKVILMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRILD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DGVNKLNEAQKSLLGSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDRIRKEAYAGA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 VGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRILD 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TGIFAEQTVEVVKSAIETADGALDLYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                           Complete proteome; Cytolysis; Hemolysis; Toxin; Transmembrane.

INIT MET 0 0 By similarity.

TRANSMEM 178 198 Potential.

DISULEID 86 284 In monomeric form (By similarity)

SEQUENCE 302 AA; 33658 MW; 2BDFDB35D044FDAE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HLYE ECOLI STANDARD, PRT, 302 AA.
P77335; Q47276; Q8VU70; Q9R3G4;
01-NOV-1997 (Rel. 35, Created)
29-MAR-2004 (Rel. 43, Last sequence update)
10-CT-2004 (Rel. 45, Last annotation update)
Hemolysin E, chromosomal (Hemolysis-inducing protein) (Silent hemolysin sheA) (Cytotoxin clyA) (Latent pore-forming 34 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=hlyE; Synonyms=clyA, sheA, hpr; OrderedLocusNames=b1182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97.2%; Score 1467; DB 1; Length 302; 97.4%; Pred. No. 4.6e-89; vative 2; Mismatches 6; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=K12 / XL1-BLUE;
McNamara P.J., Iandolo J.J., Uhlich G.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
[2]
SIMILARITY: Belongs to the hemolysin E family.
                                                                                                                                                                                                        EMBL; AJ113032; CAC38360.1; -.
EMBL; AJ113034; CAC38363.1; -.
EMBL; AL627270; CAD01758.1; ALT_INIT.
EMBL; AE016839; AA069115.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enterobacteriaceae, Escherichia
                                                                                                                                                                                                                                                                                               HSSP; P77335; 100Y.
InterPro; IPR010356; HlyE.
Pfam; PF06109; HlyE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 294; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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DISULFIDE BOND FORMATION.
                                                                                                                                                                                                                                                                                                                                        MEDLINE-99157562; PubMed=10027972;
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"Analysis of the Slya-controlled expression, subcellular localization
and pore-forming activity of a 34 kDa haemolysin (ClyA) from
Escherichia coli K-12.";
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Wai S.N., Lindmark B., Soederblom T., Takade A., Westermark M.,
Oscarsson J., Jass J., Richter-Dahlfors A., Mizunoe Y., Uhlin B.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
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STRAIN=KL2 / XL1-BLUE;
King C.H., Shinnick T.M.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
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MEDLINE=97061202; PubMed=8905232;
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                                                                                             haemolysin.";
Mol. Microbiol. 25:107-115(1997)
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regulator SlyA."
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3D-structure; Complete proteome; Cytolysis; Direct protein sequencing; Hemolysis; Toxin; Transmembrane.
INIT MST 0 0
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K -> R (in strain CH9802).
G -> A (in strain CH9802)
       EMBL; AE000216; AAC74266 1; ALT INIT.
EMBL; D90751; BAA36016.1; ALT_INIT.
EMBL; D90752; BAA36030.1; ALT_INIT.
EMBL; D90753; BAA36030.1; ALT_INIT.
EMBL; AP240780; AAL55667.1; -
EMBL; U12466; AAA92081.1; -
EMBL; U13410; -; NOT_ANNOTATED_CDS.
PDB; 1QQY; X-ray; A=1-302.
ECOGOR, EG13243; hlyE.
InterPro; IPR010356; HlyE.
Pfam; PF06109; HlyE; 1.
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X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).

X-RAY CRYSTALLOGRAPHY (2.0 AUGSTROMS).

X-RAY CRYSTALLOGRAPHY (2.0 AUGSTROMS).

X-RAY CRYSTALLOGRAPHY (2.0.4 Shea): X-ray crystal structure of Green J., Artymiuk P.J.; Edilman T.J., Artymiuk P.J.; Shea): X-ray crystal structure of X-C-11 100:265-276(2000).

C-11 100:265-276(2000).

C-11 100:265-276(2000).

C-12 FUNCTION: Toxin, which has some hemolytic activity towards mammalian cells. Acts by forming a pore-like structure upon context with mammalian cells.

C-12 FUNCTION: Toxin and oligomer. In periplasm, it is present as a monomer, while in outer membrane vesicles, it oligomerizes to form a pore structure that is active. Probably forms an octamer.

C-12 FUNCTION: During anaerobic growth. Weakly or not expressed in most strains. It is activated by slyA, while it is slienced by H. NS. Its expression is also regulated by CRP and FNR.

C-12 FUNCTION: During anaerobic growth. Weakly or not expressed in most strains. It is activated by slyA, while it is slienced by H. NS. Its expression is also regulated by CRP and FNR.

C-12 FUNCTION: During anaerobic growth. Weakly or not expressed in most strains. It is activated by slyA, while it is slienced by H. NS. Its expression is also regulated by CRP and FNR.

C-13 FUNCTION: During anaerobic growth. Weakly or not expressed in most strains are oligomerization. In outer membrane vesicles, the redox status prevents formation of the disulfide vesicles, the redox membrane. Membrane vesicles. Membrane. Membrane. Membrane. Membrane. Membrane. Membrane. Membrane. Membrane. Membrane. Membrane. Membrane. Membrane. Membrane. Membrane. Membrane. Membrane. Membrane. Membrane. Membrane. Membrane. Membrane. Membrane. Membrane. Membrane. Membrane. Membrane. Membrane. Membrane. Membrane. Membrane. Membrane. Membrane. Membrane. Membrane. Membrane. Membrane. Membrane. Membrane. Membrane. Membrane. Membrane. Membrane. Membrane. Membrane. Membrane. Membrane. Membrane. Membr
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     assembly of pore-forming oligomers of the
                                                                                                                                                                                                                                                                                                                                                                               Westermark M., Oscarsson J., Mizunoe Y., Urbonaviciene J., Uhlin B.E., "Silencing and activation of ClyA cytotoxin expression in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22053220; PubMed=12057949;
Spory A., Bosserhoff A., von Rhein C., Goebel W., Ludwig A.;
"Differential regulation of multiple proteins of Escherichia coli and
Salmonella enterica serovar Typhimurium by the transcriptional
                                                                                                       SPECTROMETRY, DISULFIDE BOND, AND MUTAGENESIS OF TYR-96; ASN-156;
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MEDLINB-22829856; PubMed=12949101;
Wai S.N., Westermark M., Oscarsson J., Jass J., Maier E., Benz
Uhlin B.E.;
                                                                                                                          TYR-164 AND ARG-260.
MEDLINE=20576278; PubMed=11006277; DOI=10.1074/jbc.M005420200; Atkins A., Wyborn N.R., Wallace A.J., Stillman T.J., Black L.K. Fielding A.B., Hisakado M., Artymiuk P.J., Green J.; Structure-function relationships of a novel bacterial toxin, hemolysin E. The role of alpha G.";
J. Biol. Chem. 275:41150-41155 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Characterization of dominantly negative mutant ClyA cytotoxin
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EMBL; X98615; CAA67204.1; ALT_INIT.
EMBL; AJ001829; CAA05035.1; --
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J. Bacteriol. 185:5491-5499(2003).
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       "Vesicle-mediated export and asse
enterobacterial clyA cytotoxin.";
Cell 115:25-35(2003).
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activity.
Y->C: Strongly reduces cytotoxic
activity.
Missing: In PWWK16; retained in cytosol.
Loss of function.
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                                                  Missing. ...
Loss of function.
AG-SDD: Abolishes cytotoxic activity.
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Pred. No. 4.7e-83;
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(Rel. 44, Last annotation update)
(Cytotoxin clyA) (Silent hemolysin sheA).
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                                                                                                                        activity.
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ID HLYE E8

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DT 29-MAR

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DE Hemoly
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STRAIN-0157:H7 (RIMD 0509952 / EHBC;

STRAIN-0157:H7 (RIMD 0509952 / EHBC;

MEDLINE=21156231; PubMed=11258796;

A Hayashi T., Makino K., Ohhishi M., Kurokawa K., Ishii K., Yokoyama K.,

Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

Ida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,

Ruhara S., Shiba T., Hattorii M., Shinagawa H.;

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DNA Res. 8:11-22[2001].

I. DNA Res. 8:11-22[2001].

I. PUNCTION: Toxin, which has some hemolytic activity towards mammalian cells. Acts by forming a pore-like structure upon contact with mammalian cells (By similarity).

Contact with mammalian cells (By similarity).

Contact with mammalian cells (By similarity).

Contact with mammalian cells (By similarity).

A pore structure that is active. Probably forms an octamer (By alminatory).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                              STRAIN=O157:H7 / EHEC;
MEDLINE=20322319; PubMed=10865950; DOI=10.1016/S0923-2508(00)00143-1;
del Castillo F.J., Moreno F., del Castillo I.;
"Characterization of the genes encoding the SheA haemolysin in
Becherichia coli 0157:H7 and Shigella flexneri 2a.";
Res. Microbiol. 151:229-230(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTM: In periplasm, it forms a disulfide bond, which prevents the oligomerization. In outer membrane vesicles, the redox status prevents formation of the disulfide bond, leading to oligomerization and pore formation (By similarity). SIMILARITY: Belongs to the hemolysin E family.
                                                                                                                                                                                                                                                                                                                                             STRAIN=C15:H7 (EDL933 / ATCC 700927 / EHEC;
MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
MADLINE=21074935; PubMed=111; Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
Name=hlyE; Synonyms=clyA, sheA; OrderedLocusNames=z1944, ECs1677;
Escherichia coli O157:H7.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            In monomeric form (By similarity). F261E29E1DE5FC87 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity).
SUBCELLULAR LOCATION: Secreted. Exported from the cell by omembrane vesicles. Also found in the periplasmic space (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hemolysis; Toxin; Transmembrane. By similarity.
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EMBL, AE005335; AAG5603.1; ALT_INIT.
EMBL, AP002055; BAB35100.1; ALT_INIT.
PIR; E85696; E85696.
PIR; E90838; E90838.
                                                                    Enterobacteriaceae; Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome; Cytolysis; INIT MET 0 0 B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 409:529-533(2001).
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SEQUENCE FROM N.A.
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                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                               NCBI_TaxID=83334;
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DISULFID
SEQUENCE
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33585 MW;

302 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 KLTTELAAIGEIKTETETTRFYVDYDDLMLSLLKEAANKMINTCNEYQKRHGKKTLFEVP 300
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                                                                                                                             2 TGIFAEQTVEVVKSAIETADGALDFYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVL
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Reingold J., Starr N., Maurer J., Lee M.D.;
"Identification of a new Escherichia coli She haemolysin homolog in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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90.1%; Score 1361; DB 1; Length 302; 88.7%; Pred. No. 4.6e-82; ive 20; Mismatches 14; Indels
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Vet. Microbiol. 66:125-134(1999).

HEND, ARGO2225, AAD28079.1; -.

HSSP, P77335; 1QOY.

INTERPRO, IDRO10356; HIVE.

PÉEM; PF06109; HIVE.

SEQUENCE 300 AA; 33555 MW; 6580B66C44A7B4BC CRC64;
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Last annotation update)
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   Query Match
Best Local Similarity 88.7
Matches 268; Conservative
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Matches 213; Conserv
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Escherichia coli.
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EV 302
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(See http://www.isb-sib.ch/announce/
    entities requires a license agreement ( or send an email to license@isb-sib.ch)
                                                                                                         EMBL; AF200955; AAF13995.1; -
EMBL; AJ238955; CAB65415.1; ALT INIT.
EMBL; AE015143; -; NOT ANNOTATED_CDS.
EMBL; AE016982; -; NOT ANNOTATED_CDS.
HSSP; P77335; 1QOY.
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InterPro; IPR010356; HlyB.
Pfam; PF06109; HlyB; 1.
Complete proteome.
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InterPro; IPR010356; HlyE.
Pfam; PF06109; HlyE; 1.
SEQUENCE 113 AA; 12879 N
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OrderedLocusNames=c1630;
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ID HLEL_ECOL6
AC Q8FIZ7;
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SEQUENCE 5250274 / ATCC 700930 / Serotype 2a;

MEDINE=22550274; PubMed=12704152;

MEDINE=25590274; PubMed=12704152;

Med J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,

Med J., Goldberg M.B., Purland S.M., Runyen-Janecky L.J., Zhou S.,

A chartz D.C., Blatner F.R.;

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"Infect. Immun. 71:2775-2786(2003).

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                         VAGPFGLIISYSIAAGVIEGKLIPELNDRLKAVQNFFTSLSVTVKQANKDIDAAKLKLAT 245
                                                               STRAIN=301 / Serotype 2a, MEDLINE=22272406; PubMed=12384590; Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H., Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J., Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S., Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
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MEDLINE=2032319; PubMed=10865950; DOI=10.1016/S0923-2508(00)00143-1;
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Bescherichia coli 0157:H7 and Shigella flexmeri 2a.";
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Enterobacteriaceae; Shigella.
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                                                                                                                                                                                                                                    244 EISVIGDLKTETETTRFFVDYDDLMLKQLQDSAIKLILSCNEYQKRHGKK 293
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OrderedLocusNames=SF1171, S1259;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SETATN=06.HI / CFT073 / ATCC 700928 / UPEC;

STRANN=06.HI / CFT073 / DIMEC;

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To uropathogenic Escherichia coll.";

Proc. Natl. Acad. Sci. U.S.A.

C. -I - STMILARITY: Belongs to the hemolysin E family.

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Enterobacteriaceae; Escherichia.
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                                                                 Query Match
34.0%; Score 513; DB 1; Length 113;
Best Local Similarity 90.1%; Pred. No. 1.7e-26;
Matches 100; Conservative 5; Mismatches 6; Indels
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25.3%; Score 382; DB 1; Length 93
Best Local Similarity 79.6%; Pred. No. 6.2e-18;
Matches 74; Conservative 11; Mismatches 8; Indels
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12879 MW; C328908D14C5C4EB CRC64;
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29-MAR-2004 (Rel. 43, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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348 IVMTSNIASQYLLTSDDFVQIDDQXIQAELNQTFRPEFLNRIDNÍVY--FNALSVQTÍ-- 403
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11 (1]
2 SEQUENCE FROM N.A.
2 STARIN-ATCC 25416;
2 STRAIN-ATCC 25416;
3 MEDLINE-97148974; PubMed=8995799;
3 MEDLINE-97148974; PubMed=8995799;
3 MEDLINE-97148974; PubMed=8995799;
4 Talph M., Cupta R.S.;
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5 BMBL; U51225; Fincteoride binding; IEA.
5 GO; GO:000165; Fincteoride binding; IEA.
6 GO; GO:000165; Fincteoride binding; IEA.
7 InterPro; IPR001270; Chaprnin_clpA/B.
7 RINTE; PR00300; CLPPROTEASEA.
7 RAPINTS; PR00300; CLPPROTEASEA.
7 RAP-binding.
7 MP-binding.
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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24.3%; Pred. No. 1.5;
tive 47; Mismatches 115; Indels
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Name=PY01185;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=17XNL;
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                                    211 INDRLKAVQNFFTSLSVTVKQANKDIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDLM 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          274 EKVEILSSEVVRLKGLLDSTAESEESKNRETEELV--KNLESEVSVLKGKLEEARIIEER 331
                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54
                                                                  332 LAETEKLIEELKSEVADAKKAESEARQLFEEWKHKAGLLEMELEA-VTLSDKFKGESLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SQEASVLVGDIKVLLMDSQDKYFEATQTVYEW---CGVVTQLLSAYILLFDEY-NEKKAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 AQKDILIRILDDGVNKLNEAQKSLLGSSQSFNNASGKLLALD---SQLTNDFSEKSSYF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----QSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGV-IEG-----KLIPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            439 ASQQEVFGLQTTIDVLRNKLEAAEEAASEA-----LINNEKAANVKIEGLTEENVKLISE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QTVEVVKSAIETADGALD-----FYNKYLDQVIPWKTFDETIK-----ELSRFKQEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=2095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.0%; Score 136.5; DB 2; Length 895; 22.4%; Pred. No. 1.6; ative 67; Mismatches 121; Indels 79
                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Similar to an Arabidopsis thialiana chromosome BAC genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Haing Y.C., Chow T., Chen C., Wu H., Chu M., Chao Y., Liu Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
Babli, APO1111; BAA90502.1; -.
Gramene; Q9LIW7; -.
SEQUENCE 895 AA; 100520 MW; BA4F7EFDF70FFAA3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         258 ETTR----FYVDYDDLMLSLLKGAAKKMINTCNEYQQR-HGKKT 296
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Last sequence update)
Last annotation update)
                                                                                                                                                    LSLLKGAAKKMINTCNEYQQRHGKKTLLEVPDI 303
                                                                                                                                                                                   61 LSLLKEAAQKMINTCNEYQKRHGKKTLFEIPEV 93
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01-0CT-2000 (TrEMBLrel. 15, Last seq
01-0CT-2002 (TrEMBLrel. 22, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 22.4%
nes 77; Conservative
                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                        Q9LIW7;
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P71497
ID P7144
AC P7144
DT 01-E
DT 01-E
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SWART; SM00382; AAA; 2.
PROSITE; PS00871; CLAB 2; 1.
ATP-binding; Complete proteome; Protease.
SEQUENCE 713 AA; 80782 MW; 1B5D204A9E29BE50 CRC64;
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SEQUENCE
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CAE77235;
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                                                                                                                                                                                                                                                                                                       54 --YSQEASVLVGDIKVLLMDSQDKYPEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASA 111
                                                                                                                                                                                                                                                                                                                                                        112 QKDILIRILDDGVNKLNEAQKSLLGSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVD 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Westberg J., Persson A., Holmberg A., Goesmann A., Lundeberg J., Johansson K.-E., Pettersson B., Uhlen M.; "The genome sequence of Mycoplasma mycoides subsp. mycoides SC type strain PG1T, the causative agent of contagious bovine pleuropneumonia
                                                                                                                                                                                                                                                                                                                                  ----ILOADKSEOKINT
                                                                                                                                                                                                                                                                                                                                                                                                             172 RIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNDRLKAVQNFFTSLSVTVKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                232 ANKDIDAAKLKLAT-------EIAAIGEIKTETETTRFYVDYDDLMLS
                            "Genome sequence and comparative analysis of the model rodent malaria
                                                                                                                                                                                                                              Gaps
 S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
                                                                                                                                                                                                                            96; Indels 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=clpB; OrderedLocusNames=MSC 0613;
Name=clpB; OrderedLocusNames=MSC 0613;
Mycoplasma mycoides (subsp. mycoldes SC).
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                          paratice Plasmodium yoelli yoelii.";
Nature 419:512-519(2002).
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which preliminary data.
EMBL, AABLO1000312; EAA20475.1; -.
                                                                                                                                                                                                  DB 2; Length 2723;
                                                                                                                        Interpro; IPR011561; Pox II rel.
InterPro; IPR006499; ReticulocyteBP.
Prodom; PD014111; Pox II rel; I.
TIGRRAMS; TIGR01612; Z35KDa-fam; I.
SEQUENCE 2723 AA; 320451 MW; 08CD9C2EF7672ED2 CRC64;
                                                                                                                                                                                                                                                      11 EVVKSAIETADGALDFYNKYLDQVIPWKTFDETIKELSRFKQE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
ATP dependant procease Clp8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              713 AA
                                                                                                                                                                                                   / Match 8.6%; Score 130; DB Local Similarity 19.7%; Pred. No. 16; nes 62; Conservative 54; Mismatches
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GENBL; BX842644; CAE77235.1; --

GO, GO:0008233; F:peptidase activity; IBA.

InterPro; IPR003593; AAA_AIPase.

InterPro; IPR001359; AAA_AIPase centr.

InterPro; IPR001270; Chaprnin_CIpA/B.

PEam; PF000004; AAA; 2.

PRINTS; PR00300; CLPPROTEASEA.
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LIKPTIENLISSFN 1713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLKGAAKKMINTCN 286
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Q6MT03
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13-APR-2004 (TrEMBLrel. 27, Last annotation update)
ATP dependant protease ClpB.
CLPB OR MSC_0613.
Mycoplasma mycoides (subsp. mycoides SC).
Bacteria: Firmicutes; Mollicutes; Mycoplasma.
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                                                                           -----ASGKLLALDSQLTNDFSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYS 197
                                                                                                                                                                  IAAGVIEGKLIPELNDRLKAVQNFFTSLSVTVKQANKDIDAAKLKL--ATEIAAIGEIKT 255
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                                                                                                                                                                                              ITGDFSKGFSDLVNFKMKLPNRGDGNLETPPPAYYFLPFYIDQIKSWSSPWNSFENLGQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=TT01;
MEDLINE=2957627; PubMed=14528314;
MEDLINE=2957627; PubMed=14528314;
Duchaud E., Rusniok C., Frangeul L., Buchrieser C., Givaudan A., Taourit S., Bocs S., Boursaux-Eude C., Chandler M., Charles J.-F., Dassa E., Derose R., Derzelle S., Freyssinet G., Gaudriault S., Medigue C., Lanois A., Powell K., Siguier P., Vincert R., Wingate V., Zourne M., Glaser P., Boemare N., Danchin A., Kunst F.;
"The genome sequence of the entomopathogenic bacterium Photorhabdus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---DETIKELSRFKQEYSQEASVLVGDIKVL------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Photorhabdus luminescens (subsp. laumondii).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.4%; Score 126.5; DB 2; Length 577;
19.0%; Pred. No. 4.2;
tive 55; Mismatches 132; Indels 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        280 DYKFAVBSIPTDYLECPLCGTLHDNSLPNRALLLSEKDSLLNEA---
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SEQUENCE 577 AA; 65287 MW; B7F86EE4B34BEDE1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 26, Created)
(TrEMBLrel. 26, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                    577 AA
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EMBL; BX571865; CAE14130.1; -.
PhotoList; plu1837; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similar to putative phage protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OrderedLocusNames=plu1837;
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Best Local Similarity 19.0<sup>†</sup>
Matches 80, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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429 SKLLANIEALGSTGINLSKVKSPTDÝKQLLGGGAAEAARGLLAYQLSVLQQIHGAKTCVV 488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Almark U.C.M., Frank A.C., Karlberg B.O., Legault B.-A., Ardell D.H., Canbaeck B., Eriksson A.-S., Naeslund A.K., Handley S.A., Huvet M., La Scola B., Holmberg M., Andersson S.G.E.;
La Scola B., Holmberg M., Andersson S.G.E.;
In Scola B., Holmberg M., Andersson S.G.E.;
In Encouse-borne human pathogen Bartonnella quintana is a genomic derivative of the zoonotic agent Bartonella henselae.";
Proc. Natl. Acad. Sci. U.S.A. 101:9716-9721(2004).
EMBL; BX897700; CAF26028.1;
InterPro; IPR002017; Spectrin.
InterPro; IPR010989; t-snare.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bartonella quintana (Rochalimaea quintana).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bartonellaceae; Bartonella.
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SEQUENCE 1521 AA; 169742 MW; 12CC93BCB2C97920 CRC64;
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Last annotation update)
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Sordariomycetidae; Sordariales; Sordariaceae; Neurospora
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Best Local (
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Q7REL0
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                                                                                                                                                                                                                                                                                                                     "Genome sequence and comparative analysis of the model rodent malaria parasite Plasmodium yoelii yoelii.";
Nature 419:512-519(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 GALDFYNKYLDQVIPWKTFDETIKELSRFKOEYSQ---EASVLVGDIKVLLMDSQDKYFE
                                                                                                                                                                                             carlton J.M., Angluoli S.V., Suh B.B., Kooij T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.B., Selengut J.D., Koo H.L., Peterson J.D., Pop M., Kosack D.S., Shunway M.F., Bidwell S.L., Peterson J.J., van Aken S.B., Riedmuller S.B., Feldblyum T.V., Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M., Florens L., Yates F.R. III, Raine J.D., Sinden R.B., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.M., Vaidya A.B., Van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67;
                                                                                                                                                                                                                                                                                                                                                             -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----EIAAIGEIKTETETTRFYVDYDDLMLSLLKGAAKKMINTCN 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.2%; Score 124.5; DB 2; Length 1825;
21.1%; Pred. No. 23;
Ive 56; Mismatches 105; Indels 67;
                                                                                                                         Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
NCBL_TaxID=73239;
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InterPro; IPR006499; ReticulocyteBP.
TIGRFAMB; TIGR01612; 235kDa-fam; 1.
SEQUENCE 1825 AA; 213817 MW; 2956DB1596385940 CRC64;
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Last annotation update)
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Last annotation update)
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                              PRT; 1825 AA
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                                                                                                                Plasmodium yoelii yoelii
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                             PRELIMINARY;
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Name=NCU00658.1;
                                                                                                                                                                                                                                                                                                                                                                                         preliminary data.
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                                                                                                                                                                  SECUENCE FROM N.A.
                                                                                                                                                                                         PubMed=12368865;
                                                                                            Rhoptry protein.
                                                                                                                                                                                                                                                                                                                  Carucci D.J.;
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01-MAR-2004
01-MAR-2004
                                                                                                      Name=PY03534;
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ID Q7RIT2
AC Q7RIT2;
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54 YSQEASVLVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYI----LLFDEYNEKKA 109
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                                                                                                                                           Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
La Blkins T., Engels R., Mang S., Nielsen C.B., Butler J., Endrizzi M.,
Qui D., Ianaktev P., Pedersen D., Nielsen W., Scher A., Schulte U.,
Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
Kamal M., Kamwysselis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
Cogoni C., Macino G., Catchenide D., Li W., Pratt R.J., Osmani S.A.,
DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
Narden O., Plaann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
Parden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.,
I'll Geneme Sequence of the Filamentous Fungus Neurospora crassa.",
I'll The Genome Sequence shown here is derived from an
EMBLOGERARA PURCH P. S. Ebbel E. D. S. Ebbel E. D. S. Ebbel E. D. S. Ebbel E. D. S. Ebbel E. D. S. Ebbel E. D. S. Ebbel E. D. S. Ebbel E. D. S. Ebbel E. D. S. Ebbel E. D. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebbel E. S. Ebb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 QTVEVVKSAIETADGALDF-----YNKYLDQVIPWKTFDETIK-----ELSRFKQE
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Last annotation update)
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21.0%; Pred. No. 78;
ve 63; Mismatches 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF06818; Fez1; 1.
Pfam; PF02524; KLD; 5.
PROSITE; PS01039; SBP_BACTERIAL_3; UNKNOWN_1.
Hypochetical protein.
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EMBL; AABX01000001; EAA36562.1; -.
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InterPro; IPR003900; KID repeat.
InterPro; IPR001638; SBP_bac_3.
Pfam: PF06818; Fezl; 1.
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(TrEMBLrel: 26, I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21.0%;
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NCBI_TaxID=5141;
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Hypothetical protein.
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1679 DVNQYKKDYBIGIVEKINBIAKANKDKIBSTKESIEPIIQNIMSSFNSSDLEDIASNEAL 1738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : : | : : | :: | :: | 1.3 | 1.4 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 VGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAY--ILLFDEYNEKKASAQKDILIRI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 LDDGVN--KLNEAQKSLLGSSQSFNNASGKLLALDS--QLTNDFSEKSSYFQSQVDRIRK 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 EAYAGAAAGIVAGPFGLIISYSIAAGVIEGKL-----IPELNDRLKAVQNFFTSLSV 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              228 TVKQANKDIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDLMLSL-----L 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 OTVEVVKSAIET--ADGALDFYNKYLDQVIPWK-TFDETIKELSRFK---QEYSQEASVL
                                                                                                                                                                                                                                                                                                                                                                                                 Genome sequence and comparative analysis of the model rodent malaria
                                                                                                                                                 Carlton J.M., Angluoli S.V., Suh B.B., Kooij T.W., Pertea M., Silva J.C., Exmolaeva M.D., Allen J.E., Salengut J.D., Koo H.L., Shereson J.D., Koo H.L., Shallon S.J., Summay M.F., Bidwell S.L., Shallon S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V., Cho J.K., Quackenbush J., Sedegah M., Shoabla A., Cummings L.M., Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A., van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J., Carucci D.J.;
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Helicobacteraceae; Wolinella.
                                                                                                                                                                                                                                                                                                                                                                                                                          parasite Plasmodium yoelii yoelii.";
Nature 419:512-519(2002)
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBU whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.0%; Score 121; DB 2; Length 2664; 21.3%; Pred. No. 60; ative 67; Mismatches 140; Indels 56
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBL_TaxID=73239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2664 AA; 312670 MW; FDE72DB05743F4AB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             275 KGAAKKMINTCNEYQQRHG----KKTLLEVPDI 303
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InterPro; IPR006499; ReticulocyteBP.
TIGRFAMS; TIGR01612; 235kDa-fam; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         preliminary data.
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SEQUENCE FROM N.A.
STRAIN=DSMZ 1740;
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Matches 71, Conserv
                                                                               SEQUENCE FROM N.A.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     368 SLREQLGEGANEVLSLLQKSSQESSAFLL----EQEKWAKESTLVLFAKLKERFERLSEA 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131 ----QKSLLGSSQSFNN-----ASGKLLALDSQLTNDFSEKSSYFQSQV 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         424 FLTONKGALEGMALDFRGFWEEYATRWRESSELTQGTLLETNOOVRASFAELSEGVLAON 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DRIRKEAYAGAAAGIVAGPF-GLIISYSIAAGVIEG--KLIPELNDRLKAVQNFFTSLSV 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2
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22.9%; Pred. No. 16;
ve 54; Mismatches 122; Indels 103; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        316 EEVTSSTKEAQESLTQSSRWLQERIQ-----SDISLAQQHFTEHLGGLSTEFKALVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : :: || |: | || || || 484 SAMGEQIKAG-FEGMTQGALSGLMILAKALEGGIDGVKKSVSEMNQTL-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TVKQANKDIDAAKLKLATEIAAIGEIKTETTRFYVDYDDLMLSLLKGAAKKMINTCNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 531 ----AKETLOTLONHSOSOLGLLGESTTAIOTR------LLELEEGAOKSLKNLALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 VKSAIETADGALDFYNKYLDQV-----IPWKTFDETIKELSRFKQEYSQEASVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 EVVKSAIETADGALDFYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVLVGDIKVLLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71 DSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRILDDGVNKLNËA
MEDLINE=22882897; PubMed=14500908;
Baar C., Eppinger M., Raddatz G., Simon J., Lanz C., Klimmek O.,
Nandakumar R., Gross R., Rosinus A., Keller H., Jagtap P., Linke B.,
Meyer F., Lederer H., Schuster S.C.;
"Complete genome sequence and analysis of Wolinella succinogenes.";
Proc. Natl. Acad. Sci. U.S.A. 100:11690-11695 (2003).
EMBL; BX571659; CAE09993.1;
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Helicobacteraceae; Helicobacter.
NCBI_TaxID=32025;
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EMBL, AB017146; AAP77368-1; ---
Complete proteome; Hypothetical protein.
SEQUENCE 555 AA; 61077 MW; 1E2515BCB839A804 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                        61;
                                                                                                                                                                                                                                                                                                                                             DB 2; Length 693;
                                                                                                                                                                                                                                                                                                                                                                                                        124; Indels
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                                                                                                                                                                                                                                                                           693 AA; 77641 MW; CE57A1F23CFACCC2 CRC64;
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                      ch 8.0%; Score 120.5; 1 Similarity 21.3%; Pred. No. 13; 64; Conservative 52; Mismatches
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STRAIN=ATCC 51449 / 3B1;
MEDLINE=22709201; PubMed=12810954;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 22.9%
Matches 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OrderedLocusNames=HH0771;
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189 PFGLIISYSIAAGVIEGKLIPELNDRLKAVQNFFTSLSVTVKQANKDIDAAKLKLATEIA 248
                                                                                                                                                                                                      1178
                                                                                                                                                                                                                                                                                                                                                  316 RNWEEVVPEPIQSQL------NQKDEQIKDLTKQVNQIN---KDKVGIEQQFNT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----LINDFSEKSSYFQSQVDRIRKBAYAGAAAGIVAG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   268 DVYDTYFIVNVYSWS--DENSYD-KYFKFNYTR-----TGDTVSIDFDSKTEVF----MT 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84 YEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRILDDGVNKLNEAQKSLLGSSQSFNN 143
                             : | : : | : : | 1012 LIBEEKDDLEQDRADVSATKDDIAKKLNKITIECEDAKDEIAKLEQELEDEENKNKDLTN 1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DFYNKY-LDQVIPWKTFDBTIKELSRFKQBYSQEASVLVGDIKVLLMDSQDKYFBATQTV
                                                                                   82 TVYEW----CGVVTQLLSAYILLFDEYNEKKASAQKDILIRILDDGVNKLN-----E
                                                                                                          130 AQKSLIGSSQSF------NNASGKLLALDSQLTNDFSEKSSYFQSQVDRIRK
                                                                                                                                                                                       176 BAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNDRLKAVQNFFTSLSVTVKQANKD
                                                                                                                                                                                                                                                                       236 I------DAAKLK--LATEIAAIGEIKTETETTRFYVDYDDLML-----
      LMDSQDKYFEATQ
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Viruses: dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Lazarevic V., Duesterhoeft A., Soldo B., Hilbert H., Mauel
Karamata D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF020713; AAC13027.1; -.
PIR; T12818; T12818.
Hypothetical protein.
SEQUENCE 478 AA; 55050 MW; 6FF7495A957D4A4F CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                           1273 QKKLDDMTADNEKLKAKAKDLEAQLNEVQDNHEK 1306
                                                                                                                                                                                                                                                                                                                                                                                                            -----SLLKGAAKKMINTCNEYQQRHGK 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    478 AA.
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Pred. No. 16;
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01-OCT-2003 (TrEMBLrel. 25
Hypothetical protein yonD.
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Matches 58; Conserva
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064067;
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                                                                                                                                                                                                                                                                                                                                                            297
                                                                                                                                                                                                                                                                                                                LFGSFN-STKLTTTAQGVELISKATKDNVSAR-----EFADKEEVKKKWWGLQSNTSTWK 282
                                                                                                                                                                                                                                                                                                                                                                                   283 EYYDASNFALKGIQQSIRGYEYLLQDIGSGVKSLSIAKGNYKSYADILNA----GAKEL 337
                                                                               120
                                                                                                                                                214
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                                                                                                                                                                                                LTNDFSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNDR
                                                                                                                                                                                                                                                                               LKAVQNFFTSLSVT-----VKQANKDIDAAKLKLATEIAAIGEIK-----TETETTR
VKFTFNVKDGSLQKIKKELDSINKNSANELYALELKLHEQKMEHI-----QEYSKAYKDLQ
                                                              106 EKKASAQKDILIRILDDGVNKLNEAQK----SLLGSSQS---FNNASGKLLA--LDSQ
                                                                                                                                                                                                                         Gaps
                                         GDIKVLLMDS--------ODKYPEATQTVYEWCGVVTQLLSAYI--LLFDEYN
                                                                                                                                                                                                                                                                                                                                                            -----YDDLM------LSLLKGAAKKWINTCNEYQQRHGKKTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=HMI: IMSS;
MEDLINE=93295430; PubMed=8515774;
MEDLINE=93295430; Annsonetti P., Guillen N.;
Raymond-Denise A., Sansonetti P., Guillen N.;
"Identification and characterization of a myosin heavy chain gene (mhcA) from the human parasitic pathogen Entamoeba histolytica.";
Mol. Biochem. Parasitol. 59:123-131(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.7%; Score 117; DB 2; Length 2139;
19.0%; Pred. No. 85;
ive 47; Mismatches 114; Indels 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 2139;
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Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0003774; F:motor activity; IEA.
InterPro; IPR001609; Myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
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Bukaryota; Entamoebidae; Entamoeba.
NCBI_TaxID=5759;
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Pfam; PF00063; Myosin head; 1.
PRINTS; PR00193; MYOSINHEAVY.
SMART; SMOA42; MYSC; 1.
SEQUENCE: 2139 AA; 245225 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, L03534; AAB48065.1; -.
PIR, T18296; T18296.
HSSP; P08799; 1MND.
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01-NOV-1996 (TERMBLEEL: 01,
01-JUL-1997 (TERMBLEEL: 04,
01-OCT--2003 (TERMBLEEL: 25,
Myosin heavy chain.
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IK 339
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Q9X360
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KATAINLE 1980 44033; PubMed-9384377; DOI=10.1038/36786;

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RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA BOTTIS R., Bourster L., Brans A., Bertenell S.C., Bron S.,

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RA Chin S.Y., Glaser P., Goffeau A., Galizzi A., Galleron N.,

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RA Ghiseppi G., Guy B.J., Haga K., Haicch J., Harwood C.R., Henaut A.,

Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M.,

Jones L.-M., Joris B., Koetter P., Kontingstein G., Krogh S.,

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RA Medigue C., Medina N., Mellado R.P., Mazuno M., Moestl D., Nakai S.,

RA Persocht A.M., Persecan B., Pujic P., Purnelle B., Rapoport G.,

Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,

Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,

Scoffone F., Sadaie Y., Stanian S., Purnelle B., Rapoport G.,

Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Serror P.,

Romoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F.,

Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H., Yamane K.,

Wastranedger T., Wandens S., Wipat A., Yamamoto M., Yamane K.,

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Wastranedger T., Wandens P., Wandenbol M., Yamane K.,

Yoshikawa H., Danchin A.,

Phylic P., Parror V., Wohlyama S., Vandenbol M., Yamane K.,

Topnoni A., Tosato V., Wohlyama S., Vandenbol M., Yamane K.,

Wasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E.,

H., H., H., H., H., Wander B., Wandenbol M., Wanders P.,

Wohlikawa H., Danchin A.,

Robikawa H., Panchin A.,

Robikawa H., Panchin A.,

Robikawa H., Panchin A.,

Robikawa H., Panchin A.,

Robikawa H., Panchin A.,

Robikawa H., Panch
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                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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                                                                                                                  01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                             478 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.7%; Score 116.5; I 23.0%; Pred. No. 16; rative 39; Mismatches
                                                                                                                                                                                                                                           Name=yonD; OrderedLocusNames=BSU21130;
                                                          PRT;
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EMBL; 299115; CAB14031.1; -.
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                                                          PRELIMINARY;
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SEQUENCE 478 AA;
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                                                                                                                                                                                                                                                                 Bacilius subtilis.
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                                                                                                                                                                                                               YonD protein.
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01-JAN-1998
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                                                                                                                                                                                                                                                                                                                    MEDLINE-22061436; PubMed-12004073;
Read T.D., Salzberg S.L., Pop M., Shumway M., Umayam L., Jiang L.,
Holtzapple E., Busch J.D., Smith K.L., Schupp J.M., Solomon D.,
Keim P., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.7%; Score 116.5; DB 2; Length (Local Similarity 19.0%; Pred. No. 22; Length (es 59; Conservative 65; Mismatches 106; Indels
                                                                                                                                                                                                        Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               652 AA; 76210 MW; 723F5FBE03516355 CRC64;
                                         05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
652 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Composition anthracis.";
Science 296:2028-2031(2002).
BMBL, AE011190, AAM26077.1; -.
InterPro; IPR011199; SLH.
InterPro; IPR0110989; t-snare.
InterPro; IPR0110989; t-snare.
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PRT;
                                                                                                                                                                 Bacillus anthracis str. A2012.
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Q9X360;
01-NOV-1999 (TrEMBLrel. 12, 0
01-NOV-1999 (TrEMBLrel. 12, 1
01-OCT-2004 (TrEMBLrel. 28, 1
                                                                                                           S-layer protein, (PXO1-90).
Name=BXA0124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PXO1-90 (S-layer protein,).
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  285 CNEYQQRHGKK 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AKEINKKLAEK 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00395; SLH;
                                                                                                                                                                                                                                 NCBI_TaxID=191218;
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                            05-JUL-2004
05-JUL-2004
                                                                                                                                                                                          Plasmid pXO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8444¥6
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STRAIN=Ames 0581;
Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B., wilson M., Stanley S., Decker S., Read T.D., Salzberg S., Fraser C.M.; Bacillus anthracis comparative genomics.";
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus,
                 Bacillus cereus group; Bacillus anthracis
NCBI_TaxID=261594;
                                                                                                                                        submitted (MAY-2004) to the EMBL; AE017336; AAT28865.2; Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                       59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              496 AKEINKKLAEK 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmodium yoelii yoelii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2004 (TrEMBLrel
                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI TaxID=73239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2004
01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           171
                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                         Local
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Q7RM79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      354 IAESKELAKKKAELNTKLVELFKVQEALNKKSGQYLYYINKLDNELRELADKYKNSDNKI 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNDRLKAVQNFFTSLSVTVK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DVINOKIDE---FDKINSQRKDLERMLEELNQKLSQLKQQSPQLQDLKNKLKESQSRLLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79 ATQ------TVYEWCGVVTQLLSAYILLFDEYNE--KKASAQKDILIRILDDGVNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DFYNKYLDQVI PWKTFDETIKELSRFKQEYSQEASVL-----VGDIKVLLMDSQDKYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------BLE
                                                                                                                                                                                                                                                                                STRAIN=Ames / isolate 0581; PLASMID=DXO1;
Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B. Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81; Gaps
                                                                                                                  ATRAINESTED PLASMIDE virulence plasmid PX01; MEDLINE = 99445483; PubMed=10515943; Okinhaka R.T., Cloud K., Hampton O., Hoffmaster A.R., Hill K.K., Keim P., Kochler T.M., Lamke G., Kumano S., Mahillon J., Manter D., Martinez Y., Ricke D., Svensson R., Jackson P.J.; Sequence and organization of pX01, the large Bacillus anthracis plasmid harboring the anthrax toxin genes."; Bacteriol. 181:6509-6515(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                    virulence plasmid PX01, and Plasmid pX01.
a; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                  "Bacillus anthracis comparative genomics.";
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AR065404; ARD32394.1; -.
EMBL, AR017336; ART28865.2; -.
PIR; B59102; B59102.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              723F5FBE03516355 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT28865 PRELIMINARY; PRT; 652 AA.
AAT28865;
01-JUN-2004 (TrEMBLrel. 27, Created)
01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
51 ayer protein, (PXOI-90).
GBAA PXOI 0124.
Bacillus anthracis str. Ames 0581.
Plasmid pXOI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 116.5; I
; Pred. No. 22;
65; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGR, GBAA_DXO1_0124; -.
INCEPEVO.; PEROBIL19; SLH.
PEROS15; SLH; 3.
PROSITE; PS01072; SLH_DOMAIN; UNKNOWN_1.
       OrderedLocusNames=GBAA_pXO1_0124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76210 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                652 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                       SEQUENCE FROM N.A.
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AAT28865
ID AAT2
AC AAT2
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DT 01-J
DT C1-J
DT CBAA
CS Baci
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354 IAESKELAKKKAELNTKLVELFKVQEALNKKSGQYLYYINKLDNELRELADKYKNSDNKI 413
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                                                                                                                                                                                                                                                                                                                                                                                                            294 INKKDSNRIELNSEIKKINDRKAELLSLIMELIKQQSEFDKKIKNEKDELNKKREDLINR 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 LNEAQK----SILGSSQSFNNASGKLLALDSQLTNDFSEKSSYFQ---SQV 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNDRLKAVQNFFTSLSVTVK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   414 SRLKNH------ELE 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QANKDIDAAKLKLAT-EIAAIGEIKTETETTRFYVDYDDL-----MLSLLKGAAKKMINT 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genome sequence and comparative analysis of the model rodent malaria parasite Plasmodium yoelii yoelii.";
Nature 419:512-519(2002).
-!- CAUTION: The sequence shown here is derived from an
                                                                                                                                                                                                      25 DFYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVL-----VGDIKVLLMDSQDKYFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L., Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L., Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V., Plorens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Valdya A.B., van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Carucci D.J.; Raberg S.L., Gardner M.J., Gardner M.J.,
                                                              7.7%; Score 116.5; DB 2; Length 652; 19.0%; Pred. No. 22; tive 65; Mismatches 106; Indels 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
652 AA; 76210 MW; 723F5FBE03516355 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
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Name=PY02306;
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Pfam; PF00015; MCPsignal; 1.
PRINTS; PR00266; CHEWTRNSDUCR.
SMART; SM00304; HAMP; 1.
SMART; SM00283; MA, 1.
                                                                                                                                                             66; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=PCA / ATCC 51573;
PubMed=14671304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
  Pfam; PF00672; HAMP; 1.
                                                                                                                                                  Similarity
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Best Local S
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Best Local
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                                                                                                                                                                                                                                                                                                                                                     226
                                                                                                                                                                                                                                                                                                                                                                              257 KPGDAENA------LEFYKKGSNKENKLIEEVNFFKPQKGYAEEKRISTFSDQMF 305
                                                                                                                                                                                                                                                                                                                                                                                                         277
                                                                                                                                                                                                                                                                                               124 VNKLNEAQKSLLGSSQSFNNASGKLLALDSQLTND----FSEKSSYF----QSQVDRIR 174
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                                                                                                                                                                                                                                           87 CGVVTQLLSAYILLFDEYNEKKASAQKD-----GVTLTRILDD-----G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FRUM N.A.
STRAINBECA / ATCC 51573;
PubMed=14671304; DOI=10.1126/science.1088727;
PubMed=14671304; DOI=10.1126/science.1088727;
Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,
Heidelberg J.F., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J.,
Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,
Davidson T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.
Weidman J.F., Khouri H.M., Feldblyum T.V., Utterback T.R.,
Weidman J.F., Lovley D.R., Fraser C.M.;
                                                                                                                                                                                      27 YNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVLVGDIKVLLMDSQDKYFEATQTVYEW
                                                                                                                                                                                                        KEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELN------DRLKAVQNFFTSLS
                                                                                                                                                                                                                                                                                                                                                                                                         227 VTVKQANK-----DIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDLMLSLLKGA
                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                             97;
                                                                                                                                    DB 2; Length 779;
                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            366 VKASLKYKKENIIKNNLNENLLCGRVKVHWFPKFWKRIIMKIPD 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                            278 AKKMI-----NTCNE-----YQQRHGKKTLLEVPD 302
                                                                            Pfam; PF01926; MMR HSR1; 1.
TIGRFAMs; TIGR00650; MG442; 1.
SEQUENCE 779 AA; 92336 MW; 7F51893C396B0B52 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Methyl-accepting chemotaxis protein.
Name-hylB; ORFNames-GSU1374;
                                                                                                                                                            126;
                                                                                                                                 7.7%; Score 116.5;
10.3%; Pred. No. 28;
ve 51; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003660; HAMP. __
InterPro; IPR004090; Me chemotaxis.
InterPro; IPR005629; Sug_transporter.
InterPro; IPR010989; t-snare.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR004089; Chmtaxis_transd
                          EMBL; AABL01000631; EAA21743.1; -. 600, GO:0005525; F:GTP binding; IEA. InterPro; IPR005289; GTP-binding. InterPro; IPR002917; WMR HSRI
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                                                                                                                              Query Match 7.7%;
Best Local Similarity 20.3%;
Matches 70; Conservative 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135 LSAEDABALTAFTVSELYPAIDPVSAKFSSLVDDQLKIAKQEYDHSSGLYRASRTISLVA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         195 IIVGVLIÄGTÄGLLITRSITGPLÄEGVEVANRLAAGDLTVEVRAGGRDETGQLMAÄMGNM 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                    79 ATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRILDDGVNKLNEAQKSLLGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 TADGALDFYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVLVGDIKVLLMDSQDKYFE
                                                                                                                                                                                                                                                                                                                                           36 TANNGLD--TVYRDRVLP-----LKDLKIIADMY----AVNIVDVSHKVRNGNITWTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 GAAAGIVAGPFGLIISYSIAAGVIEGKLI--------PELNDRLKAVQNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 TADGALDFYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVLVGDIKVLLMDSQDKYFE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C., Heidelberg J.F., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J., Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S., Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J., Davidsen T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A. Weidman J., Khouri H.M., Feldblyum T.V., Utterback T.R., Wan Aken S.E., Lovley D.R., Fraser C.M.; "Genome of Geobacter sulfurreducens: metal reduction in subsurface
                                                                                                                                                                                                                                       Gaps
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Bacteria, Proteobacteria, Deltaproteobacteria, Desulfuromonadales,
Geobacteraceae, Geobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              222 FTSL-----SVTVKQANKDIDAAKLKLAT---EIAA-IGEIKTETE 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        255 VTSLRHLIABAISISHGIASASNQLHATSBQIATGSBEVASQVGAVATASE 305
                                                                                                                                                                                                                                       72;
                                                                                                                                                                     Length 541;
                                                                                                                                                                  7.7%; Score 116; DB 2; Length 54
22.7%; Pred. No. 19;
tive 42; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42; Mismatches 111; Indels
PROSITE; PS50111; CHEMOTAXIS_TRANSDUC_2; 1.
PROSITE; PS50885; HAMP; 1.
PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN 1.
SEQUENCE 541 AA; 57093 WW; 3C9BEDAEAP7C3812 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-WAR-2004 (TrEMBLrel. 27, Created)
02-WAR-2004 (TrEMBLrel. 27, Last seq
02-WAR-2004 (TrEMBLrel. 27, Last ann
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HYLB OR GSU1374.
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TIGR; GSU1374; -.
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7;

62; Gaps

88; Indels

45; Mismatches

us-09-993-292b-24.rup

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49; Conservative
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792 LSQA 795
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792 LSQA 795
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Best Local &
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HLY1_ECOLI
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  Matches
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                                                                                                                                                                                                                                                  79 ATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRILDDGVNKLNEAQKSLLGSS 138
                                                                                                                        ----- 179
                                                                                                                                                         --PELNDRLKAVQNF 221
                                                                       83 GRKSVEEAKKTIAEKLOAYLATNLAEEEKKHLEEAKPLIKVAD------ATLERLASI 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Read T.D., Peterson S.N., Tourasse, N.J., Baillie L.W., Paulsen I.T., Relon K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R., Relson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R., Rolonay J.F., Okstad O.A., Helgason E., Rilstone J., Wu M., Kolonay J.F., Beanan M.J., Dodson R.J., Brinkec L.M., Gwinn M.L., DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H., Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D., Rannan D.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F., Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C., Alzhomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolstoe A.-B., Fraser C.M.; Koehler T.M., Closely related bacteria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Ames / isolate 0581;
Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K., Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R., Richhardson P., Rubin B., Tice H.;
Submitted (JAN.2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AE017025; AAP24404.1; --
EMBL; AE017334; AAT5269.1; --
EMBL; AB017225; AAT52691.1; --
EMBL; BA0374; --
                                                                                                                                                                                                                                                                                                                                                 FTSL------SVTVKQANKDIDAAKLKLAT---EIAA-IGEIKTETE 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=Ames / isolate Porton;
MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus anthracis.
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=1392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Bacillus anthracis comparative genomics.";
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OrderedLocusNames=BA0374, BAS0360; ORFNames=GBAA0374;
                                                                                                                          OSFNNASGKLLALDSQLTNDFSEKSSYFQSQVD---RIRKEAY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q81298 PRELIMINARY; PRT; 941 AA.
Q81228; Q61440; Q6KXVO;
O1-UJN-2003 (TrEMBLrel. 24, Created)
O1-UJN-2003 (TrEMBLrel. 24, Last sequence update)
O1-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Conserved domain protein.
                                                                                                                                                                                                                         180 GAAAGIVAGPFGLIISYSIAAGVIEGKLI------
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Pred. No. 37;
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20.1%;
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                                                                                                                          139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 176 EAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELND----RLKAVQNFF----TSLSVT 228
                                   IKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRILDDGV 124
                                                                                                                                                                                                         125 NKLNEAQKSLLGSSQSFNNASGKLLALDSQ-----LTNDFSEKSSYFQSQVDRIRK 175
                                                                                                                                                                                                                                       176 BAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELND---RLKAVQNFF----TSLSVT 228
                                                                                                                                                                                                                                                                                                                                           ::| | ::: | | ::: | 32 KLFAMPNYGSAMSPFYTVLALWVGALLMVSLLTVEVHEEGANYKSHEIYFGRLLTFLTMG 791
  64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B., Wilson M., Stanley S., Decker S., Read T.D., Salzberg S., Fraser C.M.; "Bacillus anthracis comparative genomics."; Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
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EQTVEVVKSALETADGAL-DFYNKYLDQVIP-WKTFDETIKELSRFKQEYSQEASVLVGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.7%; Score 116; DB 2; Length 941
20.1%; Pred. No. 37;
tive 45; Mismatches 88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus anthracis str. Ames 0581.
Bacteria; Firmicutes; Bacillales; Bacillus;
Bacillus cereus group; Bacillus anthracis.
NCBI_TaxID=261594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE017334; AAT29469.1; -.
SEQUENCE 941 AA; 103896 MW; 78AF6B5381D7B6C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        941
                                                                                                                                                         656 VKKLLEDSSK-------GLV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT29469;
01-UUN-2004 (TrEMBLrel. 27,
01-UUN-2004 (TrEMBLrel. 27,
01-UUN-2004 (TrEMBLrel. 27,
Conserved domain protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 20.1 49; Conservative
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Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=2190;
 7777
786
795
806
816
825
843
8643
865
689
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058718:
                                                                                                                                                                                   LIPID
LIPID
VARIANT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lab-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                  Nicaud J.-M., Mackman N., Gray L., Holland I.B.; "Characterisation of HlyC and mechanism of activation and secretion of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO0313; CABNONGRPT.
PRINTS; PRO1488; RTXTOXINA.
PROSITE; PS00330; HEMOLYSIN CALCIUM; 4.
TACILUM; CYtolygis; Hemolysis; Lipoprotein; Palmitate; Repeat; Toxin;
Transmembrane.
TRANSMEM 237 259 Potential.
                                                                                                                                                                                                                                                                     Felmlee T., Pellett S., Welch R.A.; "Nucleotide sequence of an Escherichia coli chromosomal hemolysin."; J. Bacteriol. 163:94-105(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MISCELLANEOUS: The hemolysin of E.coli is produced predominantly by strains causing extraintestinal infections, such as those of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Secreted.

DOMAIN: The Gly-rich region is probably involved in binding calcium, which is required for target cell-binding or cytolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: Bacterial hemolygins are exotoxins that attack blood cell membranes and cause cell rupture by mechanisms not clearly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            involved in pore formation by the cytotoxin. PTM: Palmitoylated by hlyC. The toxin only becomes active when
                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       activity.

DOMAIN: The three transmembrane domains are believed to be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the urinary tract. SIMILARITY: Belongs to the RTX prokaryotic toxin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Potential.
16 X REPEATS, GLY-RICH.
1.
2.
3.
4.
6.
                                                      (Rel. 10, Last sequence update) (Rel. 44, Last annotation update)
 PRT; 1023 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M10133; AAA23975.1;
EMBL; X02768; CAA26546.1;
PIR; A24433; LEECA.
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR001995; RtxA.
InterPro; IPR011049; Serralysn_like_C.
Pfam; PP00353; HemolysinCabind; 6.
Pfam; PF02382; RTX; 1.
                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-J96 / Serotype 04;
MEDLINE-85234404; Pubmed-3891743;
                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=85258115; PubMed=3894051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     haemolysin from E. coli 2001.";
FEBS Lett. 187:339-344(1985).
                                   (Rel. 10, Created)
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-44 FROM N.A.
 STANDARD;
                                                                                             Hemolysin, chromosomal.
                                                                                                                                Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             237
267
364
723
732
741
750
759
                                                                                                                                                                                   NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified.
                                                                                                                                                                                                                                                                                                                                                                                STRAIN=2001;
                                       01-MAR-1989
                                                        01-MAR-1989
                                                                            05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               defined
 ECOLI
                                                                                                                 Name=hlyA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         218 VONFFTSLSVTVKQANKDIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDLMLSLLKGA 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        208 INKLGSVISNTKHINGVGN-KLQNIPNLDNIGAGLDTV---SGILSAISASFILSNADAD 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105 NEKKASAQKDILIRILDD---GVNKLNEAQKSLLGSSQSFNNASGKLLALDSQLTNDFSE 161
                                                                                                                                                                                                                                                                                                                            23
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STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

STRAIN=9633999; DND6d=8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weidman J.-F., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         162 KSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIIS----YSIAAGVIEGKLIPELNDRLKA
                                                                                                                                                                                                                                                                                                                            2 TGIFAEQTVEVVK-----SAIETADGALDFYNKYLDQVIPWKTFDETIKELSRFKQE
                                                                                                                                                                                                                                                     98; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -! - FUNCTION: Involved in DNA double-strand break repair (DSBR). The
563 563 N(6)-palmitoyl lysine (By similarity).
689 N(6)-palmitoyl lysine (By similarity).
6 A - Y (in strain 2001).
1023 AA; 109867 MW; 196D5C0A9A28B54D CRC64;
                                                                                                                                                                              Length 1023;
                                                                                                                                                                           7.7%; Score 116; DB 1; Length 102
20.2%; Pred. No. 41;
tive 59; Mismatches 112; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Methanococcus jannaschii.
Archaea; Euryarchaeota; Methanococci; Methanococcales;
Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               278 -----278 ------278 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                401 VTGIISGILEASKQAMFEHVASKWADVIAEWEKKHGK 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-ULL-2004 (Rel. 44, Last annotation update)
DNA double-strand break repair rad50 ATPase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=rad50; OrderedLocusNames=MJ1322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 273:1058-1073(1996)
                                                                                                                                                                                                                                                         68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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PRELIMINARY;
Q928G7 F
Q928G7;
01-DEC-2001 (
                                     01-DEC-2001
                                                 01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   446
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstationthe European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----SQLTNDFSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLI 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              758 ILEVNKEINDIEERISYINOKLDE----EHKKI 792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       209 PEL----NDRLKAVONFFTSLSVTVKOANKDIDAAKLKLATEIAAIGEIKTETETTRFYV 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EASVL-----VGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFPDEYNEKKAS 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 AQXDILIRILDDGVNKLNEAQKSLLGSSQSFNNASGKLLALD------ 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                662 ELNKLREDEREINRLKDKLNELKNKEKE------LIEIENRRSLKFDKYKEYLGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
  complex possesses single-strand endonuclease activity
                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF02483; SMC_C; 1.
Pfam; PF02463; SMC_N; 1.
Probom; P0000006; ABC_transporter; 1.
SWAT; SM00382; AAA; 1.
TIGRRAMS; TIGR01725; phge HK97 gp10; 1.
ATP-binding; Coiled coil; Complete proteome; DNA repair; Hydrolase;
                                                     rad50/mrell complex possesses single-strand endonuclease activand App-dependent double-strand-specific 3'-5' exonuclease activity. Rad50 provides an Anp-dependent control of mrell by unwinding and/or repositioning DNA ends into the mrell active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 1005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    32 39 ATP (By similarity)
158 849 Coiled coil (Potential).
502 502 Zinc (By similarity).
505 505 Zinc (By similarity).
1005 AA; 119387 MW; 9BBBB48173E788F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.6%; Score 115; DB 19.4%; Pred. No. 47; tive 54; Mismatches
                                                                                                                                                                                                                                                                            HAMAP; ME_00449; -; 1.
InterPro; IPR003593; ABA ATPase.
InterPro; IPR003593; ABC transporter.
InterPro; IPR007517; Rad50_zn_hook.
InterPro; IPR003405; SMC_C.
InterPro; IPR003405; SMC_N.
InterPro; IPR003405; SMC_N.
InterPro; IPR003405; SMC_N.
                                                                                                                                                                                                                            EMBL; U67572; AAB99331.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 19.49
hes 59; Conservative
                                                                                                                                                                                                                                          PIR; A64465; A64465.
HSSP; P58301; 1F2T.
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                                                                                                                                                                                                                                                       HSSP; P58301; 11
FIGR; MJ1322; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Zinc.
NP BIND
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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RESULT 33 Q928G7

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137 SSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLI--- 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : | | : : | | : : | | 497 NIVKVLIAMG------DLNGELGAVQGKYDDVKGASEKLTETNSKQDLTKWMHELQTA 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  330 EKALAFSKTFDSDMNETLRGANALMETYGLSAEQSFDLMTVGAQNGLNKTDELGDNLAEY 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  445
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                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

STRAIN=CLIP 11262 / Serovar 6a;

STRAIN=CLIP 11262 / Serovar 6a;

STRAIN=CLIP 11262 / Serovar 6a;

STRAIN=LIP 11262 / Serovar 6a;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  194 --ISYSIAAGVIEGKLIPELNDRLKAVQNFFTSL---SVTVKQANKDIDAAKL--KLATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 1093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.6%; Score 115; DB 2; Length 10:
2.6%; Pred. No. 52;
ve 40; Mismatches 127; Indels
                                                                                                                                                                                                                          Listeria innocua.
Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1093 AA; 121152 MW; 67AAA59058B9B4D4 CRC64;
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Last annotation update)
                                   Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF05017; TMP; 11.
TIGRFAMs; TIGR01760; tape_meas_TP901; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 TGIFAEQTVEVVKSAIETADGALDFYNKYL-
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Listilist; LINESGS; Tape_meas_TP901.
InterPro; IPR010090; Tape_meas_TP901.
InterPro; IPR007713; TMP.
    Created)
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(TrEMBLrel. 19, (TrEMBLrel. 19, (TrEMBLrel. 26,
                                                                                                                                                                         OrderedLocusNames=lin2568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Simitare,
nés 71; Conservative
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SEQUENCE 1093 AA
                                                                                                                                                                                                                                                                                            NCBI_TaxID=1642;
                                                                                                                                 Lin2568 protein.
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01-NOV-1996
01-OCT-2003
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Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=17XNL;
PubMed=12368865;
                                                                                           SEQUENCE
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Best Local (
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                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                  68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------INNLNDDNLKVVQDKLIKNETLKLKEAE
                                                                                                                                                                                                                                                                                                                 10 VEVVKSAIETADGALDFYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVLVGDIKVL-
                                                                                                                                                                                                                                                                                            Gaps
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STRAIN=ATCC 35092 / DSM 1617 / P2;
STRAIN=ATCC 35092 / DSM 1617 / P2;
STRAIN=21332286; PubMed=11427726;
She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BPS2 protein homolog (Bps2).
Mame-bps2, OrderedlocusNames=SSO2241;
Sulfolobus solfataricus.
Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                 SGD; $0005721; $LK19.
GO; $00007721; $LK19.
GO; GO:00007126; C:condensed nuclear chromosome kinetochore; IDA.
GO; GO:0005129; C:spindle; IDA.
GO; GO:0007126; P:meiosis; IMP.
GO; GO:0030472; P:mitotic spindle assembly (sensu Fungi); IGI.
SEQUENCE 821 AA; 95380 MW; 994CCE2EFB7C4B67 CRC64;
                                                                                                                                                                                                                                                                                            .66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IDAAKL---KLATEIAA-----IGEIKTET-----ETTRFYVDYDDL
                                                                                                                                                                                                                                                                    DB 2; Length 821;
                                                                                                                                                                                                                                                                  7.6%; Score 114.5; DB 2; Length 20.8%; Pred. No. 40; Ative 52; Mismatches 115; Indels
                                                                            SEQUENCE FROM N.A.
Hughes B., Pohl T.M.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                   Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
cerevisiae chromosome XV reading frame ORF YOR195w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --MLSLLKGAAKKMINTCNEYQQRHGKKTLLEVPDI 303
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                                                                                                                                                           EMBL; Z75103; CAA99408.1; -. PIR; S67087; S67087.
                                                                                                                                                                                                                                                                                         70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                           SEQUENCE FROM N.A.
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                                                         NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 NKLYYRRIKRIRNGLGEEKNLIMDDDRALLL----TYFSPENR-----LVTQ1LSGDGN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                        41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96
Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N., Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T., Garret R.A., Regan M.A., Sensen C.W., Van der Oost J.; "The complete genome of the crenarchaeon Sulfolobus solfataricus P2."; Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97 ---YILLFDEYNEKKASAQKDILIRILDDGVNKLNEAQKSLLGSSQSFNN---ASGKLLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 GIFAEQTVEVVK------SAIETADGALDFYNKYLDQVIPWKTFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42 ETI--KELSRFKQEYSQEASVLVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151 LDSQLTNDFSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               211 INDRLKAVQNFFTSLSVTVKQANKDIDAAKLKLATEIAAIGEIKTETETTRFYVDYDD--
                                                                                                                                                                                                                                                                                                                                                                                      87; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.B., Selengut J.D., Koo H.L., Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bladwell S.L., Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V., Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M., Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Carucci D.J., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                          DB 2; Length 587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmodium yoelii yoelii.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                    7.5%; Score 113.5; DB 2; Length 19.5%; Pred. No. 31; ive 68; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genome seguence and comparative analysis of the model
                                                                                                                                                                                                                                                           587 AA; 68436 MW; B90DBC1E19C05E86 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1478 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     269 --- LMLSLLKGAAKKM-----INTCN 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           parasite Pľasmodium yoelii yoelii.";
Nature 419:512-519(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AABL01001665; EAA17280.1; -.
InterPro; IPR001990; Granin.
                                                                                                                             Proc. Natl. Acad. Sci. U.S.A
EMBL; AE006828; AAK42408.1;
PIR; A90394; A90394.
Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                         64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
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SYR_SYNY3
Q55486;
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                                                                                                             200
                                                                                                                                                                                                                                                                                                        501 LYNVNIEMEQANKDMRDDIDILLAN----IDKLNDEKNVTENEKEQKELKYNELKINYEH 556
                                                                                                                                             EYSQEASVLVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQ 112
                                                                                                                                                             383 ---KESEEIINEKNTLILELQQKLAQAS---YE------ISMIENKSNKKSN-- 422
                                                                                                                                                                                            KDILIRILDDGVN---KLNEAQKSLLGSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQV 170
                                                                                                                                                                                                                                            221
                                                                                                                                                                                                                                                                                          FTSLSVTVKQANKDI-DAAKLKLATEIAAIGEIKTETETTRFYVDYDDLMLSLLKGAAKK 280
                                                                                                                                                                                                                     -----ITNSYRGERNSEYEKKL----EELNN------ITNSYEKEINELNKEK 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- FUNCTION: May be involved in recombinational repair of damaged DNA (By similarity).
                                                                                                                                                                                                                                             DRIRK----EAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELND-----RLKAVQNF
                                                                                                                                                                                                                                                                 5 FAEQTVEVVKSAIETADGALDFYNKYL------DQVIPWKTFDE-TIKELSRFKQ
                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-98196666; PubMed=9537320; DOI=10.1038/32831; Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Carham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber Beldman R.A., Short J.M., Olsen G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex
                                                                      Indels 109;
                                                Length 1478;
             Hypothetical protein.
SEQUENCE 1478 AA; 176615 MW; 9AE7AB0AAABF6EAE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aquifex aeolicus.
Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2004 (Rel. 45, Last annotation update)
DNA repair protein recN (Recombination protein N).
Name=recN; OrderedLocusNames=AQ_561;
                                                                        98;
                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                              520 AA
                                                7.5%; Score 113.5; 20.9%; Pred. No. 94;
                                                                      51; Mismatches
                                                                                                                                                                                                                                                                                                                                         281 MINTCN-----EYQORH 292
                                                                                                                                                                                                                                                                                                                                                                  557 KVKECNKFFNMLPPKMKKKIEYEKKH 582
PROSITE; PS00422; GRANINS_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003439; ABC transporter.
InterPro; IPR004604; RecN.
InterPro; IPR003405; SMC_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE000695; AAC06789.1; -.
                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 392:353-358(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                             RECN AQUAE
066834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=VF5;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         315 KEEE--LREEVEKLREE------345
                                                                                                                                                                                                                                                                                                                                                                                        -VGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLS---AYILLFDEYNEKKASAQKDI-- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----LIRILDDGVNKLNEAQKSLLGSSQSFNNASGKLL----ALDSQLTN----DF 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  160 SEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELN-DRLKAV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Arginyl-tRNA synthetase (EC 6.1.1.19) (Arginine--tRNA ligase) (ArgRS).
Name=argS; OrderedLocusNames=s110502;
                                                                                                                                                                                                                                                                                                                                                  10 VEVVKSAIETADGALDFYNKYLDQVIPWKTFDE----TIKELSRFKQEYSQ---EASVL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96127529; PubMed=8590279;

Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,

Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,

Sugiura M., Tabata S.;

"Sequence analysis of the genome of the unicellular cyanobacterium

Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb

region from map positions 64% to 92% of the genome.";

PDNA Res. 2:153-166(1995).

-1 - CATALYTIC ACTIVITY: ATP + L-arginine + tRNA(Arg) = AMP +

diphosphate + L-arginyl-tRNA(Arg).

diphosphate + L-arginyl-tRNA(Arg).

-1 - SUBUNIT: Monomer (By similarity).

-1 - SUBCELLULAR LOCATION. Cytoplasmic.

-1 - SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      346 EDLEERIEELLKELN--LERAKLKV------EIK-ESEPTKYGKDKIEFLFS 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             219 ONFFISLSVTVKQANKDIDAAKLKLATEIAAIGEIKTETTTRFYVDYDDLMLS
                                                                                                                                                                                                                                                                                 71;
                                                                                                                                                                                                                    DB 1; Length 520;
                                                                                                                                                                                                                                                                                     94; Indels
Pfam; PF02483; SNC C; ...
TIGRFAMS; TIGR00634; recN; 1.
ATP-binding; Complete proteome; DNA repair.
36 ATP (Potential).
36 ATP (Potential).
37 ATP (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
NCBI_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   584 AA.
                                                                                                                                                                                                                    7.5%; Score 112.5;
20.1%; Pred. No. 32;
tive 70; Mismatches
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HAMAP; MF 00123; -; 1.
InterPro; IPR005148; ArgtRNAsynthet N.
InterPro; IPR001278; Arg tRNA-synt Ic.
InterPro; IPR0018099; tRNA-synt Ic.
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                                                                                                                                                                                                                                               Best Local Similarity 20.1
Matches 59; Conservative
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Escherichia coli
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                  SARRERE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NYRLNTDGAEKIIYVTDAGQANHFAQFPQVAEKAGILTDPTQVV---HVPFGLVKGEDGK 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 GIFAEQTVEVVKSALETADGALD-----FY---NKYLDQVIPWKTFDETIKELSRFKQE
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InterPro; IPR001412; tRNA-synt I.

InterPro; IPR009080; tRNA-synt I.

InterPro; IPR009080; tRNA-synt I.

Pfam; PF007485; tRNA-synt I.

Pfam; PF00750; tRNA-synt I.

Pfam; PF00750; tRNA-synt I.

Pfam; PF00718; TGR00485; I.

PRINTS; PR01038; TRNASYNTHARG.

TIGRPAM8; TGR00486; args; 1.

PROSITE; PS00178; AA_TRNA_LIGASE I; 1.

Aminoacyl-tRNA synthetase; ATP-binding; Complete proteome; Ligase; Protein blosynthesis.
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01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to tr|OBWZS2 Neurospora crassa Dynactin.
ORFNames=YALIOA205049;
Yarrowia lipolytica (Candida lipolytica).
Eukaryota; Fungi; Ascomycota; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 584;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 7.5%; Score 112.5; DB 1; Length Local Similarity 23.2%; Pred. No. 36; es 76; Conservative 45; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 136 "HIGH" region.
584 AA; 65212 MW; 89602A1A5A3BD85B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomycetales; Dipodascaceae; Yarrowia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2004 (TrEMBLrel. 28, Created)
01-OCT-2004 (TrEMBLrel. 28, Last seqn
01-OCT-2004 (TrEMBLrel. 28, Last ann
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Hess J., Wels W., Vogel M., Goebel W.;
"Nucleotide sequence of a plasmid-encoded hemolysin determinant and
its comparison with a corresponding chromosomal hemolysin sequence.";
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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MEDLINE-96404790; PubMed-88008931;
Ludwig A., Garcia F., Bauer S., Jarchau T., Benz R., Hoppe J.,
Goebel W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 941;
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                                                                                                                                                                                                                                                                                                                                          Genoscope;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; CR382127; CAG84227.1; -.
SEQUENCE 941 AA; 106891 MW; EF36A7BBE6D40AFB CRC64;
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01-JAN-1988 (Rel. 06, Last sequence update)
02-ULJ-2004 (Rel. 44, Last annotation update)
Hemolygin, plasmid.
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"Genome evolution in yeasts.";
Nature 430:35-44(2004).
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                                                                                                                                                              MEDLINE=98065943; PubMed=9403685; DOI=10.1038/37551;
MEDLINE=98065943; PubMed=9403685; DOI=10.1038/37551;
MEDLINE=98065943; PubMed=9403685; DOI=10.1038/37551;
Inthigra R., White O., Ketchum K.A., Dodson R.J., Hickey E.K.,
Gwinn M.L., Dougherty B.A., Tomb J.-F., Fleischmann R.D.,
Richardson D.L., Peterson J.D., Kerlavage A.R., Quackenbush J.,
Salzberg S.L., Hanson M., van Vugt R., Palmer N., Adams M.D.,
Gocayne J.D., Weidman J.F., Utterback T.R., Watthey L., McDonald L.A.,
Artiach P., Bowman C., Garland S.A., Fujii C., Cotton M.D., Horst K.,
Roberts K.M., Hatch B., Smith H.O., Venter J.C.;
"Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----LDQVIPWKTFDETIKELSR
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                                                                                                                                                                                                                                                                    218 VQNFFTSLSVTVKQANKDIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDLMLSLLKGA
                                                                                                             162 KSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIIS----YSIAAGVIEGKLIPELNDRLKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122; Indels 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 1098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGR; BBG10; -.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0004811; P:chemotaxis; IEA.
GO; GO:0004815; P:chemotaxis; IEA.
GO; GO:0007165; P:signal transduction; IEA.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPR004089; Chmtaxis_transd.
Pfam; PF00015; MCPsignal; 1.
Complete proteome; Hypothetical protein; Plasmid.
SEQUENCE 1098 AA; 123861 MW; F465D18421F05935 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 1-JUN-1999 (TrEMBLrel. 26, Last annotation update) Hypothetical protein BBG10. OrderedLocusNames=BBG10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    402 VTGIISGILEASKQAMFEHVASKMADVIAEWEKKHGK 438
                                                                                                                                                                                                                                                                                                                                                                                                                                   -----AKKMINTCNEYQORHGK 294
265 TRTKAAAGVELTTKVLGNVGKGISQYIIAQRAAQGLSTS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Borrelia burgdorferi (Lyme disease spirochete).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1098 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.5%; Score 112.5;
0.6%; Pred. No. 77;
ve 60; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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EMBL; AE000786; AAC66075.1; -.
PIR; B70232; B70232.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGIFAEQTVEVVK-----SAIETADGALDFYNKYLDQVIPWKTFDETIKELSRFKQE
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                                                                                                                                                                                                                                                                                                     activity.

DOMAIN: The three transmembrane domains are believed to be involved in pore formation by the cytotoxin.

FTM: Palmitoylated by hlyC. The toxin only becomes active when modified.

MISCELLANDOUS: The hemolysin of E.coli is produced predominantly by strains causing extraintestinal infections, such as those of
                                                                                                                                                                                                           DOMAIN: The Gly-rich region is probably involved in binding calcium, which is required for target cell-binding or cytolytic
                                                         FUNCTION: Bacterial hemolysins are exotoxins that attack blood cell membranes and cause cell rupture by mechanisms not clearly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO0313; CABDNGRPT.
PRINTS; PRO01489; RTXTOXINA.
PROSITE; PSO0330; HEWOLYSIN CALCIUM; 4.
CAlcium; Cycolysis; Hemolysīs; Lipoprotein; Palmitate; Plasmid;
Repeat, Toxin; Transmenbrane.
TRANSMEM 238 260 Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the urinary tract. SIMILARITY: Belongs to the RTX prokaryotic toxin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N(6)-palmitoyl lysine.
N(6)-palmitoyl lysine.
W; 83944917F76C945B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Potential.
Potential.
16 X REPEATS, GLY-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR001343; Hemlysn_Ca_bind.
Interpro; IPR003995; RtxA.
Interpro; IPR011049; Serralysn_like_C.
Pfam; PF00353; HemolysinCabind; 6.
Pfam; PF03182; RTX; 1.
                                                                                                                                                                               SUBCELLULAR LOCATION: Secreted.
                            Bacteriol. 178:5422-5430(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110201
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Matches 69; Conserv
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EMBL; AL008505; CAA15432.3; --
BMBL; ABL125; CAAA16432.3; JOINED.
EMBL; AL008505; CAB03386.3; JOINED.
EMBL; Z81125; CAB03385.3; --
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MEDLINE-99069613; PubMed-9851916;
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EMBL; AF074902; AAC26793.1; -.
PIR; P87908; F87908.
PIR; T23064; T23064.
PIR; T43291; T43291.
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Science 282:2012-2018(1998).
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Submitted (FEB-2004)
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Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
A Goffard N., Frangeul L., Aigle M., Anthouard V., Babbour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne B., Bleykasten C.,
Boisrame A., Boyer J., Catrolico L., Confanioleri F., de Daruvar A.,
Barnay S., Fairhead C., Ferry-Dumazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniauw N., Joyet P., Kachouri R.,
A Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
Mincker P., Souciet J.L.;
Genome evolution in yeasts.";
DRIRKEAYAG-----AAAGIVAGPFGLIISYSIAA-----GVIEGKLIPELNDRLKAV 218
                                                                                                ::: : | : | : | : | : | | : | | : | | : | | : | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
                                                                                                                                                             219 ONFFISLSVTVKQANKDIDAAKLKLATEIAAI-----GEIKTETETTRFYVDYDDLMLSL 273
                                                                                                                                                                                          GDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRILDD
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01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to DEHACOGOSEG Debaryomyces hansenii IPF 1836.1.
ORFNames=YALIOF023879;
Yarrowia lipolytica (Candida lipolytica).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Dipodascaceae; Yarrowia.
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Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR382132; CAG77705.1; -.
SEQUENCE 1906 AA; 210346 MW; F6ED7D1AF7B7562B CRC64;
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                                                                                                                                                                                                                                                                                 Created)
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Best Local Similarity
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-----LLSSFKEKLQTSKDDHSTEVSKLTEQVRESTLKAENFEHDISSLKDDLAQA 1392
183 AGIVAGPFGLIISYSIAAGVIE-----GKLIPELNDRLKAVQNF---FTSLSVTVKQA 232
                                                                                                                                                                                                             233 NKDIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDLMLSLLKGAAKKMINTCNEYQQR 291
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STRAIN=Bristol N2;
MFDLINE=2266894; PubMed=12783803;
HUANG C.C., Hall D.H., Hedgecock B.M., Kao G., Karantza V.,
Vogel B.E., Hutter H., Chisholm A.D., Yurchenco P.D., Wadsworth W.G.;
"Laminin alpha subunits and their role in C. elegans development.";
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                   045614 PRELIMINARY; PRT; 3102 AA.
045614; P91834; O9TZR4;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
C. elegans LAM-3 protein (Corresponding sequence T22A3.8) (Laminin alpha chain) (Hypothetical protein T22A3.8).
Name=lam-3; Synonyms=lamal/2; ORFNames=T22A3.8;
Caenorhabditis elegans.
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R HSSP; PO2468; INPE.

R GO; GO:0005506; C:extracellular matrix; IEA.

R GO; GO:0005102; F:receptor binding; IEA.

R GO; GO:0005102; F:receptor binding; IEA.

R GO; GO:0005108; F:receptor binding; IEA.

R GO; GO:0030134; P:regulation of cell adhesion; IEA.

R GO; GO:0030134; P:regulation of cell migration; IEA.

R GO; GO:003034; P:regulation of cell migration; IEA.

R GO; GO:0045995; P:regulation of embryonic development; IEA.

R INCERPRO; IPRO08999; EGF like.

R INCERPRO; IPRO09099; GGT like.

R INCERPRO; IPRO00034; Laminin_GG.

R INCERPRO; IPRO00034; Laminin_GG.

R INCERPRO; IPRO00191; Laminin_GG.

R INCERPRO; IPRO01991; Laminin_GG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to the EMBL/GenBank/DDBJ databases.
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Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
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PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2090 KNESSLSN------VDNSNAVKIVEELKKEKKDLTDRLGHLNELKTSI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               232 ANKDIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDLMLSLLKGAAKKM-INTCNEYQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 ---YEWCGVVTQLLSAYILLFDEYNEK------KASAQKDILIRILDDGVNKLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 AEQTVEVV-----KSAIETADGALDFYNKYLDQVIPWKTFDETIKELSRFKQEYSQEAS
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Hypothetical protein.
Hypothetical farican clawed frog).
Eukaryota Metazoa; Ghordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----YFEATQTV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 3102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50025; LAM G DOWAIN; 3.
Hypothetical protein; Laminin BGF-like domain.
SEQUENCE 3102 AA; 343790 MW; 2EE9305D5C591PAB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.5%; Score 112.5; ~~.,
19.9%; Pred. No. 2.6e+02;
tive 64; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 VLVG-----DIKVLLMDSQDK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PSO0022; EGF 1; 12.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS01248; LAMININ_TYPE_EGF; 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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MEDLINE=22388257; PubMed=12477932;
   Laminin I.
Laminin II.
Laminin N.
                                                                   InterPro; IPR008211; Laminin_N.
InterPro; IPR003129; TSP N.
Pfam; PF00052; Laminin B; 2.
Pfam; PF00053; Laminin EGF; 17.
Pfam; PF02210; Laminin G2; 3.
                                                                                                                                                                                                                                                                                                                                       ProDom; PD003031; Laminin B; 2. SMART; SM00180; BGF Lam; 17. SMART; SM00281; LamB; 2. SMART; SM00282; LamG; 4. SMART; SM00136; LamNT; 1.
                                                                                                                                                                                                                          pfam; PP06008; Laminin_I; 1.
Pfam; PP06009; Laminin_Ii; 1.
Pfam; PP00055; Laminin_N; 1.
PRINTS; PR00011; EGFLAMININ.
PRODOM; PD003031; Laminin_B; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
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                                                InterPro;
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Q6GNE7
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Loquellano N.A., Peters G.J., Abramson R.D., Hulyk S.W.,
Villalon D.K., Wuzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Marking M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman U.W., Green E.D., Dickson M.C.,
Jones S.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Worder M.I., Skalaka U., Smallus D.E., Schnerch A., Schein J.E.,
T and mouse ConN sequences.";
T and mouse ConN sequences.";
T and mouse ConN sequences.";
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Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
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InterPro; IPR007794; Rib_recept_KP.
Pfam; PP05104; Rib_recp_KP_reg; 1.
Hypothetical protein.
SEQUENCE 1012 Aa; 112965 MW; CF23ABBE0D9EDAEA CRC64;
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073565; AAH73565.1; -.
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1081 AA

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Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      parasite Plasmodium yoelii yoelii.";
Nature 419:512-519(2002).
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
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Pred. No. 81;
                                                                                                                                                       Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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                  01-MAR-2004 (TrEMBLrel. 26, Created)
1-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
235 kba rhoptry protein (Fragment)
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Best Local Similarity 19.0.
Best Local 75; Conservative
                                                                                                                               Plasmodium yoelii yoelii
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                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                            NCBI_TaxID=73239;
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PubMed=12368865;
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1338 RELNLKRVNIIKC-LQQQI------NEQTKLYKEYTDELNNEIKTLKQSKHIHTDNT 1387
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                                                                                                                                                                                                                                               MEDLINE=22255705; PubMed=12368864; Mail Co., Berriman M., Hyman R.W., Gardner M.J., Fung E., White O., Berriman M., Hyman R.W., Carlton J.M., Pain A., Nelson K.B., Bowman S., Paulsen I.T., James K., Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Chan M.S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S., Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B., Martin D.M., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C., Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MTGIFAEQTVEVVKSAIETADGALDFYNKYLDQV----IPWKTFDETIKELSRFKQEYS
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Bukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1464;
Plasmodium falciparum (isolate 3D7).
Bukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genome sequence of the human malaria parasite Plasmodium
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tive 70; Mismatches 112; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1464 AA; 175530 MW; 7316F16F516897CD CRC64;
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MEDLINE=85254917; PubMed=2861910;
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1388 SNNNQKNNGYNDNIEL 1403
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ProDom; PD088957; DUF327; 1.
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EMBL; AE014839; AAN35802.1;
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                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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NCBI_TaxID=5691;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VSG expression site-associated protein
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Rudenko G., Chaves I., Dirks-Mulder A., Borst P.;
"Selection for activation of a new variant surface glycoprotein
expression site in Trypanosoma brucei can result in deletion of
old one.";
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N-linked (GlcNAc. .) (Potential).
N-linked (GlcNAc. .) (Potential).
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   [ 42:173-182(1985). FUNCTION: Not known but may be related to activation of the
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163 WEDVGEILWKETEAKCGSOKVEGVGEIQTE 192
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                                                                     variant surface glycoprotein genes.
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329 AA; 36603 MW;
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134 LLGSSQSFNNASGKLLALDSQLTNDFSEKSSY-----FQSQVDRIRKEAYAGAAAGIV 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         187 AGPFGLIISYSIAAGVI---EGKLIPELNDRLKAVQ-----NFPTSLSVTVKQA 232
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----LISYGNKMGNIVAKAGGLFAALBDSLKBVRKEIPGALIKTNKYYTSVABIVRTV 162
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5691;
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"The architecture of Variant Surface Glycoprotein gene expression sites in Trypanosoma brucei.";
                                                                                                                                                                                       C., Melville S.E.
Berberof M., Borst P., Rudenko G.; "The architecture of variant surface glycoprotein gene expression sites in Trypanosoma brucei."; Mol. Biochem. Parasitol. 122:131-140(2002).
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Rudenko G., Chaves I., Dirks-Mulder A., Borst P.;
"Selection for activation of a new variant surface glycoprotein
expression site in Trypanosoma brucei can result in deletion of
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                                                                                                                                                                                    Zeng C., Zhao B., Hierl M., Catanese J., Gerrard C., Melv Hoek M., Navarro M., Cross G.A.M., El-Sayed N., Berberof Studenko G., Borst P., de Jong P.; Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases. EMBL, AL671259, CAD21890.1; ...
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EMBL, AL671259, CAD21890.1; -.
SEQUENCE 329 AA; 36603 MW; 4D19F59477D9CEE8 CRC64;
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7.4%; Score 111; DB 2;
Best Local Similarity 22.9%; Pred. No. 23;
Matches 48; Conservative 33; Mismatches 63
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22.9%; Pred. No. 23;
ive 33; Mismatches
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187 AGPFGLIISYSIAAGVI---EGKLIPELNDRLKAVQ------NFFTSLSVTVKQA 232
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-----EYNEKKASAQKDILIRILDDGVNKL-NEAQKS 133
                                                                         LLGSSQSFNNASGKLLALDSQLTNDFSEKSSY-----FQSQVDRIRKEAYAGAAAGIV 186
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4 EIVELVVLLFSVTCVDAWLQGADCTRVADHKEHAPVTEAVCYLRCLSDALNKLYSEGEKK 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.4%; Score 111; DB 2; Length 465; 22.0%; Pred. No. 35; tive 51; Mismatches 129; Indels
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Bacillus cereus (strain ATCC 10987).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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InterPro; IPR001029; Flagellin C.
InterPro; IPR001492; Flagellin N.
Pfam; PF00700; Flagellin N; 1.
PRINTS; PR00207; FLAGELLIN,
PROD0m; PD000316; Flagellin C; 1.
Complete Protecome; Flagellin C; 1.
SEQUENCE 465 AA; 49855 MW; E4C307E7717381D5 CRC64;
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1 WIGIFAEQTVEVVKSAIETA......TCNEYQQRHGKKTLLEVPDI
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(c) 1993 - 2005 Compugen Ltd.
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US-10-437-96-197045
US-10-369-493-10918
US-10-282-122A-46343
US-09-884-696-5
US-10-369-493-5220
US-10-369-493-5220
US-10-369-493-5220
US-10-369-493-5220
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US-10-369-493-5220
US-10-282-122A-70920
US-10-0282-246A-106
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Maximum Match 100%
Listing first 100 summaries
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Sequence 12211, A
Sequence 17323, A
Sequence 4, Appli
Sequence 248508,
Sequence 26451,
Sequence 11332, A
Sequence 7458, A
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Sequence 226623,
Sequence 64494, A
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Patent No. US20020146430A1

GENERAL INFORMATION:

APPLICANT: JULY SETSITY OF MARYLANG

TITLE OF INVENTION: USE OF CLY A HEMOLYSIN FOR EXCRETION OF

TITLE OF INVENTION: USE OF CLY A HEMOLYSIN FOR EXCRETION OF

TITLE OF INVENTION: USE OF LAY A HEMOLYSIN FOR EXCRETION OF

TITLE OF INVENTION: USE OF LAY A HEMOLYSIN FOR EXCRETION OF

CURRENT APPLICATION NUMBER: US/09/993,292A

CURRENT FILING DATE: 2001-11-23

PRIOR APPLICATION NUMBER: 60/252,516

PRIOR FILING DATE: 2000-11-22

NUMBER OF SEQ ID NOS: 19

SOFTWARE FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
97.1%; Score 1466; DB 9; Length 305;
Best Local Similarity 97.0%; Pred. No. 9e-118;
Matches 294; Conservative 2; Mismatches 7; Indels
4 US-10-156-761-14486

5 US-10-282-1223-14

4 US-10-369-493-17323

5 US-10-369-493-17323

10S-09-815-32-4

10S-09-815-35-4

10S-10-425-115-286451

4 US-10-369-493-11332

5 US-10-369-493-1132

6 US-10-369-493-115622

6 US-10-282-122A-63115

7 US-10-282-122A-63115

7 US-10-282-122A-63115

7 US-10-425-115-226623

5 US-10-425-115-226623
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; ORGANISM: Salmonella Typhi
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RESULT 2 US-10-437-963-197045 ; Sequence 197045, Application US/10437963

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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wei
APPLICANT: Buckharov, Andrey A.
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 103-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 197045
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APPLICANT: Galdan, Barry S.
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9.0%; Score 136.5; DB 16; Length
Best Local Similarity 22.4%; Pred. No. 0.011;
Matches 77; Conservative 67; Mismatches 121; Indels
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US-10-437-963-197045
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Publication No. US20030233675A1
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Buckharov, Andrey A.
APPLICANT: Barbazuk, Brad
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ORGANISM: Oryza sativa
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Matches 68
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                                                                                                                                                                                                                                                                                  564 QYENEYIRYSSIISG-----MDPGAIKKEIEAAGESFTTFKNRINELLS-QIGFVPEYN 616
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                                                                                                                                                                                                                                                                                                                                                                                                                                        -----AGNIESRYKSAYQENIKWKTLVDSYT 708
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
                                                                                                                        Gaps
                                                                              ; Score 116; DB 14; Length 891;
; Pred. No. 0.62;
46; Mismatches 129; Indels 66;
                                                                                                                                                                4 IFAEQTVEVVKSAIETADGALDFYNKYLDQVI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 46343, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PELING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR PELING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
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FILING DATE: 2001-02-09
APPLICATION NUMBER: 60/269,308
; TYPE: PRT
; ORGANISM: Ferroplasma acidarmanus
US-10-369-493-10918
                                                                                7.78;
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APPLICANT: Zamudio, Carlos
APPLICANT: Walone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
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Wall, Daniel
Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                Query Match 7.7% Best Local Similarity 22.3% Matches 69; Conservative
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 IKVILLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRILDDGV 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54 YSQEASVL-----VGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILL-FDEY 104
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                                  - See File Wrapper or PALM
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                                                                                                                                                                                                                                                                                                              DB 15; Length 941;
                                                                                                                                                                                                                                                                                                           Query Match 7.7%; Score 116; DB 15; Length 94
Best Local Similarity 20.1%; Pred. No. 0.67;
Matches 49; Conservative 45; Mismatches 88; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             656 VKKLLEDSSK------GLV----
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 46343
LENGTH: 941
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Publication No. US20030035809A1
GENERAL INFORMATION:
                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Bacillus anthracis
US-10-282-122A-46343
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ORGANISM: Escherichia coli
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APPLICANT: Cao, Yorgwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REPERENCE: 38-10(52052)8
FILE REPERENCE: 38-10(52052)8
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 5221
LENGTH: 2823
APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPENSE WITH IMPROVED PROPERTIES
TITLE OF INVENTION: EXPENSE WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(5205)B
CURRENT PAPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR PRINTING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 5220
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                                                                                                                                                                                                                                                                                                                                                                   Query Match
7.5%; Score 112.5; DB 14; Length 2823;
Best Local Similarity 19.9%; Pred. No. 6;
Matches 73; Conservative 64; Mismatches 106; Indels 123; Gaps
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Publication No. US20030233675A1
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, ORGANISM: Caenorhabditis elegans
US-10-369-493-5221
                                                                                                                                                                                                                                                                                                       ; ORGANISM: Caenorhabditis elegans
US-10-369-493-5220
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Sequence 1061, Application US/10369493

Publication No. US2003023675A1

GENERAL INFORMATION:

APPLICANT: Chao, Yongwei

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

TITLE OF INVENTION: UNMER: US/10/369,493

CURRENT APPLICATION NUMBER: US/0360,039

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 1061

FEMALE OF SEQ ID NOS: 47374
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                        162 KSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIIS----YSIAAGVIEGKLIPELNDRLKA 217
                                                   ----SQLTNDFSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLI
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                                                                                                          218 VQNFFTSLSVTVKQANKDIDAAKLKLATELAAIGEIKTETETTRFYVDYDDIMLSLLKGA
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401 VIGIISGILEASKQAMFEHVASKMADVIAEWEKKHGK 437
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758 ILEVNKEINDIEERISYINQKLDE---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , APPLICANT: Cao, Yongwei
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Best Local Similarity
Matches 59; Conserv
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Sequence 212070, Application US/10424599

Sequence 212070, Application No. US20040031072A1

GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5)223) B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 212070

LENGTH: 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 EVEREKIRVAEANLE-----KQAMDWMLAQEELKRIGEDAARHAEESSETLEDFRRVKK 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 LIMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQ-----KDILIRILD 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            255 E-----IQRLKSEKASLQGILEEKDLELS----SARKMLGDVNQEIYDLKMLMHSKET 303
                 -LLALDSQLTNDFSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGK 206
                                                        -----IGAKIMNKE 910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 DGVNKLNEAQKSLLGSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDRIRKEAYAGA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 EVVKSAIETADGALDFYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVLVGD---IKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | :::: | ::: | :: | | :-----ESERTKLRVAESRNRELERDLKMEKELISELEKERTSLEQAVKE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 KLATEIAAIGEIKTETETTRFYVDYDDLMLSLLKGAAKKMINTCNB--YQQR---HGKKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 AAGIVAGPFGLIISYSIAAGVIEGKLIPELNDRLKAVQNFFTSLSVTVKQANKDIDAAKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.3%; Score 110.5; DB 15; Length Best Local Similarity 18.9%; Pred. No. 0.99; Matches 57; Conservative 59; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: PAT_MRT3847_33525C.1.pep
US-10-424-599-212070
                                         ::|| ||| :::|
872 DMVALASQL-EBLQHKLVVGESQVENVKEEL-
                                                                                                 207 LIPELN----DRLKAVQNFFTSLSVT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 70920, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION: APPLICANT: Mang, Liangeu APPLICANT: Zamudio, Carlos
                                                                                                                                                                                                            : |||:|
970 SAQHSTETSR 979
                                                                                                                                                                                  252 EIKTETETTR 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     297 LL 298
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APPLICANT: Cac, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Gldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILLE OF INVENTION: 2003-02-28
FILLE PRILING DATE: 2003-02-28
FRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
                                                                                                                            : |: : | : | : | : | 1.2090 KNESSLSN------VDNSNAVKIVEELKKEKKDLTDRLGHLNELKTSI----- 2131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174 RKEAYAGAAAGIVAGPFGLIISYSIAAGVIE--GKLIPELNDRLKAVONFFTSLSVTVKQ 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          232 ANKDIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDLMLSLLKGAAKKM-INTCNEYQQ 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 VGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASA-----QKDI 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----OSFN---NASGK- 147
                                                                                                                                                                                                                                                                       84 ---YEWCGVVTQLLSAYILLFDEYNEK------KASAQKDILIRILDDGVNKLN 128
                                                                                                                                                                                                                                                                                                                                                       -----EAQKS---LLGSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDRI 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 AEQTVEVVKSAIETADGALDFYNKYLDQVIPWKTFDET----IKELSRFKQEYSQEASVL
                                                                                                 6 AEQTVEVV-----KSAIETADGALDFYNKYLDQVIPWKTFDETIKELSRFKQEYSQEAS
                                                                                                                                                                                  60 VLVG-----YFEATQTV-----
                 7.5%; Score 112.5; DB 14; Length 2823;
19.9%; Pred. No. 6;
tive 64; Mismatches 106; Indels 123; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1295;
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Publication No. US20030233675A1
GENERAL INFORMATION:
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Query Match
Best Local Similarity 19.5%
T3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2174 SEĞIKT 2179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             291 RHGKKT 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Caen
US-10-369-493-6440
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LENGTH: 1295
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Best Local
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AVONFFTSLSVTVKQANKDIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDLMLSLLKG 276
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                                                                                                                                                                                                                                                                                                                   APPLICANT: X0. H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITAA. 034A
CURRENT APPLICATION NUMBER: 00/20-20
PRIOR APPLICATION NUMBER: 60/191, 078
PRIOR PILING DATE: 2000-05-21
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207, 727
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230, 335
PRIOR FILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
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Pest Local Similarity 18.3%; Pred. No. 3;
Matches 61; Conservative 60; Mismatches 130; Indels 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               277 AAKKMINTCNEYQQ------RHGKKTLLEV 300
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Malone, Cheryl
Haselbeck, Robert
Oblsen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Granch
Yamamoto, Robert
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LENGTH: 1189
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APPLICANT: Rothenberg, Mark
TITLE OF INVENTION: No. US20030235882Alel Nucleic Acids and Polypeptides and Methods of
TITLE OF INVENTION: Thereof
FILE REFERENCE: 21402-22
CURRENT APPLICATION NUMBER: US/10/028,248A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/256619
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---RIKLSFSTKLKQTEDEKNALKEQLEEEEEAKRNLE 1356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----EHKRKKVDÄÖLQE 1256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         166 FOSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGK---LIPELNDRLKAVQNFF 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 QEASVLVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDI 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 EQTVEVVKSAIE----TADGALDFYNKYLDQVI PWKTFDETIKE-----LSRFKQEYS
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Pest Local Similarity 21.0%; Pred. No. 8.1;
Matches 66; Conservative 43; Mismatches 107; Indels
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PRIOR APPLICATION NUMBER: 60/308039
PRIOR FILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: 60/311266
PRIOR FILING DATE: 2001-08-09
NUMBER OF SEQ ID NOS: 211
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 106
LENGTH: 1959
Application US/10028248A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/262959
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: 60/272408
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/285189
                                                                                                                                                                                                                                                                                                   Taupier Jr, Raymond
Kekuda, Ramesh
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                                                                                   Patturajan, Meera
Vernet, Corine
Casman, Statie
Malyankar, Uriel
Shenoy, Suresh
Spytek, Kimberly
Gangolli, Esha
Miller, Charles
Boldog, Ferenc
        Sequence 106, Application US/100
Publication No. US20030235882A1
GENERAL INFORMATION:
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Zerhusen, Bryan
Liu, Xiaohong
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Millet, Isabelle
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Inger, Shlomit
                                                                  APPLICANT: Shimkets, Richard
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, ORGANISM: Gallus gallus
US-10-028-248A-106
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APPLICANT:
APPLICANT:
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APPLICANT: Sciore, Paul
APPLICANT: Millet, Isabelle
APPLICANT: Rothenberg, Mark
TITLE OF INVENTION: No. US20030235882Alel Nucleic Acids and Polypeptides and Methods of TITLE OF INVENTION: Thereof
                                                                                                                                                                                                                                                                                                                                              | : :::|
| 1310 LQDTQELLQEET------RLKLSFSTKLKQTEDEKNALKEQLEEEEEEAKRNLE 1356
                                                                                                                                                               1257 LOVKFTEGERVKTELAERVNKLOVEL------DNVTGLLNQSDSKSIKLAKDFSALESO 1309
                                                                     ------EHKRKKVDÄÖLQE 1256
                                                                                                                                                                                                                                                                                                                ----NKDIDAAKLKLATEIAAIGEIKTETE 258
                        56 QEASVLVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDI 115
                                                                                                                                                                                                               166 FQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGK---LIPELNDRLKAVQNFF 222
                                                                                                                     116 L-----IRILDDGVNKLNEAQKSLLGSSQSFNNASGKLLALDS---QLTNDFSEKSSY 165
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CURRENT APPLICATION NUMBER: US/10/028,248A
CURRENT FILING DATE: 2001-12-19
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1224 SERAELSNEVKVLLQGKGDA------
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PRIOR FILING DATE: 2001-04-20
PRIOR APPLICATION NUMBER: 60/308039
PRIOR PILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: 60/311266
PRIOR APPLICATION NUMBER: 60/311266
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PATENTIN VEY: 2.1
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APPLICATION NUMBER: 60/285189
FILING DATE: 2001-04-20
APPLICATION NUMBER: 60/308039
FILING DATE: 2001-07-26
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APPLICATION NUMBER: 60/256619
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APPLICATION NUMBER: 60/272408
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1415 KTRLQQELDDIAVDL 1429
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Vernet, Corine
Casman, Stacie
Malyankar, Uriel
Shenoy, Suresh
Spytek, Kimberly
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Zerhusen, Bryan
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Miller, Charles
Boldog, Ferenc
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GENERAL INFORMATION
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LENGTH: 1999
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES AND METHODS OF USE THEREOF
FILE REFERENCE: 21402-222CIP
CURRENT APPLICATION NUMBER: US/10/107,782
CURRENT FILING DATE: 2002-03-27
                                --NKDIDAAKLKLATEIAAIGEIKTETE 258
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PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2000-12-19
PRIOR PILING DATE: 2000-12-19
PRIOR PELING DATE: 2001-01-19
PRIOR PELING DATE: 2001-02-28
PRIOR PELING DATE: 2001-02-28
PRIOR PELING DATE: 2001-02-28
PRIOR PELING DATE: 2001-04-20
PRIOR PELING DATE: 2001-04-20
PRIOR PELING DATE: 2001-04-26
PRIOR PELING DATE: 2001-04-26
PRIOR PILING DATE: 2001-07-26
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PRIOR PILING DATE: 2001-08-09
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PRIOR PILING DATE: 2001-08-09
PRIOR PILING DATE: 2001-08-09
PRIOR PILING DATE: 2001-08-09
PRIOR PILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 215
PRIOR PILING DATE: 2001-03-28
NUMBER OF DATE: 2001-03-28
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fchernev, Velizar,
Vernet, Corine,
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                                                                                         259 TTRFYVDYDDLMLSL 273
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Shimkets, Richard,
Si, Jingsheng,
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Best Local Similarity 21.0%;
Matches 66; Conservative 4
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Spytek, Kimberly,
Stone, David,
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Gangolli, Esha,
Kekuda, Ramesh,
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Miller, Charles,
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APPLICANT: Casman, Stacie
APPLICANT: Colman, Steve,
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TYPE: PRT
CRGANISM: Homo sapiens
US-10-107-782-106
223 TSLSVTVKQA-
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APPLICANT: Barbazuk, Brad
APPLICANT: Li, Finge Brad
APPLICANT: Li, Finge Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 19-21 (53221)
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 191043
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                                                                                                                                                                                                                                                                                                                                                                                                                                              13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 BOTVEVVKSAIE----TADGALDFYNKYLDQVIP--WKTFDET---IKELSRFKQEYSQE
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US-10-437-963-191043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1225 RGELANEVKVLLQGGRD-------
PRIOR APPLICATION NUMBER: 60/285,189
PRIOR PILING DATE: 2001-04-20
PRIOR APPLICATION NUMBER: 60/308,039
PRIOR FILING DATE: 2001-07-26
PRIOR FILING DATE: 2001-08-09
PRIOR PILING DATE: 2001-08-09
PRIOR PILING DATE: 2001-08-09
PRIOR PILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 215
SEQ ID NO 107
LENGTH: 1999
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
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ORGANISM: Oryza sativa
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES AND METHODS OF USE THEREOF
FILE REFERENCE: 21402-222CIP
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                                                                                      Query Match
7.2%; Score 108.5; DB 14; Length 1999;
Best Local Similarity 19.5%; Pred. No. 8.3;
Matches 66; Conservative 53; Mismatches 124; Indels 95; Gaps
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1225 RGELANEVKVLLQGGRD--------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 10/028,248
PRIOR FILING DATE: 2001-12-19
PRIOR FILING DATE: 2000-12-19
PRIOR PILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/262,959
PRIOR APPLICATION NUMBER: 60/262,959
PRIOR APPLICATION NUMBER: 60/202,408
PRIOR FILING DATE: 2001-01-19
PRIOR FILING DATE: 2001-02-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Taupier, Raymond, jr.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shimkets, Richard,
Si, Jingsheng,
Smithson, Glennda,
Spytek, Kimberly,
Stone, David,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tchernev, Velizar,
Vernet, Corine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liu, Xiaohong,
Malyankar, Uriel,
Miller, Charles,
Millet, Isabelle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patturajan, Meera,
Rothenberg, Mark,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Edinger, Shlomit,
Gangolli, Esha,
Kekuda, Ramesh,
                       , ORGANISM: Rattus norvegicus US-10-028-248A-107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sciore, Paul,
Shenoy, Suresh,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Boldog, Ferenc,
APPLICANT: Casman, Stacie
APPLICANT: Colman, Steve,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vernet,
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78 EATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRILD-----DGVNKLNEAQ 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 GAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNDRL-KAVQNFFTSLSVTVKQANKDI-- 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        237 -DAAKLK-----LATEIAAIGEIKTETETTRFYVDYDDLMLSLLKGAAKKMINTCNEY 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   449 LDKABEAKLPRVVEEILTTSLKLSGNAQESISLIR------BRLPLAKGMLDDLIDTLSKI 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          334 SEKLSNIQSLNDTLVDFLTKINQLTSNNRLDDVIDNLEDSSNKIDSSISTLNDIKNKVIS 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       236 KTVDLASDATSKLSDTVKDIKSDLPTIKKT-----LNDTKLLSSDLKKFLEDTNDNLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 53523
LENGTH: 742
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                     Sequence 53523, Application US/10282122A Publication No. US20040029129A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-05-23
PRIOR PELICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PLING DATE: 2000-05-66
PRIOR PELING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/255,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2001-12-27
PRIOR PILING DATE: 2001-12-27
PRIOR PILING DATE: 2001-12-27
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
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PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
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R APPLICATION NUMBER: 60/206,848

R FILING DATE: 2000-05-23

R APPLICATION NUMBER: 60/207,727

R FILING DATE: 2000-05-26

R APPLICATION NUMBER: 60/230,335

R RILING DATE: 2000-09-06

R APPLICATION NUMBER: 60/230,347

R RILING DATE: 2000-09-06
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                                                                                                                                                                                                             Wang, Liangsu
Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                        Zyskind, Judith
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trawick, John
Carr, Grant
                                                                                                                                                                                                                                                                                                                                                                                                                                               Wall, Daniel
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Gldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTRINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILLE OF DATE: 2003-02-28
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            217
                                                                                                                                                                                                                                                                                           87 CGV----VIQLLSA----YILLFDEYNEKKASAQ-KDILIRILDDGVNKLNEAQKSLLGS 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                           138 -----SQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPF 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191 GLIISYSIAAGVIEGKLIPELNDRLKAVQNFFTSLSVTVKQANKDIDAAKLKLATEIAAI 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        450 - LLLEKDNMIKQLDGKLSDALSDSSKDREN-----IAALNKELDATKAMLENEVAAV 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104 YNEKKASAQKDILIR---ILDDGVNKLNEAQKSLLGSSQSFNNASGKLLALDSQLTNDFS 160
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                                                                         Gaps
                                                                     80;
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21.3%; Pred. No. 8.9;
tive 47; Mismatches 113; Indels
                                                                         95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 AEQTVEVVKSAIETADGALDFYNKYLDOVIPWKTFD--
                                      Pred. No. 2.7;
                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3279, Application US/10369493
Publication No. US20030233675A1
20.7%; ***
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                                                                         62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64; Conservative
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Best Local Similarity
Matches 64; Conserv
                                  Best Local Similarity
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LENGTH: 1965
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Green, Xianfeng
TITLE OF INVENTION: EXPESS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: EXPESS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(5205)B
CURRENT FILING DATE: 2003-02-8
PRIOR PLILING DATE: 2003-02-8
PRIOR PLILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO SILO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52 QEXSQ-----EASVLVG--DIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEY 104
                                                                                                                                                                                                                                             1373 SEISÕWKARYEGEGLVGSEELEELKRKOMNRVMDLOEALSAAQNKVISLEKAKGKLLAET 1432
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                                                                                                                                                                                                                                                                                                                                                                                                152
                                                                                                                                                                                                             5 PAEQTVEVVK------SAIETADGALDFYNKYLDQVIPWKTFDETIKELSRFK 51
                                                                                                                                                                                                                                                                                                                                                                                                105 NEKKASAQKDILI------RILDDGVNKINEAQKSLLGSSQSFNNASGKLLALD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  213 DRLKAVQNFFTSLSVTVKQANKD-----IDAAKLKLATEIAAIGEIKTETETTRFYVD
                                                                                                                                                                                                                                                                                                     52 QEYSQ-----EASVLVG--DIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEY
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                                                                                                                       DB 14; Length 1938;
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17.3%; Pred. No. 12;
tive 63; Mismatches 112; Indels
                                                                                                                       Query Match
7.1%; Score 106.5; DB 14; Length
Best Local Similarity 17.3%; Pred. No. 12;
Matches 52; Conservative 63; Mismatches 112; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1493 SSMDN-----LSEQIETLRRE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10.369-493-5110
Sequence 5110, Application US/10369493
Publication No. US20030233675A1
GRNERAL INFORMATION:
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; ORGANISM: Caenorhabditis elegans
US-10-369-493-5110
              LENGTH: 1938
TYPE: PRT
ORGANISM: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 7.1
Best Local Similarity 17.3
Matches 52; Conservative
                                                                                     US-10-369-493-5109
SEQ ID NO 5109
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US-10-369-493-5109
Sequence 5109, Application US/10369493
Sequence 5109, Application US/10369493
Sequence 5109, Application US/0030233675A1
GENERAL INFORMATION:
APPLICANT: Gao, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Marry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROFEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROFERIES
TITLE OF INVENTION: US/01369,493
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT PILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
                                                                                                                                                                           Sequence 9374, Application US/10369493

Sequence 9374, Application US/10369493

Sequence 9374, Application US/10369493

Sequence 9374, Application No. US20030233675A1

Sequence 9374, Application No. US200338675A1

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: BLANTS WITH IMPROVED PROPERTIES

TITLE OF INVENTION: BLANTS WITH IMPROVED PROPERTIES

TITLE OF INVENTION: UNMBER: US/10/369,493

CURRENT APPLICATION NUMBER: US 60/360,039

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR PRILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 9374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 LVGDIKVLLMDSQDKYFEAT-----QTVYEWCGVVTQLLSA---YILLFDEYNEKKAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 BQTVEVVKSAIETADGALDFYNK-----YLDQVIPWKTFDETIKELSRFKQEYSQEASV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 107.5; DB 14; Length 857; Fred. No. 3.2; 45; Mismatches 104; Indels 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          231 QANKDIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDLMLSLL 274
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Best Local Similarity 23.9%;
Matches 68; Conservative 45
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; ORGANISM: Xylella fastidiosa
US-10-369-493-9374
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SNGEDMKKLVSL 513
                                    289 QQRHGKKTLLEV 300
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PRIOR APPLICATION NUMBER: 60/272408
PRIOR PILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/285189
PRIOR FILING DATE: 2001-04-20
PRIOR FILING DATE: 2001-07-26
PRIOR FILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: 60/301266
PRIOR FILING DATE: 2001-07-26
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o. US20030235882A1
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Vernet, Corine
Casman, Stacie
Malyankar, Uriel
Shenoy, Suresh
Spytek, Kimberly
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Zerhusen, Bryan
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Edinger, Shlomit
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Millet, Isabelle
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Miller, Charles
Boldog, Ferenc
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 105
LENGTH: 1961
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liu, Xiaohong
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                                                                                                                                                                                                                                                    280 KMINTCNEYQ-
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Best Local Si
Matches 68
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--- NKIFSQEIRDIN 1520
                                                                                                                          1521 EQITQGGRTYQEVHKSVRRLEQEKDELQHALDEAEAALEAEESKVLRLQIEVQQIRSEIE 1580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112 OKDILIRILDDGVNKINEAOKSILGSS-----OSFNNASGKILALDSQLTNDFS 160
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PRIOR PELLING DATE: 2000-03-21
PRIOR PELLING DATE: 2000-03-21
PRIOR PELLING DATE: 2000-03-21
PRIOR PELLING DATE: 2000-05-23
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-09-65
PRIOR PELLING DATE: 2000-09-69
PRIOR PELLING DATE: 2000-09-69
PRIOR PELLING DATE: 2000-09-69
PRIOR PELLING DATE: 2000-09-69
PRIOR PELLING DATE: 2000-09-69
PRIOR PELLING DATE: 2000-01-23
PRIOR PELLING DATE: 2000-01-22
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PRIOR PELLING DATE: 2001-02-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION WIMBER: US/10/282,122A
CURRENT FILING.DATE: 2003-02-20
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7.1%; Score 106.5;
Best Local Similarity 21.5%; Pred. No. 28;
Matches 71; Conservative 49; Mismatches
                                                                                                                                                                                                                                                                               Sequence 71235, Application US/10282122A
Publication No. US20040029129A1
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                                                              213 DRLKAVQNFFTSLSVTVKQANKD--
   1493 SSMDN-----LSEOIETLRRE
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Carr, Grant
APPLICANT: Famamoto, Robert
APPLICANT: Famamoto, Robert
APPLICANT: Famamoto, Robert
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APPLICANT: Richembergy, Mark
TITLE OF INVENTION: No. US20030255882Alel Nucleic Acids and Polypeptides and Methods of
TITLE OF INVENTION: Thereof
FILE REFERENCE: 21402-222
CURRENT APPLICATION NUMBER: US/10/028,248A
PRIOR APPLICATION NUMBER: 60/256619
PRIOR PLING DATE: 2000-12-19
PRIOR FILING DATE: 2000-12-19
PRIOR PLING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/256519
PRIOR APPLICATION NUMBER: 60/256519
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                                                                                                                                                                        161 EKSSYFQSQVDRIRK-EAYAGAAGIVAGPFGLIISYSIAAGVIEGKLIPELNDRLKAVQ 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 EQTVEVVKSAIETADGALDFYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVLVGDIK 66
                                                               --IAKIGEAETDTTVNE---ARD
                                                                                                                                     220 NFFTSLSVTVKQANKDIDAAKLKLATBIAAIGEIKTETETTRFYVDYDDLMLSLLKGAAK
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                                                                                                                                                                                                                                                                                                             822 EAIQNINTAQGNDDVTEAQNNGTNTIQQVP 851
                                                                                                                                                                                                                                                                      -ORHGKKTLLEVP 301
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APPLICANT: Cao, Yongwei
APPLICANT: Hinle, Gregory J.
APPLICANT: Hinle, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
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APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfew B.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: ASPERSION OF MICROBIAL PROPERTIES
FILE REFERENCE: 38-10(52052)8
FILE REFERENCE: 38-10(52052)8
CURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2003-02-21
PRIOR PILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 497
LENTH: 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130
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                                                                                                                                                                                                                                                                                                                                                                                                          1259 VKFSEGERVRTELADKVSKLOVELDSVTGLINQSDSKSSKLTKDFSALESQLODTQELLQ 1318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1166 BOBVSILKKTLE------DEA---KTHEAQIQEM---ROKHSQAVEELABQLE 1206
                                                                                                                                                                                                                                                                                        67 VLLMDSQDXYFEAT----QTVYEWCGVVTQLLSAYILL----FDEXNEKKASAQ-KDIL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------DFSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLII8YSIAAGVI 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 QDKYFEATQTYYEWCGYVTQLLSAYILLFDEYNEKKASAQKDI---LIRILDDGVNKLNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131 GGNDLDAT-VVY---GVNHELLSA-----EDCIVSNASCTINCIIPIIKVLDD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 SAIETADGALDFYNKYLDQVIPWKT--PDETIKELSRFKQEYSQEASVLVGDIKVLLMDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 204 EGKLIPELNDRLKAVQNFPTSLSVTVKQA----NKDIDAAKLKLATEIAAIGBIKTETET
                                                                                                                                                                                                           7 EQTVEVVKSALETADGALDFYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVLVGDIK
                                                                                                                                                                                                                                                                                                                                                                      117 IRI-----LIDDGVNKLNBAQKSLLGSSQSFNNASGKLL----ALDSQLTN----
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                                                                                                                                                                         96;
                                                                                                                             7.0%; Score 106; DB 15; Length 1961; 21.7%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.0%; Score 105.5; DB 14; Length 21.2%; Pred. No. 1.4; trive 53; Mismatches 102; Indels
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1319 EENRQKLSLSTKLKQMEDEKNSFREQLEEEEEEEAKRNLEKQIAT----
                                                                                                                                                                         Indels
                                                                                                                                                                         50; Mismatches 100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , ORGANISM: Xenorhabdus nematophilus US-10-369-493-497
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 105
LENGTH: 1961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1417 TRLOQELDDLLVDL 1430
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Best Local Similarity 21.29
Matches 56; Conservative
                                                                                                                                                7.0%
Best Local Similarity 21.7%
Matches 68; Conservative
                                                                            , ORGANISM: Homo sapiens
US-10-107-782-105
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US-10-369-493-497
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                                            LENGTH: 19
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TLE OP INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES AND METHODS OF USE THEREOF
LE REFERENCE: 21402-222CIP
                                                                                                                                                                                                                                                                                                                     1166 EQEVSILKKTLE------DEA---KTHEAQIQEM---RQKHSQAVEELAEQLE 1206
                                                                                      ----- OTKRVKATLEKAKOTLENERGELANEVKA--LLOGKGDSEHKRKKVEAOLOELO 1258
                                                                                                                                                               1362
                                                                                                                                                                                                                                                                                              259
                                                  67 VLLMDSQDKYFBAT----QTVYBWCGVVTQLLSAYILL----FDEYNEKKASAQ-KDIL 116
                                                                                                                               117 IRI-----LDDGVNKLNEAQKSLLGSSQSFNNASGKLL----ALDSQLTN----- 157
                                                                                                                                                                                                             ------DFSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVI
                                                                                                                                                                                                                                                                                              EGKLIPELNDRLKAVONFFTSLSVTVKOA----NKDIDAAKLKLATEIAAIGEIKTETET
                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/107,782
CURRENT FILING DATE: 2002-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 10/028,248
PRIOR PELING DATE: 2001-12-19
PRIOR PELING DATE: 2001-12-19
PRIOR PELING DATE: 2000-12-19
PRIOR FILING DATE: 2000-10-19
PRIOR FILING DATE: 2000-10-19
PRIOR PELING DATE: 2001-01-19
PRIOR PELING DATE: 2001-02-28
PRIOR PILING DATE: 2001-02-28
PRIOR PILING DATE: 2001-04-20
PRIOR APPLICATION NUMBER: 60/285,189
PRIOR APPLICATION NUMBER: 60/308,039
PRIOR PILING DATE: 2001-04-20
PRIOR PILING DATE: 2001-04-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2001-U8-U7
PRIOR APPLICATION NUMBER: 60/279,344
PRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 215
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PRIOR FILING DATE: 2001-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 105, Application US/10107782
Publication No. US20040018970A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Taupier, Raymond, jr.,
Tchernev, Velizar,
Vernet, Corine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shimkets, Richard,
Si, Jingsheng,
Smithson, Glennda,
Spytek, Kimberly,
                                                                                                                                                                                                                                                                                                                                                                                                              || : |||:: |
1417 TRLQQELDDLLVDL 1430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boldog, Ferenc,
Casman, Stacie
Colman, Steve,
Edinger, Shlomit,
Gangolli, Esha,
Kekuda, Ramesh,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patturajan, Meera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rothenberg, Mark,
                                                                                                                                                                                                                                                                                                                                                                                     260 TRFYVDYDDLMLSL 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 yankar, Uriel,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Miller, Charles,
Millet, Isabelle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shenoy, Suresh,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sciore, Paul,
                                                                                                          1207
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182 ADAIVDDYPVLGYAVKNGQKLQLVGDKETGSSYGFAVKKGQNPELIKKFNAGLKNLKDNG 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89 VVIQLESAYILLFDEYNEKKASAQKDILIRILDDGVNKLNEAQKSLLGSSQS-----FN 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143 NASGKLLALDSQLTNDFSEKSSY-----FQSQVDRIRKEAYAGAAAGIVAGPFGLII 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                291 NAQGDYVGIDVDLVKRAABLQGFTVEPKFIGFSSAVQAVE----SGQADGMVAG----- 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             195 SYSIAAGVIEGKLIPELNDRLKA----VQNFFTSLSVTVKQAN----KDIDAAK-----LK 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 ÄVKKGNDKIKSYDDLKGKTVAAKVGTESANFLEKNKEKYDYTIKNFDDATGLYKALENGE 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 341 -------MIITDDRKKAFDFSVPYFDSGIQIAVKKGNDKIKSYDDLKGKKVGVK 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 AIETADGALDFYNKYLDQVIPWKTFDETIKELSRFKQEY------SQE
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Publication No. US20030175700A1
GENERAL INFORMATION:
APPLICANT: Bhatia, Ajay
APPLICANT: Probst, Peter
APPLICANT: Stromberg, Erika Jean
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND DIAGNOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 108;
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                                                                                                                                                                                                                                             APPLICANT: Indianal Prokarty
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REPERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/25,625
PRIOR APPLICATION NUMBER: 60/25,625
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/25,931
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-16
PRIOR PILING DATE: 2000-12-16
PRIOR PILING DATE: 2000-12-16
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
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larity 19.8%; Pred. No. 5;
Conservative 51; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243 LATEIA-AIGEIKTETETTRFYVDYDDLMLSLLK 275
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                                                                                                                                         Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
                                             Ohlsen, Kari L.
Zyskind, Judith W.
       Haselbeck, Robert
                                                                                                              Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 ASVLVGDIKVL
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66; Conserva
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US-09-841-260-139
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APPLICANT:
APPLICANT:
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Best Local S:
Matches 66
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 107270

LED IN NO 107270

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249 LVAEQKLNICEAEIERLKMELGALTEANE----AAAKAFDTQNEEITKELEDLKTKLEE 303
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US-10-437-963-107270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 107270, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
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Patent No. US20020061569A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Oryza sativa
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US-09-815-242-10796
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Match 6.9%; Score 103.5; DB 16; Length Local Similarity 21.7%; Pred. No. 4.9; es 68; Conservative 48; Mismatches 119; Indels
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Sequence 139, Application US/10762058
Sequence 139, Application No. US20040137007A1
GENERAL INFORMATION:
APPLICANT: Bhatia, Ajay
APPLICANT: Stromberg, Erika Jean
APPLICANT: Stromberg, Erika Jean
APPLICANT: Stromberg, Erika Jean
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APPLICANT: Stromberg, Erika Jean
APPLICANT: NUMBER: US/10/762,058
APPLICANT: NUMBER OF SEQ ID NOS: 140
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; Sequence 58016, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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Best Local S
Matches 68
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                                                                                                                                                                                                                                 DB 10; Length 660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 139, Application US/10007693
; Sequence 139, Application US2002046776A1
; Publication No. US20020146776A1
; GENERAL INFORMATION:
    APPLICANT: Bhatia, Ajay
; APPLICANT: Bracia, Peter
    TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT
    TITLE OF INVENTION: AND DIAGNOSIS OF CHLAMYDIAL INFECTION
    FILE REFERENCE: 210121.515C2
    CURRENT APPLICATION NUMBER: US/10/007,693
    CURRENT FILING DATE: 2001-12-05
    NUMBER OF SEQ ID NOS: 157
    SEQ ID NOS: 157
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6.9%; Score 103.5; DB 13; Length
Best Local Similarity 21.7%; Pred. No. 4.9;
Matches 68; Conservative 48; Mismatches 119; Indels
                                                                                                                                                                                                                                                                         Indels
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Best Local Similarity 21.7%; Pred. No. 4.9;
Matches 68; Conservative 48; Mismatches 119;
TITLE OF INVENTION: OF CHLAMYDIAL INFECTION PILE REFERENCE: 210121.515
CURRENT APPLICATION NUMBER: US/09/841,260
CURRENT FILING DATE: 2001-04-23
NUMBER OF SEQ ID NOS: 140
LENGTH: 660
                                                                                                                                                                                                                                                                                                                   8 QTVEVVKSAIETADGALDFYNKYL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRGANISM: Chlamydia trachomatis US-10-007-693-139
                                                                                                                                                                        , ORGANISM: Chlamydia trachomatis
US-09-841-260-139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         262 FYVDYDDLMLSLLK 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----DALAQALK 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 29
US-10-007-693-139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        155
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159 FSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGK-----LIPE 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       312 AEBĢISQAQKDIQEIKP---SGSDIPIV-GPSGSAASAGSAAGALKSSNNSGRISLLLDD 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     211 INDRLKAV----QNFFTSLSVTVKQANKDIDAAKLKLATE----IAAIGEIKTETETTR 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   368 VDNEMAAIALQGFRSMIEQFNVNNPATAKELQAMEAQLTAMSDQLVGADGELFAEIQAIK 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99 ILFDEYNEKKASAQKDILIRILDDGYNKLNEAQKSILGSSQSFNNASGKLLALDSQLTND 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   268 LOAQONNSPDNIAATKELIDAAETKVNELKOEHTGL-------TDSPLVKK 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             155 EEVNNIKKALEAQKDTIDKLNKLVTLQNQNKSLTEVLKTTDSADQIPAINSQLEINKNSA 214
                                                                         112 AEEQISQAQKDIQEIKP---SGSDIPIV-GPSGSAASAGSAAGALKSSNNSGRISLLLDD 367
                                                                                                                                       211 INDRLKAV-----QNFFTSLSVTVKQANKDIDAAKLKLATB----IAAIGBIKTETETTR 261
                                                                                                                                                                   368 VDNEMPALALQGFRSMIEQFNVNNPATAKELQAMEAQLTAMSDQLVGADGELPAEIQAIK 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 DETIKELSRFKOEVSQEASVLVGDIKVLLMDSQD--KYFEATOTVYEWCGVVTQLLSAYI
                                           159 FSEKSSYFOSOVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGK-----LIPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TREATMENT AND DIAGNOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79;
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268 LQAQQNNSPDNIAATKELIDAAETKVNELKQEHTGL--
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CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PAPLICATION NUMBER: 60/230,347
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PAPLICATION NUMBER: 60/253,625
PRIOR PAPLICATION NUMBER: 60/253,625
PRIOR PAPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Clostridium acetobutylicum
US-10-282-122A-51864
                                                            Wang, Liangsu
Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
Mall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
Publication No. US20040029129A1
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Best Local S
Matches 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50 FKQEYSQ-EASVLVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             246 AQLAKFNL-----ELGKLSESIQEQESILAKQRKENAQADRLIEKNQQVLLDLSEKLKQ 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  218 LKETLTQTDVSLMVAEIKTAKKD----------WDNKQ 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109 ASAQKDILIRILDDGVNKLNEA---QKSLLGSSQSFNNASGKLLALDSQLTNDFSEKSSY 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          166 FQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNDRLKAVQNFFTSL 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              226 SVTVKQANKDIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDLMLSLLKGAAKK---- 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----vioertkhtoxssoer 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --HFEKLQESLMKAAAEKETEIQ 354
                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: 05/10/282,122A

CURRENT FILING DATE: 2003-02-20

FRIOR PAPLICATION NUMBER: 60/191,078

FRIOR APPLICATION NUMBER: 60/206,848

FRIOR APPLICATION NUMBER: 60/206,848

FRIOR APPLICATION NUMBER: 60/207,727

FRIOR APPLICATION NUMBER: 60/230,335

FRIOR PILING DATE: 2000-05-26

FRIOR APPLICATION NUMBER: 60/230,335

FRIOR PILING DATE: 2000-09-06

FRIOR APPLICATION NUMBER: 60/230,347

FRIOR APPLICATION NUMBER: 60/230,347

FRIOR PILING DATE: 2000-10-23

FRIOR APPLICATION NUMBER: 60/253,625

FRIOR APPLICATION NUMBER: 60/253,625

FRIOR APPLICATION NUMBER: 60/257,931

FRIOR PILING DATE: 2000-12-22

FRIOR APPLICATION NUMBER: 60/257,931

FRIOR PILING DATE: 2001-02-09

FRIOR PILING DATE: 2001-02-09

FRIOR PILING DATE: 2001-02-09

FRIOR PILING DATE: 2001-02-09

FRIOR PILING DATE: 2001-02-09

FRIOR PILING DATE: 2001-02-06

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FRIOR FILING DATE: 2001-02-06

FRIOR FILING DATE: 2001-0
                                                                                                                                APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: APLICANT: APLICANT: XU
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 GIFAEQTVEVVK-----SAIETADG---ALDFYNKYLDQVIPWKTFDETIKELSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.9%; Score 103.5; DB 15; Length 1020;
19.8%; Pred. No. 8.9;
tive 41; Mismatches 90; Indels 133; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----MINTCNEYQ--QRHGKKTLLEVPD 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  322 QTSLAEAQK-----KVK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Enterococcus faecium
US-10-282-122A-58016
                        Zyskind, Judith
Wall, Daniel
Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 19.89
Matches 65; Conservative
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LENGTH: 1020
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US-10-282-122A-51864 ; Sequence 51864, Application US/10282122A

RESULT 32

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14:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               183 AGIVAGPFGLIISYSIAAGVIEGKLIPELNDRLKAVQNFFTSLSV-----TVKQANKD 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                236 IDAAKLKLATELAAIGEIKTETETTRFYVDYDDLMLSLLKGAAKKMIN-----TCNEYQ 289
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                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-23

PRIOR PLILNG DATE: 2000-05-26

PRIOR PLILNG DATE: 2000-09-06

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PRIOR PLILNG DATE: 2000-09-06

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PRIOR PLILNG DATE: 2000-10-23

PRIOR PLILNG DATE: 2000-10-23

PRIOR PLILNG DATE: 2000-11-27

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PRIOR PLILNG DATE: 2000-11-27

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PRIOR PLILNG DATE: 2000-12-22

PRIOR PLILNG DATE: 2001-02-06

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             290 PYIDNYENTLKQIDILKEQILSRENTMKAISLEKEDMEKKLSIAKDNKEK-----
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95; Gaps
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                                               FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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109 AS-----AQKDILIRILDDGVNK--LNEAQKSLIGSSQSFNNASGKLLALDSQLTND 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 AKDDRFGKALFQEFG------LDEG--KLKDIIKQVRGSQKVTDQNPEGKYE 161
                                                                                                                                                                                                                                     38 KTEDETIKELSRFKQEYSQEASVLVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAY 97
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                                                                                                                                                                                                                                                                                                                     98 I-----LLFDEYNEKKASAQKDILIRILDDGVNKLNEAQKSLLGSSQ-SFNNASGKLL
                                                                                                                                                                                                                                                                 61 KIRDRTEQFFQRQPKVSGTSSSVYLGRSLDTLLDRADVYRKEFQDEY1---SIEHLLLAY
                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                 41; Mismatches 111; Indels 102;
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                                                                                                                                                          Length 862;
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; Sequence 66, Application US/10080608A
; Publication No. US20030198956A1
; Publication No. US20030198956A1
; GENERAL INFORMATION:
; APPLICANT: Hyman, Paul
; APPLICANT: Hyman, Paul
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STARED ASSEMBLY OF NANOSTRUCTURES
; TITLE OF INVENTION: STARED
; CURRENT PRILIG DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE FEASERE FOR WINDOWS Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     231 QANKDIDAAKLK-----LATEIAAIGEIKTETETT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.8%; Score 103; DB 14;
22.0%; Pred. No. 9.1;
tive 53; Mismatches 129;
                                                                                                                                                          6.8%; Score 103; DB 14; 23.7%; Pred. No. 7.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | : :|:|:| :: | | | 341 DQPSVEDSISILRGLRER-----YENHHGVK 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DYDDL--MLSLLKGAAKKMINTCNEYQQRHGKK 295
                                                                                     TYPE: PRT ORGANISM: No. US20030233675Altoc punctiforme
                                                                                                                                                                                                                                                                                                                                                                                                        150 ALDSQLTNDFSEKSSYFQ----SQVDRIR----
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Matches 70, Conservative
                                                                                                                                                                                                           79; Conservative
PRIOR FILING DATE: 2002-02-:
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 19762
LENGTH: 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
CORGANISM: Bos taurus
US-10-080-608A-66
                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                              US-10-369-493-19762
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1424 DIEKAILEQOVLSBELITKKEQVSEAIKTSQİPLAKHG-HKLSEKEKKQI--SEQLNALN 1480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1481 KAYHDLCDGSANQLQQLQSQLAHQTEQKT--LQKQQNTCHQQLEDLCSWVGQAERALAGH 1538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89 VVTQLLSAYILLFDEYNEKK---ASAQKDILIRILDDGVNKLNEAQKSLLGSSQSFN--- 142
        396 IDSLTLKIQNLESKIDNLKVPEE----YKNKINEGIFLLRNYDEKLKHKNKLGLDCDKFQ 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29 KYLDQVIPWKTFDETIKELSRPKQEYSQEASVLVGDIKVLLMDSQDKYFEATQTVYEWCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 5373;
                                                                                                                                                                                                                                                                                    APPLICANT: Zhang, Bling
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale B.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.9%; Score 103.5; DB 16; Length !
llarity 23.0%; Pred. No. 86;
Conservative 49; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/408,765A CURRENT FILING DATE: 2003-04-04 NUMBER OF SEQ ID NOS: 3077 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 19762, Application US/10369493
Publication No. US20030233675A1
                                                                                                                                                                                                 Sequence 741, Application US/10408765A Publication No. US20040101874A1 GENERAL INFORMATION: APPLICANT: Ghosh, Soumitra S. APPLICANT: Fahy, Eoin D.
                                                            ---- QRHGKKTLL 298
                                                                                                  452 VDFEKAKSKKEML 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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611 LSOKEDVILKEHITOLEKKLOLMVEEQDNLNKLLENEQVOKLFVKTOLY----GFLKEMG 666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 IKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYI-LLFDEYNEKKASAQKDILIRILD-- 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     208 -----IPELNDRLKAVQNFFTSLSVTVKQANKDIDAAKLKLATEIAAIG----- 251
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
                                                                                                                                                                                                                                                                                                                                                                                                                                                              89; Indels 150;
                                                                                                                                                                                                                                                                                                                                                                                                           DB 16; Length 1583;
              APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
FITLE OF INVENTION: TERRIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FESSISE FOR WINDOWS VERSION 4.0
SEQ ID NO 1635
LENGTH: 1583
                                                                                                                                                                                                                                                                                                                                                                                                                                                              55; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 6.8%; Score 103; D
Best Local Similarity 19.9%; Pred. No. 18;
Matches 73; Conservative 55; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 55283, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
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Yamamoto, Robert
Forsyth, R.
  Glenn, Gary M.
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                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           297 LLEVPDI 303
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APPLICANT:
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APPLICANT: Goldberg, Edward
TITLE OF INVENTION: Nanostructures Containing PNA Joining and Functional Elements
FILE REFERENCE: NANF.P-004
CURRENT APPLICATION NUMBER: US/10/370,685
CURRENT FILING DATE: 2003-02-21
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 159
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
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FSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKL-----IPELN 212
                                                                                                        DRLKAVQNFFTSLSVTVKQANKDIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDLMLS 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               599 DOYNL-----LKVQLGKDSQHQGPYTDGAQ----MNGVQPEEISR---LREEIEELK 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 AS-----AQKDILIRILDDGVNK--LNEAQKSLLGSSQSFNNASGKLLALDSQLTND 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1635, Application US/10408765A
Publication No. US20040101874A1
GENERAL INFORMATION:
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Fahy, Boin D.
APPLICANT: Zhang, Bing APPLICANT: The APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: Taylor, Steven W.
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 155, Application US/10370685; Publication No. US20030215903A1; GENERAL INFORMATION:
                                                                                                                                                        861 NEIKALSEERTAIKEQLDSSNSTI
                                                                                                                                                                                                                LLKGAAKKMINTCNEYQO 290
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LLADQDQKIFSLKNKLKE 928
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Best Local Similarity 22.0%
Matches 70; Conservative
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; ORGANISM: Bos taurus
US-10-370-685-155
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57 BASVLVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYI-----LLFDEYNEKKAS 110
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249 NSADVYTREESDSKFVRIDGINATTEKLDTRLASAEKSIADHDTRLNGLDKTVSD---- 303
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Sequence 155, Application World 10670A1

Publication No. US20040110670A1

GENERAL INFORMATION:

APPLICANT: BAITCO, Maria B., et al.

TITLE OF INVENTION: Heterologous Expression of Neisserial Proteins

TITLE OF INVENTION: Heterologous Expression of Neisserial Proteins

TITLE OF INVENTION: Heterologous Expression of Neisserial Proteins

CURRENT APPLICATION UNDER: US010/20, 481

CURRENT FILING DATE: 2003-05-05

PRIOR APPLICATION NUMBER: PCT/1B01/00452

PRIOR FILING DATE: 2001-02-28

NUMBER OF SEQ ID NOS: 633

SOFTWARE: SeqWin99, version 1.02
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                                                                                                                                                                                Query Match 6.8%; Score 102; DB 15; Length 590; Best Local Similarity 21.4%; Pred. No. 5.7; Smatches 74; Conservative 62; Mismatches 129; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              263 ----YVDYDDLMLSLLKGAAKKMINTCNEYQQRHGKKTLLEVPDI 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :: | :: | : | | : | 404 DFIRQIEVDGQLITLESGEFQ-----VYKQSHSALTAFQTEQI 441
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6.8%; Score 102; DB 16; Length 5
Best Local Similarity 21.4%; Pred. No. 5.7;
Matches 74; Conservative 62; Mismatches 129; Indels
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ORGANISM: Artificial Sequence
ORGANISM: Artificial Sequence
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US-10-220-481-155
                                                      ; FEATURE:
; CTHER INFORMATION: 961C-741
US-10-220-480-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-220-481-155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -DGVNKINEAQKSLLGSSQSFNNA----SGKLLALDSQLTNDF----SEKSSYFQSQVD 171
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                     25 DFYNKYLDQVIPWKTFDETIK------ELSRFKQEYSQEASVLVGDIKVLLAMDS
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VBS-10-120-480-50

Sequence 50, Application US/10220480

Publication No. US20040092711A1

GENERAL INFORMATION:

APPLICANT: Chiron SpA

TITLE OF INVENTION: Hybrid Expression of Neisserial Proteins

FILE REFERENCE: POS-708-WO

CURRENT APPLICATION NUMBER: US/10/220,480

CURRENT APPLICATION NUMBER: US/00-02-28

PRIOR APPLICATION NUMBER: GB 0004695.3

PRIOR FILING DATE: 2000-02-28

PRIOR FILING DATE: 2000-11-13

NUMBER OF SEQ ID NOS: 121

SOFTWARE: SeqWin99, version 1.02

SEQ ID NO 50

LENGTH: 590
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Pred. No. 3.8; 42; Mismatches 105;
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312 LIDDYPGLKITDLRARARRM 331
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Best Local Similarity 23.11
Matches 74; Conservative
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LENGTH: 1903
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US-10-766-993-3
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353 HKDKGLQ-----SLTLDQSVRKNE--KLKLAAQGAEKTYGNGDSLNTGKLKND-KVSRF 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             271 NSADVYTREESDSKFVRIDGLNATTEKLDTRLASAEKSIADHDTRLNGLDKTVSD---- 325
                                                    213 DRLKAVQNFFTSLSVTVKQANKDIDAAKLKLATEIAA------IGEIKTETETTRF 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111 AQKDILIR-----ILDDGVNKLNEAQKSLLGSSQ-SFNNASGKLLALDSQLTNDFSEK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163 SSYFQSQVDRIRKEAYAG----AAAGI----VAGPFGLIISYSIAAGVIEGKLIPELN 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         213 DRLKAVONFFTSLSVTVKQANKDIDAAKLKLATELAA------IGEIKTETETTRF 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62; Mismatches 129; Indels 80; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: ARICO, Maria B., et al.
TITLE OF INVENTION: Heterologous Expression of Neisserial Proteins
FILE REFERENCE: CHIR-15883/01US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 612;
                                                                                                                                                                                                                                                                                                      APPLICANT: Chiron SpA
TITLE OF INVENTION: Hybrid Expression of Neisserial Proteins
FILE REFERENCE: P026783M0
CURRENT APPLICATION NUMBER: US/10/220,480
CURRENT FILING DATE: 2000-02-28
PRIOR PFLIANG DATE: 2000-02-28
PRIOR FILING DATE: 2000-02-8
PRIOR FILING DATE: 2000-11-13
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Seqwin99, version 1.02
SEQ ID NO 56
                                                                                                                          263 ----YVDYDDLMLSLLKGAAKKMINTCNEYQQRHGKKTLLEVPDI 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      263 ----YVDYDDLMLSLLKGAAKKMINTCNEYQQRHGKKTLLEVPDI 303
                                                                                                                                                 DFIRQIEVDGQLITLESGEFQ-----VYKQSHSALTAFQIEQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 6.8%; Score 102;
Best Local Similarity 21.4%; Pred. No. 6
Matches 74; Conservative 62; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 161, Application US/10220481 Publication No. US20040110670A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                               Sequence 56, Application US/10220480 Publication No. US20040092711A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
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; OTHER INFORMATION: 961cL-741
US-10-220-480-56
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111 AQKDILIR-----ILDDGVNKLNEAQKSLLGSSQ-SFNNASGKLLALDSQLTNDFSEK 162
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APPLICANT: Liu, Xiaowen
APPLICANT: Liu, Xiaowen
APPLICANT: Lewicki, John A.
APPLICANT: Xu, Qiang
APPLICANT: Osel, Inc.
TITLE OF INVENTION: Surface Expression of Biologically Active Proteins in
TITLE OF INVENTION: Bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 FAEQTV-----EVVKSAIETADGALDFYNKYLDQVIPWKT-FDETIKELSRFKQEYSQ
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MAME/KEY: DOMAIN
LOCATION: (1309)..(1903)
OTHER INFORMATION: CWA200 cell wall associated region with anchor
OTHER INFORMATION: motif
                                                                                                                                                                                                                                                                                                                                                                                                DB 16; Length 612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                263 ----YVDYDDIMLSLIKGAAKKMINTCNEYQQRHGKKTLLEVPDI 303
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                                                                                                                                                                                                                                                                                                                                                                                             6.8%; Score 102; DB 16;
21.4%; Pred. No. 6;
tive 62; Mismatches 129;
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CURRENT APPLICATION NUMBER: US/10/766,993
CURRENT FILING DATE: 2004-01-28
FRIOR APPLICATION NUMBER: US 60/443,619
PRIOR FILING DATE: 2003-01-29
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 3
CURRENT APPLICATION NUMBER: US/10/220,481
                       CURRENT FILING DATE: 2003-05-05
PRIOR APPLICATION NUMBER: PCT/IB01/00452
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 633
SSCPTWARE: SeqWin99, version 1.02
SEQ ID NO 161
LENGTH: 612
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Publication No. US20050003510A1
GENERAL INFORMATION:
                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                             ; FEATURE:
; OTHER INFORMATION: 961cL-741
US-10-220-481-161
                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 21.4 Matches 74; Conservative
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Sequence 164, Application US/10171311
Publication No. US20030087270A1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
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US-09-927-597-2
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Best Local S
Matches 69
                    1587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7611, Application US/10032585
Publication No. US20030180953A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Terry, Reemer D.
APPLICANT: Howard, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REFERENCE: 10182-005-999
CURRENT APPLICANTON NUMBER: US/10/032,585
CURRENT PILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: PATENTING DATE: 201-12-20
NUMBER OF SEQ ID NOS: 8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; | ; | ; | ; | ; | 118. | ; | 118. | ; | 118. | ; | 118. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 1315. | ; | 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 6.8%; Score 102; DB 17; Length 1903;
Best Local Similarity 19.1%; Pred. No. 28;
Matches 63; Conservative 42; Mismatches 109; Indels 116; Gaps 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 --TVYEWCGVVTQL------LSAYILLFDEYNEKKASAQKDILI--RIL 120
                                                                                                                                                                                                                                                                                                                                                                       .-----EEVKNNS 1390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DDGVNKLNEAQKSLLGSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDRIRKEAYAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                      48 SRFK--QEYSQEASVLVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYN 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      106 EKKASAQKDILIRILDDGVNKLNBAQKSLLGSS-----QSFNNASGKLLALDSQL 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TNDFSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNDRL 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     216 KAVQNFFTSLSVTVKQANKDIDAAKLKLATEIAAIGEIKTETETTRF----YVDYDDLMLS 272
                                                                                                                                                                                                                                                                                                                          6 AEQIVEVVKSAIETADGALD-----FYNKYLDQVIPWKT-------FDETIKEL 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 DFYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVLVGDIKVLLMDSQDKYFEATQ---
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, NAME/KEY: PEPTIDE
; LOCATION: (1868)..(1872)
; OTHER INFORMATION: anchor motif, sorting signal, cell wall targeting
; OTHER INFORMATION: region
US-10-766-993-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16;
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21.9%; Pred. No. 29;
tive 41; Mismatches 97; Indels 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1447 KFDEALKKAENVKND----SNATOKEVDD 1471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               273 LLKGAAKKMINTCNEYQQRHGKKTLLEVPD 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1362 TDKYKNASDDTKSKFDDALKKA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity Matches 60; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 44
US-10-032-585-7611
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APPLICANT: Chen, Yan
APPLICANT: Chen, Yan
APPLICANT: Chen, Xumei
APPLICANT: Chen, Xumei
APPLICANT: Chen, Xumei
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APPLICANT: Chentant Glatt, Karen
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APPLICANT: Glatt, Karen
APPLICANT: Denneyerapu, Manjula
APPLICANT: Denneyerapu, Manjula
APPLICANT: MUMER: US/10/171,311
CURRENT APPLICATION NUMBER: US 60/298,159
PRIOR APPLICATION NUMBER: US 60/298,155
PRIOR APPLICATION NUMBER: US 60/298,155
PRIOR APPLICATION NUMBER: US 60/298,155
PRIOR APPLICATION NUMBER: US 60/335,936
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-11-14
NUMBER OF SEQ ID NOS: 238
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 164
LEMOTH: 1938
TYPE: PRT
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                                                                                QNF---FTSLSVTVKQANKDIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDLMLSLLK 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52 OBYSOBASVIJVGDIKVILMDSQDKYFBATQTVYEWCGVVTQLLSAYILLFDBYNEKKASA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 OKDILIRILDDG-----VNKLNBAOKSLLGSSOSFNNASGKLLALDSOLTNDFSE 161
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181 AAAGIVAGPFGLIISYSIAAGVIEGKLIPE-LNDRLKAVON--FFTSLSVTVKQANKDID
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                                                                                                                                                                                                                                                                                                                                                 |:| | | | : :||:|::|
----PKTDI----ETKLIKENKKLQLDYEDVLL 1658
                                                                                                                                                                                                                                                                       238 AAKLKLATEIAAIGEIKTETETTRFYVDYDDLML 271
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Query Match
Best Local Similarity 21.8
Matches 69; Conservative
                                                                                                                                                                                                                                             , ORGANISM: Homo sapiens
US-10-171-311-162
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US-10-341-434-103
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                                                                                                                                                                                                               TYPE: PRT
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APPLICANT: Schlegel, Robert
APPLICANT: Chin, Yan
APPLICANT: Chao, Yan
APPLICANT: Chao, Yanei
APPLICANT: Monahan, John
APPLICANT: Monahan, John
APPLICANT: Ganavarapu, Manjula
APPLICANT: Ganavarapu, Manjula
APPLICANT: Ganavarapu, Manjula
APPLICANT: Ganavarapu, Manjula
APPLICANT: Ganavarapu, Manjula
APPLICANT: Hoersh, Sebastian
ITILE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
ITILE OF INVENTION: NOVEL GENES, CANCER
ITILE OF INVENTION: OF CERVICAL CANCER
FILE REFERENCE: MIL-035
CURRENT APPLICATION NUMBER: US/10/171,311
CURRENT PILING DATE: 2002-06-13
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 10; Length 1945;
                                                                                      APPLICANT: Beraud, Christophe
APPLICANT: Beraud, Christophe
APPLICANT: Feddman, Richard
APPLICANT: Freedman, Richard
APPLICANT: Craven, Andrew
APPLICANT: Sakowicz, Roman
APPLICANT: Hartman, James
TITLE OF INVENTION: Human smooth muscle myosin heavy chain
FILE REFERENCE: CYTOPO18
CURRENT APPLICATION NUMBER: US/09/927,597
CURRENT APPLICANTON DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2

TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTA
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21.8%; Pred. No. 32;
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Publication No. US20030087270A1
GENERAL INFORMATION:
Application US/09927597
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                                 Publication No. US20030032018A1
GENERAL INFORMATION:
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TYPE: PRT
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                                                                                                                                                                    DB 14; Length 1972;
                                                                                                                                                                  Query Match 6.7%; Score 101.5; DB 14; Length Best Local Similarity 21.8%; Pred. No. 33; Matches 69; Conservative 48; Mismatches 105; Indels
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21.8%; Pred. No. 33;
ive 48; Mismatches 105; Indels
PRIOR APPLICATION NUMBER: US 60/335,936
PRIOR FILING DATE: 2001-11-14
NUMBER OF SEQ ID NOS: 238
SEQ ID NO 162
LENGTH: 1972
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                             1260 OVQELOSKCSDGERARAELNDKVHKLONEVESVTG---MLNEAEGKAI----KLAKDVAS 1312
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                                                            162 KSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIE---GKLIPELNDRLKAV 218
                                                                                                                        ONF---FTSLSVTVKQANKDIDAAKLKLATEIAAIGBIKTETETTRFYVDYDDLMLSLLK 275
112 OKDILIRILDDG-----VNKLNEAOKSILGSSOSFNNASGKLLALDSQLTNDFSE 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 BOTVEVVKSAI--ETAD------GALDFYNKYLDQVIPWKTFDETIKELSRFK
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Best Local Similarity 21.8%; Pred. No. 33;
Matches 69; Conservative 48; Mismatches 105; Indels 95;
                                                                                                                                                                                                                                                                                                                                            APPLICANT: Malik, Fady
APPLICANT: Beraud, Christophe
APPLICANT: Beraud, Christophe
APPLICANT: Freedman, Richard
APPLICANT: Treedman, Andrew
APPLICANT: Sakowicz, Roman
APPLICANT: Hartman, James
TITLE OF INVENTION: Human smooth muscle myosin heavy chain
FILE REFERENCE: CYTOPO18
CURRENT FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 4
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                Sequence 4, Application US/09927597 Publication No. US20030032018A1 GENERAL INFORMATION:
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ORGANISM: Human
US-09-927-597-4
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RESULT 50 8-10-369-493-6362 ; Sequence 6362, Application US/10369493 ; Publication No. US20030233675A1

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APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfend S.
APPLICANT: Chen, Xianfend S.
APPLICANT: Chen, Xianfend S.
APPLICANT: Chen, Xianfend S.
APPLICANT: Chen, Xianfend S.
TITLE OF INVENTION: ELANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52062)8
FILE REPERENCE: 38-10(52062)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR PLILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 6362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         176 BAYAGAAAGIVAGPFGLIISY------SIAAGVIEGKL-----IPELNDRL 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               392 ESQTTSES-----LKYEHELVRKYMIEDMEKLEAEVLALKSQQANLEIQBFHDKI 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 QEASVINGDIKVILMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDI 115
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17.9%; Pred. No. 24;
tive 52; Mismatches 117;
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Job time : 148 secs
                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Caenorhabditis elegans
Hinkle, Gregory J. Slater, Steven C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 17.99
Matches 53; Conservative
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Perfect score:

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Searched:

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61 LVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRIL 120
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Batent No. US20020146430A1

GENERAL INFORMATION:

APPLICANT: James E. Galen

APPLICANT: University of Maryland

ITILE OF INVENTION: USE OF CLY A HEMOLYSIN FOR EXCRETION OF

ITILE OF INVENTION: PROTEINS

FILE REFERENCE: UOFMD.007A

CURRENT APPLICATION NUMBER: US/09/993,292A

CURRENT FILING DATE: 2001-11-23

PRIOR APPLICATION NUMBER: 60/252,516

PRIOR APPLICATION NUMBER: 60/252,516

NUMBER OF SEQ ID NOS: 19

SOFTWARE: FRESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
5 US-10-282-122A-46343

4 US-10-369-493-6440

4 US-10-369-493-6440

4 US-10-369-493-5110

5 US-10-282-122A-53523

6 US-10-437-963-10270

6 US-10-437-963-10270

6 US-10-369-493-497

5 US-10-369-493-497

6 US-10-369-493-497

10S-09-8185-535-4

6 US-10-408-765A-666

5 US-10-408-765A-666

5 US-10-408-765A-666

6 US-10-425-115-22623

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Pred. No. 9.9e-118;
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Best Local Similarity 100.0%;
Matches 305; Conservative 0
   ORGANISM: Salmonella Typhi
  US-09-993-292A-2
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LENGTH: 305
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Sequence 5221, Ap
Sequence 1061, Ap
Sequence 212070,
Sequence 7611, Ap
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Sequence 5, Appli
Sequence 5220, Ap
Sequence 5221, Ap
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Sequence 197045,
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Copyright (c) 1993 - 2005 Compugen Ltd
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Sequence 5. Application US/09884696

| Sequence 5. Application No. US2003003809A1
| Publication No. US2003003809A1
| Publication No. US2003003809A1
| Publication No. US2003003809A1
| APPLICANT GEORGE, LISLE W
| APPLICANT HESS, JOHN A
| APPLICANT HESS, JOHN A
| APPLICANT HESS, JOHN A
| APPLICANT HESS, JOHN A
| TITLE OF INVENTION: MORAXELLA BOVIS CYTOTOXIN GENE, ANTIBODIES
| TITLE OF INVENTION: MOY SIGNE NOT SIGNE AND TREATMENT OF MORAXELLA
| TITLE OF INVENTION: WOUNDER: US/09/884,696
| CURRENT APPLICATION NUMBER: US/09/884,696
| CURRENT FILING APTE: 2001-06-19
| CURRENT FILING APTE: 2001-06-19
| SOFTWARE: PATENTING APEL 2.1
| SEQ ID NO 5:
                                                                                                                                                                            GENERAL INFORMATION
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Gao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
TITLE OF INVENTION: SPANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION UNMERR: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR PLICATION NUMBER: US 60/360,039
PRIOR PLICATION NUMBER: US 60/360,039
PRIOR PLICATION NUMBER: 202-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 10918
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; Pred. No. 0.16;
52; Mismatches 119; Indels 70
544 KSTKESYEVMLDEANYDITCLRKNVDKLEAEVNKYREECESKET 587
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Publication No. US20030233675A1
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ORGANISM: Ferroplasma acidarmanus
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APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: APPLICANT: Cao, Yongwei
APPLICANT: Boucharov, Andrey A.
APPLICANT: Buckharov, Andrey A.
APPLICANT: Buckharov, Andrey A.
APPLICANT: Barbaruk, Brad
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                                  DDGVKKLANEAQKSILITSSQSFNNASGKILALDSQLTNDFSFKSSYFQSQVDRIRKEAYAG 180
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US-10-437-963-197045
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; Sequence 197045, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
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ORGANISM: Oryza sativa
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Gldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)8
FURENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
                                                                                                                                                                                                                                                      --VKRLG 2136
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1881 DLKNR-IDVLEQWMNDYRETIYDVSKKDTADAERMSLVVGKRINRYKEVSNEIEKLRVEA 1939
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1997 DEBYVQTAGRHAEKLEVQAQK-IVDRFVDTRTETENPLKASHAYENIVBALKNATEAVDS 2055
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                                                                                                        ----- 2097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194 ISYSIAAGVIE--GKLIPELNNRLKTVQNFFTSLSATVKQANKDIDAAKLKLATEIAAIG 251
                                                                                                                                                                            194 ISYSIAAGVIE--GKLIPELNNRLKTVQNFFTSLSATVKQANKDIDAAKLKLATEIAAIG 251
                                         134 LLTSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLI 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----YFEATQTV-----YEWCGVVTQLLSAYILLFDEY
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                                                                                                                                                                                                                                                                                                                                                                       252 BIKTETETTRFYVDYDDLMLSLLKGAAKKM-INTCNEYQQRHGKKT 296
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7.5%; Score 113.5; D
Best Local Similarity 20.8%; Pred. No. 8.5;
Matches 72; Conservative 57; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5221, Application US/10369493 Publication No. US20030233675A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 1061, Application US/10369493; Publication No. US20030233675A1; GENEAL INFORMATION: APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 5221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73 QDK-----
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Publication No. US20030233675A1

GRENEAL INFORMATION:
GAPPLICANT: Gao, Yongwei
APPLICANT: Glodman, Barry S.
APPLICANT: Glodman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54 YSQEASVL------VGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILL-FDEY 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NEKKASAQKDILIRILDD---GVKKLNEAQKSLLTSSQSFNNASGKLLALDSQLTNDFSE 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -------AAAAGLIASVVTLAİSPLSFLSİADKFKRANKİEEYSQRFKK 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             162 KSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIIS----YSIAAGVIEGKLIPELNNRLKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           218 VQNFFTSLSATVKQANKDIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDLMLSLLKGA
                                                                                                                                                                                                                                                                                                                          2 TSIFAEQTVEVVK-----SAIETADGALDLYNKYLDQVIPWKTFDETIKELSRFKQE
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7.5%; Score 113.5; DB 14; Length 2823;
Best Local Similarity 20.8%; Pred. No. 8.5;
Matches 72; Conservative 57; Mismatches 96; Indels 121;
                                                                                                                                                                               Length 1023;
                                                                                                                                                                            7.7%; Score 116; DB 10; Length 1 larity 20.5%; Pred. No. 1.3; Conservative 59; Mismatches 111; Indels
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; ORGANISM: Caenorhabditis elegans
US-10-369-493-5220
                                 TYPE: PRT
ORGANISM: Escherichia coli
                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 5
US-10-369-493-5220
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LENGTH: 2823
LENGTH: 1023
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generac 761, Application US/10032585

publication No. US20030180953A1

general INFORMATION:

GENERAL INFORMATION:

APPLICANT: Gener D.

APPLICANT: Charles, Boone

APPLICANT: Charles, Boone

APPLICANT: General, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, Beneral, 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 KLATBIAAIGBIKTBITTTRYVDYDDLMLSLLKGAAKKMINTCNB--YQQR---HGKKT 296
                                                                                                                                                                                                                                                                                            : : : | | : | : | : | | B-----1QRLKSEKASLQGILEEKDLELS----SARKWLGDVNQEIYDLKWLWHSKET 303
                                                                                                                                                                                         115 LINDVRSELVSSQQALASSRSKWERGERLLELQLSELGEGRASVMSYMENLKDAQIEV-- 172
                                                                                                                                                                                                                                                                                                                                                                              182 AAGIVAGPFGLIISYSIAAGVIEGKLIPELNNRLKTVQNFFTSLSATVKQANKDIDAAKL 241
                                                                                                                                                                                                                                                                                                                                                                                                                         61 EVEREKLRVAEANLE-----KOAMDWMLAQEELKRLGEDAARHAEESSETLEDFRRVKK 114
                                                                                                                             LLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQ-----KDILIRILD 121
                                                                                                                                                                                                                                                       122 DGVKKLNEAQKSLLTSSQSFNNASGKLLALDSQLTNDFSEKSSYFOSGVDRIRKEAYAGA 181
   EVVKSAIETADGALDLYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVLVGD---IKV 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194 ISYSIAAGVIEGKLIPE-LNNRLKTVQN--FFTSLSATVKQANKDIDAAKLKLATEIAAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38 KTFDETIKELSRFKQEYSQEASVLVGDIKVLLMDSQDKYFEATQ----TVYEWCGVVTQ
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7.4%; Score 112.5; DB 14; Length 1948;
Best Local Similarity 22.2%; Pred. No. 6.2;
Matches 58; Conservative 40; Mismatches 90; Indels 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1556 LLLVREE-----LRTTQILIKDFRIKVENLEATIEE-----
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; Sequence 70920, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Candida albicans
US-10-032-585-7611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
US-10-032-585-7611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93
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Sequence 212070, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Cao Vongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5322)B
CURRENT FILING NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 212070
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Gldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
FILE REFERENCE: 38-10(52052)8
FILE REFERENCE: 38-10(52052)8
CURRENY PAPLICATION NUMBER: US $6/369,039
PRIOR PAPLICATION NUMBER: US $6/360,039
PRIOR PAPLICATION NUMBER: US $6/360,039
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 1061
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEL--NNR--LKTVQNFFTSLSATVKQANKDIDAAKLKLATEIAAIGEIKTETETTRFYV 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     605 DEILEDIKSQLNKFK---NFYNQYLSAVSYLNSVDEEGIRNRİKEIENIVSGWNKEKCRE 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EASVL-----VGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKAS 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111 AQKDILIRILDDGVKKLNEAQKSLLTSSQSFNNASGKLLALD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91; Indels
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US-10-424-599-212070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 7.5%; Score 113; DB Best Local Similarity 19.7%; Pred. No. 2.3; Matches 60; Conservative 55; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         758 ILEVNKEINDIEĖRIŠYINOKLDE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Methanococcus jannaschii
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EYLD 852
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US-10-424-599-212070
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Wall, Daniel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 EESAGVLKYKKRKAESIQKLDHTEDNLNRVEDILYDLEGRVEPLKERAAIAKEYKQLSKE 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 LVGDIKVLLMDSQDKYFEATQTVYEWC-------GVVTQLLSAYILLFDEYNE 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 EQTVEVVK-----SAIETADGALDLYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASV 60
                                                                                                                                                                                                                                                                                                                                                               CANT: Xu, H. OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82;
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18.3%; Pred. No. 3.5;
tive 60; Mismatches 130; Indels 82
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                                                                                                                                                                                                                                                                                                                                                                                                           TILLE REFERENCE: ELITRA, 034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT PILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR PILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

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PRIOR PILING DATE: 2000-05-09

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PRIOR PILING DATE: 2000-05-09

PRIOR PILING DATE: 2000-05-09

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-12-22

PRIOR PILING DATE: 2001-12-22

PRIOR PILING DATE: 2001-12-2

PRIOR PILING DATE: 2001-12-2

PRIOR PILING DATE: 2001-02-09

PRIOR PILING DATE: 2001-02-09

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; ORGANISM: Staphylococcus epidermidis
US-10-282-122A-70920
                                 Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
                                                                                                                                                                                                                                                                                              Yamamoto, Robert
Forsyth, R.
Liangsu
dio. Carlos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 18.34
Matches 61; Conservative
                                                                                                                                                           Zyskind, Judith
Wall, Daniel
                                                                                                                                                                                                                           Trawick, John
Carr, Grant
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LENGTH: 1189
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235 DIDAAKLKLA----TEIAAIGEIKTETETTRFYVDYDDLMLSLLKGAAKKMINTCNEYQQ 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 VKKINE-AQKSLLTSSQSFNNASGKILALDSQLTNDFSEKSSYFQSQVDRIRKEAYAGAA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            320 -GMVINQFSSFYTPSEQGSSGIYADFLSESKLFQETQGNRIGELQKEIAELHMQVEQ--- 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 DIKVLIMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRILDDG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 AGIVAGPFGLIISYS-----IAAGVIEGKLIPEL-NNRLKTVQNFFTSLSATVKQANK 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 IFAEQTVEVVKSAIETADGALDLYNKYLDQVIPWKTFDBTIKELSRFKQEYSQEASVLVG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION UNBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-23

PRIOR PELING DATE: 2000-05-6

PRIOR PILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR PILING DATE: 2000-09-09

PRIOR PILING DATE: 2000-09-09

PRIOR PILING DATE: 2000-01-23

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR PILING DATE: 2000-12-22

PRIOR PILING DATE: 2001-12-22

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-16

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR PILING DATE: 2001-02-16

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR PILING DATE: 2001-02-16

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR PILING DATE: 2001-02-16

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR PILING DATE: 2001-02-16

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR PILING DATE: 2001-02-16

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Xu, H. TILLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 7.4%; Score 111.5; DB 15; Length 1158; Best Local Similarity 21.0%; Pred. No. 3.7; Matches 66; Conservative 58; Mismatches 121; Indels 69; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
Sequence 56861, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                              Trawick, John
Carr, Grant
Yamamoto, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-03-21
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APPLICANT: Taupier, Raymond, jr.,
APPLICANT: Tchernev, Velizar,
APPLICANT: Vernet, Corine,
APPLICANT: Zerhusen, Brian
APPLICANT: Zerhusen, Brian
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES AND METHODS OF USE THEREOF
FILE REFERENCE: 21402-222CIP
                                                       1258 VKFNEGERRYTELADKVTKLQVELDNVTGŁLSQSDSKSSKLTKDFSALESQLQDTQELLQ 1317
                                                                                                                                                                                                                                                     ----ROKL--SLSTKLKOVEDEKNSFREQLEEEEE 1349
                                                                                                                                                                                                                                                                                                                                                                                      :| ::: ::|| | : ::| | : :| | : :| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
                                                                                                                                                                                                                                                                                                                                  231 QANKDIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDL-MLSLLKGAAKKMINTCNEYQ 289
                                                                                                                                                          175 KEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNNRLKTVQ----NFFTSLSATVK 230
118 RILDDGVKKLNEAQKSLLTSSQSFNNASGKLLALD---SQLTNDFSEKSSYFQSQVDRIR 174
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PRIOR PELING DATE: 2001-12-19
PRIOR PELING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/266,619
PRIOR PELING DATE: 2000-10-19
PRIOR PELING DATE: 2001-01-9
PRIOR PELING DATE: 2001-02-28
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-03-28
PRIOR PELING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: 60/205,189
PRIOR APPLICATION NUMBER: 60/308,039
PRIOR PELING DATE: 2001-03-28
PRIOR PELING DATE: 2001-03-28
PRIOR PELING DATE: 2001-03-28
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PRIOR APPLICATION NUMBER: 10/028,248
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Smithson, Glennda,
Spytek, Kimberly,
Stone, David,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Edinger, Shlomit,
Gangolli, Esha,
Kekuda, Ramesh,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        himkets, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patturajan, Meera
Nothenberg, Mark,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Malyankar, Uriel
Miller, Charles,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Suresh,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Boldog, Ferenc,
APPLICANT: Casman, Stacie
APPLICANT: Colman, Steve,
                                                                                                                                                                                                                                                             1318 EEN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sciore, Paul
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; ORGANISM: Homo sapiens
US-10-107-782-107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1399 QRHEEK 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              290 QRHGKK 295
                                                                                                                                                                                                                                                         요
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APPLICANT: Millet, Isabelle
APPLICANT: Rothenboerg, Mark
TITILE OF INVENTION: No. US20030235882Alel Nucleic Acids and Polypeptides and Methods
TITLE OF INVENTION: Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --sehkrkkveaologio 1257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 EQTVEVVKSAIE----TADGALDLYNKYLDQVIP--WKTFDET---IKELSRFKQEYSQE 57
                 ----AIIQLITNEKENIPNLDKNYQE 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83; Gaps
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                 376 -LTALKKQIAATYYNDLEATPEIATDTQIKQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TILE REPERENCE: 21402-222
CURRENT APPLICATION NUMBER: US/10/028,248A
CURRENT APPLICATION NUMBER: 60/25619
PRIOR APPLICATION NUMBER: 60/25619
PRIOR PILING DATE: 2000-12-19
PRIOR PILING DATE: 2001-01-19
PRIOR PILING DATE: 2001-01-19
PRIOR PILING DATE: 2001-01-19
PRIOR PILING DATE: 2001-04-20
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PRIOR FILING DATE: 2001-04-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Taupier Jr, Raymond J
Kekuda, Ramesh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Shimkets, Richard APPLICANT: Batturajan, Meera APPLICANT: Vernet, Corine APPLICANT: Casman, Stacie APPLICANT: Malyankar, Uriel APPLICANT: Spytek, Kimberly APPLICANT: Gangolli, Esha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2001-08-09
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428 RL-EESLSEISFVS 440
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Zerhusen, Bryan
                                                                                                       291 RHGKKTLFEVPDVA 304
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1225 RGELANEVKVLLQGGRD
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Inger, Shlomit
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US-10-028-248A-107
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 107
LENGTH: 1999
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Boldog, Ferenc
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                                                                                                                                                                                                                                                                                                                                                            US-10-028-248A-107
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SOFTWARE: Patentin version 3.1
SEQ ID NO 46343
LENGTH: 941
                                                                                                                                    ; ORGANISM: Bacillus anthracis
US-10-282-122A-46343
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SEQ ID NO 6440
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US-10-369-493-6440
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                                                                                                                                                                                                                                                                                                               58 ASVLVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILI 1177
                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 RILDDGVKKLNEAQKSLLTSSQSFNNASGKLLALD---SQLTNDFSEKSSYFQSQVDRIR 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNNRLKTVQ----NFFTSLSATVK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QANKDIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDL-MLSLLKGAAKKMINTCNEYQ 289
                                                                                                                                                                       7 BQTVEVVKSAIE----TADGALDLYNKYLDQVIP--WKTFDET---IKELSRFKQEYSQE 57
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INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                           Gaps
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SEQ ID NOS: 78614
                                                                                                           83;
                                       Length 1999;
                                Query Match 7.4%; Score 111.5; DB 15; Length Best Local Similarity 19.6%; Pred. No. 7.8; Matches 60; Conservative 49; Mismatches 114; Indels
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THE REFERENCE: ELITRA.034A
THE REFERENCE: ELITRA.034A
THE REFERENCE: TOTAL OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF 
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; Sequence 46343, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
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CURRENT PILING DATE: 2003-02-20
FRIOR PELICATION NUMBER: 06/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-33
PRIOR PELICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PELING DATE: 2000-05-06
PRIOR PELING DATE: 2000-05-06
PRIOR PELING DATE: 2000-09-06
PRIOR PELING DATE: 2000-09-09
PRIOR PELING DATE: 2000-09-09
PRIOR PELING DATE: 2000-09-09
PRIOR PELING DATE: 2000-10-27
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2001-12-09
PRIOR PILING DATE: 2001-12-09
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1225 RGELANEVKVLLQGGRD-----
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
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Forsyth, R.
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Wall, Daniel
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Carr, Grant
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Gldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: EARTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PLING DATE: 2002-02-21
                                                                                                                                                   12;
                                                                                                                                                                                                                                                                                                                                             KKINEAQKSILITSSQSFNNASGKILALDSQ-----LINDFSEKSSYFQSQVDRIRK 175
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                                                                                                                                                                                                                                IKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRILDDGV 124
                                                                                                                                                                                                                                                                                  176 EAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNN---RLKTVQNFF----TSLSAT 228
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                                                                                                                7 EQTVEVVKSAIETADGAL-DLYNKYLDQVIP-WKTFDETIKELSRFKQEYSQEASVLVGD
                                                        62;
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Length 941;
                                                        Indels
                                                        90;
Query Match 7.3%; Score 111; DB Best Local Similarity 20.1%; Pred. No. 3.1; Matches 49; Conservative 43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 ILDDGVKKLNEAQKS---LLTSS-----
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Publication No. US20030233675A1
GENERAL INFORMATION:
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1493 SSMDN-----LSEQIETLRRE------NKİFSQEİ-RDINEQITQGGRT 1529
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILLE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILLING DATE: 2003-02-20
PRIOR PLILING DATE: 2000-03-21
PRIOR PLILING DATE: 2000-05-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PLLING DATE: 2000-05-26
PRIOR PLLING DATE: 2000-05-26
PRIOR PLLING DATE: 2000-05-26
PRIOR PLLING DATE: 2000-05-06
PRIOR PLLING DATE: 2000-05-06
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PRIOR PLLING DATE: 2000-09-06
PRIOR PLLING DATE: 2000-10-23
PRIOR PLLING DATE: 2000-10-23
PRIOR PLLING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153 SQLTNDFSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIE----GKL 207
                                                                                                                                                                                                                                                                                                                                                                                           5 PAEQTVEVVK------SAIBTADGALDLYNKYLDQVIPWKTFDETIKELSRFK
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                                                                                                                                                                                                                                                                                         7.3%; Score 110; DB 14; Length 1938; 18.9%; Pred. No. 9.9; tive 60; Mismatches 114; Indels 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208 IPELNNRLKTVQNFFTSLSATVKQANKDIDAAKLKLATEIAAIGEIKTETE
PILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 5110
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                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                        Similarity 18.9
55; Conservative
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                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 55
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    임
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Publication No. US200323675A1
GENERAL INPORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Gredom, Manry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Stater. Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR PEDITORION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 5109
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1315 FSSQLVEAKKAAEDELHERQEFHAACKNLEHELDQCHELLEEQINGK--DDIQRQLSRIN 1372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1373 SEISQWKARYEGEGLVGSEELEELKRKOMNRVMDLQEALSAAQNKVISLEKAKGKLLAET 1432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52 QEYSQ-----EASVLVG--DIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEY 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                105 NEKKASAQKDILI------RILDDGVKKINBAQKSLLTSSQSFNNASGKLLALD 152
                                                                                     BLNNRLKTVQNFFTSLSATVKQANKDIDAAKLKLATEIA------AIGEIKT--- 255
                                                                                                                      | | :: ::
----IGAKIMNKEMVD 913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  153 SQLTNDFSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIE----GKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.3%; Score 110; DB 14; Length 1:
18.9%; Pred. No. 9.9;
tive 60; Mismatches 114; Indels
                    Sequence 5109, Application US/10369493 Publication No. US20030233675A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 18.9
Matches 55; Conservative
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US-10-369-493-5109
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261 FQEQEASLLDQLSSTKKTVTSLSEEFRRE----KTLAEELREEIRRLESSLAQAGDDKDV 316
                                                                                                                                                        61 L-----VGDIKVLLMDSQDKYFEATQTVYEWCGV----VTQLLSA----YILLFDEYN 105
                                                                                                                                                                                     317 LEAKLKEKLGDVNIL----QEKVSLLSQEI-DNKGIRIRELSSLLSSKEADYRNLCSFSD 371
                                                                                                                                                                                                                                                                              106 EKKASAQ-KDILIRILDDGVKKINEAQKSLLTS-----SQSFNNASGKLLALDSQLTN 157
                                                                                                                                                                                                                                                                                                                 : | | : : | : | : | : | : | 312 QTKESLELAEAKIQQLBEBVHRTRNDLSSKISSIDLLNBELQALNSAKNEAEBKLSELTK 431
                                                                                                                                                                                                                                                                                                                                                                                                    158 DFSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNNRLKT 217
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                               FAEQTVEVVKSAIETADGALDLYNKYLDQVIPWKTFDETIK-ELSRFKQEYSQ---EASV
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or PALM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         528 IDEANRANQDLVLQI----SKLQDEFNEMQEGLTNK-LGEVESVS 567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE ELITAA. U34A COURRENT PEPLICATION NUMBER: U5/10/282,122A CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/2030,335
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-110-23
PRIOR PILING DATE: 2000-110-23
PRIOR PILING DATE: 2000-110-23
PRIOR PILING DATE: 2000-110-23
PRIOR PILING DATE: 2000-110-23
PRIOR PILING DATE: 2000-110-29
PRIOR PILING DATE: 2000-12-22
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PRIOR PILING DATE: 2001-02-09
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
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APPLICANT: Wu, Madrey A.

APPLICANT: Barbazuk, Brad

APPLICANT: Barbazuk, Brad

APPLICANT: Barbazuk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REPERENCE: 38-21(5321)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 191043

LENGTH: 815

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 GAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNNRL-KTVQNFFTSLSATVKQANKDI-- 236
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PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PREmaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 53523
LENGTH: 742
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 7.2%; Score 109.5; DB 15; Length Best Local Similarity 21.4%; Pred. No. 3; Matches 66; Conservative 49; Mismatches 131; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 191043, Application US/10437963; Publication No. US20040123343A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                           ) ORGANISM: Clostridium difficile US-10-282-122A-53523
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Best Local Similarity 20.5
Matches 71; Conservative
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ORGANISM: Oryza sativa
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US-10-437-963-191043
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT PILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 22285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             168 SQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNNRLKTVONFFTSLSA 227
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                                                                                                                                     358 AAEKEDIMKESDNLKRKVKEIQDSKLLVESENDELRSEILSM------KQKHGQFEVE 409
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                                                                                 170 VDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNNRLKTVQNFFTS----
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7.1%; Score 107.5; DB 14;
Best Local Similarity 19.9%; Pred. No. 15;
Matches 64; Conservative 49; Mismatches 127;
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US-10-369-493-497
US-10-369-493-497
; Sequence 497, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-369-493-22285

US-10-369-493-22285

Sequence 22285, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:
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APPLICANT: Kovalic, David K.
APPLICANT: Shou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Wi, Wei
APPLICANT: Wi, Wei
APPLICANT: Bunkharov, Andrey A.
APPLICANT: Bunkharov, Andrey A.
APPLICANT: Bunkharov, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 107270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q-----EASVLVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKA 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            613 DDLIHELQTTLINRVSASREINDKAQEMTDAVYDSTELTTEEKDT---LVDQIENHKNEI 669
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                                                                                                                                                                                                                                                    Gaps
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7.1%; Score 108; DB 16; Length 737;
Best Local Similarity 22.2%; Pred. No. 3.9;
Matches 64; Conservative 57; Mismatches 109; Indels 5
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                                                                                                                                                                                                                                                                                                                             11 EVVKSAIETADGALDLYNKYLDQVIPWKTFDETIKELSR------
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US-10-437-963-107270
                                                                                                                                                                       DB 15;
                                                                                                                                                                   Query Match 7.2%; Score 108.5; DB 15; Best Local Similarity 21.5%; Pred. No. 32; Matches 71; Conservative 49; Mismatches 128;
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724 NHEATTEEQNEAIRQVEAHSSDAIAKIGE------
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US-10-437-963-107270
; Sequence 107270, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
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US-10-282-122A-71235
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Sequence 9374, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION
APPLICANT: GEO. YONGwei
APPLICANT: Binkle, Gregory J.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
TITLE OF INVENTION: UNMER: US/10/369, 493
CURRENT PILLING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
PRIOR FILING DATE: 2002-02-21
                                                                                                        299 TVEEEKIEALNSDKSTSLEIETLNEQKNQLADKLEANKD-ELEKTKKAMEGLASALQEMS 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      171 DRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNNRLKTVQNFFTSLSATVK 230
                              ---ENFALKLELQKKKAAEEKAIRLERMI 178
                                                                                 -KLNEAOKSLLTSSOSFNNASGKLLALD 152
                                                                                                                                                               153 SQLTNDFSE-----KSSYFQSQVDRIRKEAY----AGAAAGIVAGPFGLIISYSIAAG 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 AQKDILLIRILDDGVKKINBAQKSLLTSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQV 170
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                                                                                                                                                                                                                                           202 VIEGKLIPELMNRLKTVQNFFT----SLSATVKQANKDIDAAKLKLATE--IAAIGEIK 254
        --LMDS----QDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDI-LIRIL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 LVGDIKVLLMDSQDKYPEAT----QTVYEWCGVVTQLLSA---YILLFDEYNEKKAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 EQTVEVVKSALETADGALDLYNK-----YLDQVIPWKTFDETIKELSRFKQEYSQEASV
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                                                                                                                                                                                                                                                                                                                        255 TET------ETTRFYVDYDDLMLSLLKGAAKKMINTCNEYQ 289
                                                                                                                                                                                                                                                                                                                                               Query Match 7.0%; Score 106.5; DB 14; Length Best Local Similarity 24.3%; Pred. No. 6.4; Matches 69; Conservative 45; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              231 QANKDIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDLMLSLL 274
                                            129 KGĽVDŚKVDGNRKKTAÈRIÓNLEÉ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 148, Application US/10393602
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US-10-369-493-9374
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SEQ ID NO 9374
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US-10-393-602-148
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APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Too, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPRENCE: 38-21(53113)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NOS: 73128
LENGTH: 647
TYPE. T
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROFEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROFERIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REPERENCE: 38-10(52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
                                                                                                                                                                                                                                                                                                                                             13;
                                                                                                                                                                                                                                                                                                                                                                                                        73 QDKYPBATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDI---LIRILDDGVKKLNE 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 AQKSLLTSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDRIRKEAYAGAAAGIVAGP 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      190 FGLIISYSIAAGVIEGKLIPELNNRLKTVQNFFTSLSATVKQANKDIDAAKLKLATEIAA 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 SAIETADGALDLYNKYLDQVIPWKT--FDETIKELSRFKQEYSQEASVLVGDIKVLLMDS 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 TVEVVKSAIETADGALDLYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVLVGDIKVL
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                                                                                                                                                                                                                                                                                                      Length 344;
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                                                                                                                                                                                                                                                                                                    Query Match 7.0%; Score 106.5; DB 14; Length Best Local Similarity 21.2%; Pred. No. 1.9; Matches 56; Conservative 52; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.0%; Score 106.5; DB 15; Length 22.8%; Pred. No. 4.4; tive 52; Mismatches 121; Indels
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                                                                                                                                                                                                                                                                                                  Score 106.5; I
Pred. No. 1.9;
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                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Xenorhabdus nematophilus
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Best Local Similarity 22.8*
Matches 79; Conservative
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US-10-425-114-51665
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                                                                                                                                                                               SEQ ID NO 497
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807 KSIVEVIKREGEKIATTAEPADKVKILKQLSLLDSRWEALLNKAETRNRQLEGISVVAQQ
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APPLICANT: Warnock, Dale B.
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
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APPLICANT: Heichman, Karen
APPLICANT: Bartel, Paul L.
TITLE OF INVENTION: Protein-Protein Interactions
FILE REPERENCE: 2318-266-11
CURRENT APPLICATION NUMBER: US/09/885,535
CURRENT FILING DATE: 2001-06-21
PRIOR FILING DATE: 2000-06-21
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
| : : | | | : : | | | 818 | 828 | 828 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 838 | 83
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19.4%; Pred. No. 36;
tive 76; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         279 KKMINTCNEYOQRHGKKTLFEV 300
                                                                                                                                                                                                                              Sequence 4, Application US/09885535
Patent No. US20020104105A1
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Gibson, Bradford W.
Taylor, Steven W.
                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Myriad Genetics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FDETIKELSRFK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 19.4's
Matches 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
CRGANISM: Homo sapiens
US-09-885-535-4
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APPLICANT:
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641 DLDRLKEEIEKSSKQRAMLAGATA--VYSQFITQLTDENQSCCPVCQRVFQTEAELQEVI 698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INDIVIDUAL ISOLATE: Rad50.pro-translation of SEQ ID NO:54 SEQUENCE DESCRIPTION: SEQ ID NO: 148:
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                                                                                                                                           Encoding Immunomodulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READMAGE FORM:
COMPUTER: FLOPPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COFFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/393,602
FILING DATE: 19-Mar-2003
CLASSIFICATION: 435
PRIOR APPLICATION BATE:
APPLICATION DATE:
APPLICATION DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISCHRATTON NUMBER: 38,615
REFERENCE/DOCKET WUMBER: 38,615
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Best Local Similarity 18.9%; Pred. No. 11;
Matches 75; Conservative 54; Mismatches 98;
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                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
       Publication No. US200301/v/.....
GENERAL INFORMATION:
APPLICANT: Gregory Dolganov
TITLE OF INVENTION: Transcripts E
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TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
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SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                     CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 94306
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22 FTSLSATVKQANKDIDA-----AKLKLATE----IAAIGEIKTETETTRFYV 264
                                                                                                                                                                                                                                                                                                                                                                       116 LIRILDDGV---KKLNEAQKSLLTSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDR 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :: |: :: |: :: | | : : | | : : | | :: | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : : | : : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : 
                                                                                                                                                                              173 IRKEAYAGAAAGIVAGPFGLIISYS-IAAGVIE------GKLIPELNNRLKTVQNF 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    797 QSELRVLQEDILLRKQNVDQALLNGLELLKQTTGDEVLIIQDKLEAIKARYKDITKLSTD 856
                                        LIRILDDGV---KKLNEAQKSLLTSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDR 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 IFAEQTVEVVKSAIETADGALDLYNKYLDQVIPWKTFDETIKELSRFK-QEYSQEAS-VL 61
                                                                                                                                                                                                                          187 LKKEAKNNKA------LLDSLNEVSSALLELVPWRAREGLEKMVAEDNERYRLV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 VGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69; Mismatches 113; Indels 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    265 D-----YDDLMLSLLKGAAKKMINTCNEYQQRHGKKTLFEV 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : |:: |:| |: |:| |: |:291 QVQKTFTWEILRHKDIIDDLVK-SGHKIMTACSEEEKQSMKKKLDKV 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: MAGAHAI, KENLI
APPLICANT: MAGAHAI, KENLI
APPLICANT: MAGAHAI, KENLI
APPLICANT: MAGHAIN, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT PEPLICATION NUMBER: 60/350,435
PRIOR PELING DATE: 2002-01-24
PRIOR FILING DATE: 2001-09-14
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SEQ ID NO 1911
SEQ ID NO 1911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 105; DE
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1911, Application US/10094749 Publication No. US20030219741A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUGIYAMA, TOMOYASU
OTSUKI, TETSUJI
WAKAMATSU, AI
SATO, HIROYUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISHII, SHIZUKO
YAMAMOTO, JUN-ICHI
ISONO, YUUKO
HIO, YURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAMECHIKA, ICHIRO SEKI, NAOHIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 6.9
Best Local Similarity 19.9
Matches 69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTSUKA, KAORU
NAGAI, KEIICHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IRIE, RYOTARO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ISOGAI, TAKAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
US-10-094-749-1911
                                        116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :||:::|
647 DLDRLKEBIEKSSKQRAMLAGATAVYSQFITQLTDENQSCCPVCQRVFQTEASLQEAISD 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      203 IEGKL----IPELNNRLKTVQNF 221.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :: | |
707 LQSKLRLAPDKLKSTESELKKKEKRRDEMLGLAPMRQSIIDLKEKEIPELRNKLQNV--- 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       222 FISLSATVKQANKDIDAAKLKLATEIAAIGEIKTETETT------RFYVDYDDLM 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 VGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDI----- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    508 MEVISLQNEKAD--LDRTLRKLDQEMEQLANHHTTRTQMEMLTKDKADKDEQIRKIKSRH 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55 SQEASVLVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKD 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    115 ILIRILDDGVKKLNEAQKSLLTSSQSFNNASGKLLALDSQLTNDFSEK-----SSYFQS 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---GIVAGPFGLIISYSIAAGV 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------NRDIQRLKNDIEEQETLLGTIMPEEESAKVCLTDVTIMERFQMELKDVE 812
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDELTSLLG------YPPNKKQLEDWLHSKSK------EINQTR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53; Mismatches 106; Indels 161; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 Length 1318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96;
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Publication No. US20040005560A1
GENERAL INFORMATION:
TITLE OF INVENTION: No. US20040005560Alel full length cDNA
FILLE REFERENCE: H1-A0106
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SEQ ID NO 3896
                                                                                                                                                                                                                                                                                                                                                                                                 DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 VEVVKSAIETADGALDLYNKYLDQVIPWKTFDETIK---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : : |||
813 RKIAQQAAKLQGIDLDRTVQQVNQEKQEKQHK 844
                                                                                                                                                                                                                                                                                                                                                                                                 7.0%; Score 105.5; 18.4%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.9%; Score 105; Di
19.9%; Pred. No. 10;
FILE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             169 QVDRIRKE------AYAGAAA-
                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 18.48
Matches 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69; Conservative
                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
US-10-408-765A-666
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ORGANISM: Homo sapiens
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                                                                                                                                                                                 SEQ ID NO 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       598
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APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FITLE REPERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT PILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 135452
LENGTH: 2295
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Undeled Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Undeled and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION UNBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 64494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            280 DLKGD-----MVSAAKHFEA-QLVHRDHEIEKCKQEAEQVS-----EKYFHEKSTLESE 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 I----LIRILDDGVKKIN-----EAQ-KSLLTSSQSFNNASGKLLA------LDSQL 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         328 İERLQEVVRSFBENLTKVAGEKFOLEAQVKELEQTSNDLDDSSAEIIKLQEIIKDLQGRL 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156 TNDFSEKSSYFQ--SQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELAN 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 EQTVEVVKSAJETADGALDLYNKYLDQVIPWKTFDETIKELSRFKQEY-----SQEAS 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | ::|| ::|| ::|| 388 ENDSNDKSVLEERAMELEQVRRQLEDSRAEASMK----LQTTIKNLNQVLEEK--AELEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----ATEI-AAIGEIKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |-| : | : | : | : | : | : | 412 RMKDAEQATSDINSLNGSLDGSKLKATEAQLBQLHAEKAEAILESEKQISELNQAIARLKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    502 RLB-----LLSSEKAAVDTKASALLTDVAVRDEKLKETDRHLQQLH 542
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
6.9%; Score 104.5; DB 15; Length 625;
Best Local Similarity 20.7%; Pred. No. 6.1;
Matches 73; Conservative 67; Mismatches 109; Indels 103;
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, OTHER INFORMATION: Clone ID: PAT_MRT4530_37127C.1.pep

US-10-437-963-135462
                                                                                                                                                                                                                                                                                                                           FEATURE: OTHER INFORMATION: Clone ID: LIB3060-111-G1_FLI.pep. US-10-425-114-64494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gequence 135452, Application US/10437963
; Publication No. US2004012334341
; GENERAL INFORMATION:
    APPLICANT: La Rosa, Thomas J.
    APPLICANT: Zhou, Yihua
    APPLICANT: Zhou, Yongwei
    APPLICANT: APPLICANT: Boukharov, Andrey A.
    APPLICANT: Boukharov, Andrey A.
    APPLICANT: Boukharov, Andrey A.
    APPLICANT: Brazalk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  256 ETETTRFYVDYDDLMLSLLKGAA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Zea mays
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Sequence 226623, Application US/10425115
publication No. US20040214272A1
publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFRENCE: 38 221 (5222) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 226623
LENGTH: 584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 I----LIRILDDGVKKLIN-----EAQ-KSLLTSSQSFNNASGKLLA-----LDSQL 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       287 IERLQEVVRSFEENLTKVAGEKFQLEAQVKELEQTSNDLDDSSAEIIKLQEIIKDLQGRL 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156 TNDFSEKGSYFQ--SQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNN 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 VIVGDIKVILMDSQDKYFEATQTVY----EWCGVVTQLLSAYILLFDEYNEKKASAQKD 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------ATEI-AAIGEIKT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 EQTVEVVKSAIETADGALDLYNKYLDQVIPWKTFDETIKELSRFKQEY-----SQEAS 59
                                                               222 FISLSATVKQANKDIDA-----AKLKLATE----IAAIGEIKTETETTRFYV 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       256 ETETTRFYVDYDDLMLSLLKGAA------KKOMINTCNEYQQRH 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RLE------LLSSEKAAVDTKASALLTDVAVRDEKLKETDRHLQQLH 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 6.9%; Score 104.5; DB 17; Length 584; Best Local Similarity 20.7%; Pred. No. 5.6; Ms. 5.6; Msatches 73; Conservative 67; Mismatches 109; Indels 103;
                                                                                                                                                                                                                                                265 D-----YDDLMLSLLKGAAKKMINTCNEYQQRHGKKTLFEV 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_138267C.1.pep
US-10-425-115-226623
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                                         173 IRKEAYAGAAAGIVAGPFGLIISYS-IAAGVIE-
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US-10-425-114-64494
US-10-425-114-64494
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Yihua
APPLICANT: Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Zea mays
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APPLICANT: Xu, H.,

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT APPLICATION NUMBER: 60/201,078
REIOR APPLICATION NUMBER: 60/201,078
REIOR PILING DATE: 2000-05-23
REIOR PILING DATE: 2000-05-24
REIOR PELICATION NUMBER: 60/207,727
REIOR APPLICATION NUMBER: 60/207,727
REIOR APPLICATION NUMBER: 60/203,335
REIOR APPLICATION NUMBER: 60/230,335
REIOR PILING DATE: 2000-09-06
REIOR PILING DATE: 2000-09-06
REIOR PILING DATE: 2000-10-23
REIOR PILING DATE: 2000-11-27
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                                                                                                                                                                  666 ---SQAEGIINQTTNPTLNPDEITRALTQVTDAKNGLNGEAKLATEKQNAKDAVNAMTHL 722
                                                                                                                                                                                                                                                     136 .--TSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLI 193
                                                                                                                                                                                                                                                                                                                                                                                   194 ISYSIAAGVIEGKLIPELN-----NRLKTVQNFFTSLS-----ATVKQANKDI----- 236
                                                           507 TLKQQIQANSQVPQSVDFTQAD-----QDKQQAYNNAANQAQQIANGTPTPVLTPDTVTQ 561
   TIKELSRFKQEYSQEASVLVGDIKVLLMDSQDKYFEA-----TQTVYEWCGVVTQ
                                                                                                                                                                                                                                                                                            Length 529;
                                                                                                                          93 LLSAYILLFDEYN--EKKASAQKDILIRILDDGVKKLNEAQKSLL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                237 -DAAKLKLATEIAAIGEIKTETETTRFYVDYDDLMLSL 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         723 NDAQKQALKGQIDQSPEIATVTQVKQTATSLDQAMNQL 760
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Pred. No. 5.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 48338, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Tyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Yearick, John
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Porsyth, R.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                   111 AOXDILIR-----ILDDGVKKINEA---OKSLLTSSOSFNNASGKLLALDSQLTN 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           203 IEGKLIPEL-----NNRL-----KTVQNFFISLSATVKQANKDIDAAKLKLATEIAAIG 251
                                                                                                                             6 AEQTVEVVKSAIETADGALDLYNKYLDQVIPWKTFDETIKE---LSRFKQEYSQEASVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
   Length 2295;
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Query Match 6.9%; Score 104.5; DB 16; Length Best Local Similarity 20.8%; Pred. No. 36; Matches 71; Conservative 71; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.9%; Score 104.5; DB 9; Length 24.1%; Pred. No. 55; Live 26; Mismatches 114; Indels
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APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: X, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         252 EIKTETETTRFYV-DYDDLMLSLLKGAAKKMINTCNEYQQR 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Prokaryotes
CURRENT EFERENCE: ELITRA.011A
CURRENT PELLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR PELLING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
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PRIOR PILING DATE: 2001-02-16
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PRIOR PILING DATE: 2001-02-16
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Parent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPB: PRT
ORGANISM: Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
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Best Local Similarity 24.1*
Matches 67; Conservative
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US-09-815-242-12611
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SEQ ID NO 12611
LENGTH: 3158
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14;
                                                                                                                                                                                                                                                                     157 NDFSEKSSYFQS---QVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNN 213
                                                                                                                                                                                                                                                                                              358 QQYKEMASNFESTSTTLSQVGDDTRTLVSEG---GKLKQLID-SLNQVIVEDQKFIDVSN 413
                                                                                                                                                                                                                                                                                                                                                  214 RLKTVQNPFTS-----LSATVKQANKDIDAAKLKLATEIAAIGEIKTETETTRF 262
                                                                          251
                                                                                                             49 RFKQEYSQEASVLVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKK 108
                                                                                                                                      109 ASAQKDILIRILDDGVKKLNEAQKSLLT-----SSQSFNNASGKLLALDSQLT 156
                                                                                                                                                                                                                     298 KKSNTEALVEVMKTVTEEFQKQMNSLINKLIQENFDQLNKSVEKLNTWQQENKAMISSLT 357
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CURRENT APPLICATION WINBER: US/10/282,122A
CURRENT FILING DATE: 2003-20-20
PRIOR APPLICATION WINBER: 60/191,078
                                                              EQTVEVVKSAIETAD----GALD-----LYNKYLDQVIPWKTFDETIKE-----LS
Gaps
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NUMBER OF SEQ ID NOS: 78614
16;
    63; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-22
PRIOR FILING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-06
PRIOR PILING DATE: 2000-05-06
PRIOR PILING DATE: 2000-05-06
PRIOR PILING DATE: 2000-05-09
PRIOR PILING DATE: 2000-03-09
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-20
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PRIOR PILING DATE: 2000-12-20
PRIOR PILING DATE: 2000-12-20
PRIOR PILING DATE: 2000-12-20
PRIOR PILING DATE: 2000-12-20
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                       263 YVDYDDLMLSLLKGAAKKM 281
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carr, Grant
Yamamoto, Robert
Forsyth, R.
        60; Conservative
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US-10-282-122A-51808
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xiandeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)8
CURRENT PLILIG DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 3279
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                                                                                                                                                                                                                                                                           84 YEWCGV-----VTQLLSAYILLFPEYNEKKASAQKDILIRILDDGVKKLNEAQKSLLTSS 138
                                                                                                                                                                                                                                                                                                                       306 YEWFSIPVVNQVKQDLKSQYHYTDE-----EIDSLLR--DGGLKIYTTMNTSMESNV 355
                                                                                                                                                                                                                                                                                                                                                                                 139 OSF--NNASCKLLALDSQLTNDFSEKSSYFOSQVDRIRKEAYAGAAAGIVAGPFGLIISY 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    197 SIAAGVIEGKLIPELMNRLKTVONFFTSLSATVKQANKDIDAAKLKLATEIAAIGEIKTE 256
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                                                                                                                                                                        24 LDLYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVLVGDIKVLLMDSQDKYFEATQTV
                                                                                                                                                                                                                         265 LVLYKORQNNYIDPSTYQNAINDLNNKLAFSQQ------KI----SNKY----T
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Best Local Similarity 21.2%; Pred. No. 32;
Matches 63; Conservative 45; Mismatches 119;
                                                                       Query Match
Best Local Similarity 22.3%; Pred. No. 9.6;
Matches 67; Conservative 40; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 AEQTVEVVKSAIETADGALDLYNKYLDQVIPWKTFD---
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Publication No. US20030233675A1
; ORGANISM: Clostridium acetobutylicum
US-10-282-122A-51808
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ORGANISM: Neurospora crassa
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US-10-437-963-124349
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; Sequence 267777, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REPERENCE: 38-21(5)222B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 267777
LEMOTH: 568
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BENIQQLHEK-----EALAISERRAADLADESGVI-----EAAVS 140
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                           3 SIFAEQTVEVVKSAIETADGALDLYNKYLDQVIP--WKTFDETIKELSRFKQEYSQEASV 60
                                                                                     202 VIEGKLIPELNNRLKTVQNPFTSLSATVKQANKDIDAAKLKLATEIAAIGEIKTETE 258
                                                                                                                   275 QRATDALEELYN----VKGQLAGEKRRCKKLQEELDDAVAMLEAKMPEIDELNAESE 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ::::|:| : |:
-----ESDSESTAYVSSRDE-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: MRT4577_175816C.1.pep
US-10-425-115-267777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (1)..(568)
OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 1635, Application US/10408765A; Publication No. US20040101874A1; GENERAL INFORMATION:
EKSSYFOSOVDRIRKE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Zea mays
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Sequence 124349, Application US/10437963

j Sequence 124349, Application US/10437963

j Publication No. US20040123343A1

j ENDIGATION NO. US20040123343A1

j ENDIGATI LA ROSA, Thomas J.

j APPLICANT: La ROSA, Thomas J.

j APPLICANT: Zhou, Yihua

j APPLICANT: Shou, Yongwei

j APPLICANT: Boukharov, Andrey A.

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j APPLICANT: Boukharov,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 IKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYI-LLFDEYNEKKASAQKDILIRILD-- 121
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APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Glenn, Cary M.
TITLE OF INVENTION: TAGGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660080-465;
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 16; Length 1583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (1)..(1585)
OTHER INFORMATION: unsure at all Xaa locations
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6.8%; Score 103.5; D
Best Local Similarity 19.7%; Pred. No. 26;
Matches 69; Conservative 54; Mismatches
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ORGANISM: Homo sapiens
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USE THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 LIRILDDGVKKLNFAQKSLLTSSQSFNNASGKLLALD---SQLTNDFSFKSSYPQSQVDR 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ...-----KQANKDIDAAKLKLATEIAAIG 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Taupier, Raymond, jr.,
APPLICANT: Tchernev, Velizar,
APPLICANT: Vernet, Corine,
APPLICANT: Serbusen, Brian
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES AND METHODS OF
PILE REFERENCE: 21402-222CIP
                                                                                                                                                                                                                                                                                                     7 EQTVEVVKSAIB----IADGALDLYNKYLDQVIPWKTFDETIKE-----LSRFKQEYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173 IRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNNRIKTVQ---NFF-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      252 BIKTETETTRFYVDYDDIMLSLLKGAAKKMINTCN-EYOQRHGKKTLFEVPDVAS 305
                                                                                                                                                                                                                Query Match
6.8%; Score 103.5; DB 14; Length 1959;
Best Local Similarity 19.2%; Pred. No. 35;
Matches 68; Conservative 49; Mismatches 119; Indels 119;
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CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: 10/028,248
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PRIOR APPLICATION NUMBER: 60/311266
PRIOR FILING DATE: 2001-08-09
NUMBER OF SEQ ID NOS: 211
SOUTHWARE: Patentin Ver. 2.1
SEQ ID NO 36
LENGTH: 1959
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Rothenberg, Mark,
Sciore, Paul,
Shenoy, Suresh,
Shimkets, Richard,
Si, Jingheng,
Smithson, Glemda,
Spytek, Kimberly,
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1224 NERGELANEVKVLLQGGRD-
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Malyankar, Uriel,
Miller, Charles,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Boldog, Ferenc,
APPLICANT: Casman, Stacie
APPLICANT: Colman, Steve,
APPLICANT: Bdinger, Steve,
APPLICANT: Gangeli, Esha,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isabelle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spytek, Kimbe
Stone, David,
                                                                                                                                           TYPE: PRT
CRGANISM: Homo sapiens
US-10-028-248A-36
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APPLICANT:
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TITLE OF INVENTION: No. US20030235882A1el Nucleic Acids and Polypeptides and Methods
TITLE OF INVENTION: Thereof
FILE REPERENCE: 21402-222
CURRENT APPLICATION NUMBER: US/10/028,248A
CURRENT FILLING DATE: 2001-12-19
                                                                                                                                                                                                                                                                                                         665 LYLAERQEHDETKQSLSKSQERNWELLQKVDEAEKRINKLLENAQRL-----EKHATARE 719
                                                                                                                                                                                                                                                                                                                                                                     114 DILIRIL---DDGVKKLINBAQKSLLTSSQSFNNASGKLLALD---SQLTNDFSBKSSY-- 165
                                                                                                                                                                                                                                                                                                                                                                                                            720 SLLIKTKQSHDSTTKALVEAESRNRELTKSFEDSDRKINLLEDSVNRLEERIAEKDSLLE 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                          166 FQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNNRLKTVQNFFTSL 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 VLVG-----DIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDBYNEKKASAQK 113
                                                                                                                                                                                              2 TSIRAEQ--TVEVVKSAIETADGALDLYNKYLDQVIPWKTFDETIKELSRFKQEYSQEAS
                                                                                                                                                         53;
                                                                                                           DB 16; Length 1585;
                                                                                                           Query Match
6.8%; Score 103.5; DB 16; Length
Best Local Similarity 22.1%; Pred. No. 26;
Matches 61; Conservative 48; Mismatches 114; Indels
                                    ; OTHER INFORMATION: Clone ID: PAT_MRT4530_27097C.1.pep
US-10-437-963-124349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 226 SATVKQANKDIDAAKLKLATEIAAIGEIKTETETTR 261
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PRIOR PILING DATE: 2000-12-19
PRIOR PILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/262959
PRIOR APPLICATION NUMBER: 60/272408
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-02-8
PRIOR FILING DATE: 2001-04-20
PRIOR PILING DATE: 2001-04-20
PRIOR PILING DATE: 2001-07-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 36, Application US/10028248A
Sequence 36, Application US/10028248A
Publication No. US20030235882A1
GENERAL INFORMATION:
APPLICANT: Shinkets, Richard
APPLICANT: Caturalan, Meera
APPLICANT: Caman, Stacie
APPLICANT: Caman, Stacie
APPLICANT: Shenoy, Suresh
APPLICANT: Shenoy, Suresh
APPLICANT: Shenoy, Suresh
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ekuda, Ramesh
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Tchernev, Velizar
Si, Jingsheng
Edinger, Shlomit
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Zerhusen, Bryan
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Millet, Isabelle
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Miller, Charles
Boldog, Ferenc
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ORGANISM: Zea mays
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1317 LQEEN--------RQKL--SLSTKLKQVEDEKNSFREQLEEE 1348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56 QEASVLVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDI 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 LIRILDDGVKKINEAQKSLLTSSQSFNNASGKLLALD---SQLTNDFSEKSSYFQSQVDR 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----TSLSATV-----TSLSATV5-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 173 IRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNNRLKTVQ---NFF----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 6.8%; Score 103.5; DB 15; Length 1959;
Best Local Similarity 19.2%; Pred. No. 35;
Matches 68; Conservative 49; Mismatches 119; Indels 119; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    252 EIKTETETTRFYVDYDDLMLSLLKGAAKKMINTCN-EYQQRHGKKTLFEVPDVAS 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Faby, Bounder B.
APPLICANT: Taby, Bounder B.
APPLICANT: Chang, Bing
APPLICANT: Giban, Bradford W.
APPLICANT: Giban, Bradford W.
APPLICANT: Glenn, Gary M.
APPLICANT: Glenn, Gary M.
APPLICANT: Glenn, Gary M.
APPLICANT: Glenn, Gary M.
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REPERBRECE: 660088 465
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SEQ ID NO 2687
LENGTH: 5171
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/256,619
PRIOR PILING DATE: 2000-12-19
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2001-01-19
PRIOR FILING DATE: 2001-01-19
PRIOR PELING DATE: 2001-02-28
PRIOR PELING DATE: 2001-04-20
PRIOR FILING DATE: 2001-04-20
PRIOR PELING DATE: 2001-04-20
PRIOR PELING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: 60/311,266
PRIOR FILING DATE: 2001-07-26
PRIOR FILING DATE: 2001-07-26
PRIOR FILING DATE: 2001-07-26
PRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ 1D NOS: 215
NUMBER OF SEQ 1D NOS: 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ghosh, Soumitra S. APPLICANT: Fahy, Eoin D.
                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-107-782-36
                                                                                                                                                                                                                                                                                                                                        SOFTWARE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    223
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Sequence 60225, Application US/10425114

Sequence 60225, Application US/20040034888A1

Sequence 60225, Application No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: About Yingdong

APPLICANT: Abanka, Jack E

APPLICANT: Tabanka, Jack E

APPLICANT: Cao, Yongwei

ITILE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

ITILE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REPERBNCE: 38-21(53313) B

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 60225

LENGTH: 420
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                                                                                                                                                                                                                                                                                                                                                                                                         3238 QSELRVLQEDILLRKQNVDQALLNGLELLKQTTGDEVLIIQDKLEAIKARYKDITKLSTD 3297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3298 VAKTLEQALQLARRLHSTHEELCT---WLDKVEVELLSYETQVLK--GEEASQAQMRPKE 3352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173 IRKEAYAGAAAGIVAGPFGLIISYS-IAAGVIE-----GKLIPELNNRLKTVQNF 221
                                                                                                                                                                                                                                                                                                                                                  4 IFAEQTVEVVKSAIETADGALDLYNKYLDQVIPWKTFDETIKELSRFK-QEYSQEAS-VL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 EQTVEVVKSAIETADGALDLYNKYLDQVIPWKTFDETIKELSRFKQEY-----SQEAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 VGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDI-----
                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                            96;
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                                                                                                                                                                                                                               Query Match 6.8%; Score 103; DB 16; Length 5171; Best Local Similarity 19.6%; Pred. No. 1.40+02; Matches 68; Conservative 70; Mismatches 113; Indels 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             265 D------YDDLMLSLLKGAAKKMINTCNEYQQRHGKKTLFEV 300
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US-10-425-114-60225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97;
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20.8%; Pred. No. 5.2;
:ive 66; Mismatches
; TYPE: PRT
; ORGANIEM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 4411
; COTHER INFORMATION: Xaa = Any Amino Acid
US-10-408-765A-2687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 20.8%
Matches 63, Conservative
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APPLICANT: Rothenberg, Mark
TITLE OF INVENTION: No. US20030235882A1el Nucleic Acids and Polypeptides and Methods of TITLE OF INVENTION: Thereof FILE REFERENCE: 21402-222
CURRENT APPLICATION NUMBER: US/10/028,248A
CURRENT FILING DATE: 2001-12-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           173 IRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNNRLKTVQ----NFFTSLSAT 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 229 VKQANKDIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDL-MLSLLKGAAKKMINTCNE 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 EQTYEVVKSAIE----TADGALDLYNKYLDQVIPWKTFDETIKE-----LSRFKQEYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56 QEASVLVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 14; Length 1961;
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6.8%; Score 102.5; DB 14;
Best Local Similarity 19.5%; Pred. No. 42;
Matches 60; Conservative 47; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURKENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/256619
PRIOR PILING DATE: 2000-12-19
PRIOR PILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/262959
PRIOR PILING DATE: 2001-01-9
PRIOR PELING DATE: 2001-01-28
PRIOR PILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/285189
PRIOR PILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: 60/308039
PRIOR PILING DATE: 2001-07-26
PRIOR PILING DATE: 2001-07-26
PRIOR PILING DATE: 2001-07-26
PRIOR PILING DATE: 2001-07-26
PRIOR PILING DATE: 2001-07-26
PRIOR SPELICATION NUMBER: 60/311266
PRIOR PILING DATE: 2001-08-09
NUMBER OF SEQ ID NOS: 211
                                                                                                                                                                                                                                                                                                                                                                                               Taupier Jr, Raymond
Kekuda, Ramesh
                                                                                      Patturajan, Meera
Vernet, Corine
Casman, Stacie
Malyankar, Uriel
Shenoy, Suresh
Spytek, Kimberly
Gangolli, Esha
Miller, Charles
Boldog, Ferenc
tion No. US20030235882A1
INFORMATION:
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Si, Jingsheng
Edinger, Shlomit
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smithson, Glennda
Zerhusen, Bryan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stone, David
Sciore, Paul
Millet, Isabelle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Colman, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; SEQ ID NO 103

: LENGTH: 1961

; TYPE: PRT

: ORGANISM: Homo sapiens

US-10-028-248A-103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liu, Xiaohong
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Sequence 176713, Application US/10437963

Publication No. US20040123343A1

SEQUENCE IN CORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants 18/10/437,963
CURRENT FILING DATE: 2003-05-14
CURRENT FILING DATE: 2003-05-14
SEQ ID NO 176113
LENGTH: 957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 ASAQKDILIRILDDGVKKLNEAQKSLLTSSQSFNNASGKLLALDSQLTNDFSEKSSYFQS 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 VILMDSQD--KYFEATQTVYEWCGVVTQL-------LSAYILLFDEYNEKK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 BQTVEVVKSAIETADGALDLYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVLVGDIK 66
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                                         I-----LIRILDDGVKKLN-----EAQ-KSLLTSSQSFNNASGKLLA-----LDSQL 155
                                                                                   TNDFSEKSSYFQ--SQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNN 213
                                                                                                                                                                                                            RLKTVQNFFTSLSATVKQANKDIDAAKLKL------ATEL-AAIGEIKT 255
                                                                                                                                                                                                                                                                                                                         51; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 957;
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6.8%; Score 102.5; DB 16; Length
Best Local Similarity 21.2%; Pred. No. 16;
Matches 60; Conservative 53; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATVKQANKDIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDL 269
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, OTHER INFORMATION: Clone ID: PAT_MRT4530_74436C.1.pep
US-10-437-963-176713
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US-10-028-248A-103
; Sequence 103, Application US/10028248A
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QLE 299
                                                                                                                                                                                                                                                                                                                                                                                                                            256 ETE 258
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Sequence 2102, Application US/10369493

Sequence 2102, Application US/10369493

Sequence 2102, Application No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Cap. Yongwei

APPLICANT: Slater, Steven C.

APPLICANT: Slater, Steven C.

APPLICANT: Ghoman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EPLANTS WITH IMPROVED PROPERTIES

FILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10(52052)B

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR PILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374
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                                                                                                                                                                                 1257 LOVKFNEGERVRTELADKVTKLOVELDNYTGLLSOSDSKSSKLTKDFSALESOLODTOEL 1316
                                                                                                                                                                                                                                                                                                                             173 IRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNNRLKTVQ----NFFTSLSAT 228
                                                                                                                                                                                                                                                                                                                                                                                                     229 VKQANKDIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDL-MLSLLKGAAKKMINTCNE 287
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                                                                                                             116 LIRILDDGVKKLNEAQKSLLTSSQSFNNASGKLLALD---SQLTNDFSEKSSYFQSQVDR 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48 AEDMKAAKLIJAESGKLSSSMVKRLDLSSSDKYDSMVQGVLDVKSLPDPLGRVTYARS--- 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99 LLFDEYNEKKAS-------AQKDILIRILDDGVKKLN-------FAQKSLLTSSQ 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           164 VVRSALGKSKVPQAAVQLVQSREEVSQLLKLDEYIDLVIPRGSTNLVRHIKDNTKIPVLG 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---VAGPFGL--IISYSIAAGVIEGKLIPE--LNNRLKTVQNFFTS 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       224 HAAGLCSMYVHEDADMELASKLVLDGKTDYPAACNAIETLLINEAVLSSHLPKIAETLTE 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           284 AKVTLK-----CDPASLKVLKDMPKVSALVEPSVDQDYNTEFSDLILAIKTVPSLQSAMQ 338
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Best Local Similarity 21.6%; Pred. No. 6.4;
Matches 81; Conservative 45; Mismatches 131; Indels 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 EENVKEAKNAFNILQTLSVEDRDDAL----
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| | | ::|||| :|
1224 NERGELANEVKVLLQGGRD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  281 MINTCNEYQQRHGKK 295
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|1398 LSQRHEEK 1405
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US-10-369-493-2102
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LENGTH: 451
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES AND METHODS OF USE THEREOF
FILE REPERENCE: 21402-222CIP
CURRENT APPLICATION NUMBER: US/10/107,782
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: 10/028,248
   -- DSVGCLETAEEVKRKLQKDLEG 1397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 EQTVEVVKSAIE----TADGALDLYNKYLDQVIPWKTFDETIKE-----LSRFKQEYS
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; Pred. No. 42;
47; Mismatches 114; Indels
1349 EEEAKHNLEK---QIATLHAQVADMKKKME--
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PRIOR FILING DATE: 2001-12-19
PRIOR FILING DATE: 2001-12-19
PRIOR PELING DATE: 2001-12-19
PRIOR FILING DATE: 2001-01-19
PRIOR PELING DATE: 2001-01-19
PRIOR PELING DATE: 2001-01-19
PRIOR PELING DATE: 2001-02-28
PRIOR PELING DATE: 2001-02-28
PRIOR PELING DATE: 2001-02-28
PRIOR PELING DATE: 2001-03-28
PRIOR PILING DATE: 2001-04-20
PRIOR PILING DATE: 2001-04-26
PRIOR PELING DATE: 2001-07-8
PRIOR PELING DATE: 2001-07-8
PRIOR PELING DATE: 2001-07-8
PRIOR PELING DATE: 2001-07-8
PRIOR PELING DATE: 2001-07-8
PRIOR PELING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 215
SOFTWARE: CURASCQLIST VETRION 0.1
                                                                                                                                                                                                                                                                                                                         Sequence 103, Application US/10107782
Publication No. US20040018970A1
GENERAL INFORMATION:
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Tchernev, Velizar,
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Shimkets, Richard,
Si, Jingsheng,
Smithson, Glennda,
Spytek, Kimberly,
                                                                                                                                                                                                                                                                                                                                                                                                                                   Boldog, Ferenc,
Casman, Stacie
Colman, Steve,
Colman, Steve,
Gainger, Shlomit,
Gangolli, Bsha,
Kekuda, Ramesh,
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Best Local Similarity 19.5%;
Matches 60; Conservative 4
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Malyankar, Uriel,
Miller, Charles,
Millet, Isabelle,
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Rothenberg, Mark,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sciore, Paul,
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                                                                                                                                               1398 LSORHEEK 1405
                                                                       288 YQQRHGKK 295
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ORGANISM: Homo sapiens
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LENGTH: 1961
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                                                          Sequence 3210, Application US/10369493
; Sequence 3210, Application US/10369493
; Publication No. US2030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Clam, Yanafeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: DLANTS WITH IMPROVED PROPERTIES
; TITLE OF INVENTION: DLANTS WITH IMPROVED PROPERTIES
; TITLE OF INVENTION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 3210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Terry, Roemer D.
APPLICANT: Terry, Roemer D.
APPLICANT: Charles, Boone
APPLICANT: Howard, Bussey
TITLE OF INVENTION Gene Disruption Methodologies for Drug Target Discovery
TITLE OF INVENTION Gene Disruption Methodologies for Drug Target Discovery
FILE REFERENCE: 10182-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
NUMBER OF FIG ID NOS: 8000
SOFTWARE: Patentin version 3.1
SEQ ID NO 7776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             221 FFTSLSATVK--QANKDIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDLMLSLLKGAA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 LIRILDDGVKKLNEAQKSLLTSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDRIRK 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176 BAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNNRLK------TVQN 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71 DSQDK----YFEATQTVYEWCGVVTQLLSAYILLFD-------EYNEKKASAQKDI 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 ETADGALDLYNKYL-DQVIPWKTFDETIKELSRFKQEYSQEASVLVGDIKVL----LM 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 6.7%; Score 102; DB 14; Length 1015; Best Local Similarity 20.5%; Pred. No. 19; Matches 65; Conservative 57; Mismatches 123; Indels 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7776, Application US/10032585 publication No. US20030180953A1 GENERAL INFORMATION:
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US-10-369-493-3210
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                                                    RESULT 49
US-10-369-493-3210
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426 EYENAQLSEBİSRİRAKNSOYDPEAQHYBIDQLKQENAQLKDNVKKYLMNFKELKDKEVE 485
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                                                                                                                                                                                                                                                                                           122 - DGVKKINBAQKSLITSSQSFNNASGKLIALDSQLTN--DFSEK-SSYFQSQVDRIR-KE 176
                                                                                                                                                                                                                                                                                                                    177 AYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNNRLKTVQNFFTSLSATVKQANKDI 236
                                                                                                                                                                                                                                                                                                                                                                                           237 DAAKLKLATELAAIGEIKTETETTRFYVDYDDLML--SLLKGAAKKMINTCNEYQQR--- 291
                                                                                                                                                                                   291
                                                                                                                                                                                                                       63 GDIKVILMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRILD- 121
                                                                                                                                                                         7 BQTVEVVKS---ALETADGALDLYNKYLDQVIPWKTFDETIKELSRFKQE-YSQEASVLV
                                                                                                                  Gaps
                                                                                                                  :99
                                                                              DB 14; Length 1038;
                                                                                                                Indels
                                                                                                                      59; Mismatches
                                                                                6.7%; Score 102; D
20.8%; Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: January 5, 2005, 11:08:47 Job time : 66.7056 secs
                 TYPE: PRT; ORGANISM: Candida albicans
US-10-032-585-7776
                                                                                                                        64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          292 HGKKTLF 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           486 HAHQIAF 492
                                                                                                      Similarity
LENGTH: 1038
```

GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd. Copyright

OM protein - protein search, using sw model

5, 2005, 10:43:53 January Run on:

US-09-993-292B-2

Perfect score: Title:

Sequence:

BLOSUM62 Scoring table:

1825181 segs, 575374646 residues Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000

1825181

Listing first 50 summaries Post-processing: Minimum Match 0% Maximum Match 100%

Database

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	; ;	Description		Q93rr6 salmonella	P77335 escherichia	Q9reb3 escherichia	Q9x2s8 escherichia	~	Q8fi27 escherichia	Q9liw7 oryza sativ	Q7shz4 neurospora	Q6g015 bartonella	Q6mt03 mycoplasma	Cae77235 mycoplasm	Q7m9i8 wolinella s			Q74de2 geobacter s	LO.	Q9szk7 arabidopsis			Q7qq04 giardia lam		-	Q20822 caenorhabdi	Q97wh8 sulfolobus		031954 bacillus su			Q9x360 bacillus an	Aat28865 bacillus
SUMMAKIES	ŕ	ar a	HLYE_SALTI	HLYE_SALPA	HLYE ECOLI	HLYE ECO57	Q9X2 <u>S</u> 8	HLEL_SHIFL	HLEL ECOL6	Q9LIW7	Q7SHZ4	Q6G015	Q6MT03	CAE77235	Q7M918	P71497	Q7RQB6	Q74DE2	AAR34750	Q9SZK7	Qebpde	Q7N5U5	070004	HLY1_ECOLI	Q7XEH4	SR68_CAEEL	Q97WH8	064067	031954	Q9VGA8	Q7CMF0	09X360	AAT28865
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	4	maten bengen	302	302	302	302	300	113	93	895	4007	1521	713	713	693	495	2723	541	541	1496	1877	577	1224	1023	2033	622	587	478	478	588	652	652	652
٠	Query	March	98.9	96.4	92.2	91.2	73.3	34.3	26.1	9.8	8.5	8.3	8.2	8.2	8.1	8.1	8.0	7.9	7.9	7.8	7.8	7.8	7.8	7.7	7.7	7.6	7.6	7.6	7.6	7.6	7.6	7.6	7.6
	3	acore	1498	1461	1397	1382	1110	519	395	130.5	128.5	126	123.5	123.5	122.5	122	121	119	119	118	118	117.5	117.5	116	116	115.5	115	114.5	114.5	•	114.5	114.5	114.5
	Result		-	7	m	4	Ŋ	φ	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31

Q7rm79 plasmodium	Q869b8 dictyosteli	Q9h6q7 homo sapien	Q8cpiO staphylococ	Q7rd43 plasmodium	Q9z429 pseudomonas	Q8z0n2 anabaena sp	Q9yvt6 melanoplus	_	Q7rj32 plasmodium	Q6c359 yarrowia li	045614 caenorhabdi	Q73aj3 bacillus ce	Aas40708 bacillus	P32618 saccharomyc	Q58718 methanococc	P26831 clostridium	Q71x69 listeria mo	Aat05096 listeria
Q7RM79	Q869B8	709н60	Q8CPIO	Q7RD43	Q92429	Q820N2	Q9YVT6	Q874Y4	Q7RJ32	Q6C359	045614	Q73AJ3	AAS40708	YEF3 YEAST	RASO_METJA	NAGH_CLOPE	Q71X <u>6</u> 9	AAT05096
N	~	N	0	~	~	7	~	~	~	~	N	7	~	Н	-	~	~	7
779	1885	720	1189	1611	538	727	1127	1363	1489	1906	3102	465	465	926	1005	1628	927	927
7.6	7.6	7.5	7.5	7.5	7.5	7.5	7.5	7.5	7.5	7.5	7.5	7.5	7.5	7.5	7.5	7.5	7.4	7.4
114.5	114.5	114	114	114	113.5	113.5	113.5	113.5	113.5	113.5	113.5	113	113	113	113	113	112.5	112.5
32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	40	20

ALIGNMENTS

SALTI

302 AA PRT; STANDARD;

082727. 0934C4;
29-MRR-2004 (Rel. 43, Created)
29-MRR-2004 (Rel. 43, Last sequence update)
01-0CT-2004 (Rel. 45, Last annotation update)
Hemolygin E (Cytotoxin clyA) (Silent hemolygin sheA).
Name-hlyE: Synonyms-clyA, sheA; OrderedLocusNames=STY1498, t1477;
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

NCBI_TaxID=601;

SECUENCE FROM N.A.
SENAMME-1221219, bubMed=12228306;
MEDLINE=22215-712; PubMed=12228306;
Oscarsson J., Westermark M., Loefdahl S., Olsen B., Palmgren H.,
Mizunce Y., Wai S.N., Uhlin B.E.;
"Characterization of a pore-forming cytotoxin expressed by Salmonella enterica serovars typhi and paratyphi A.";

SEQUENCE FROM N.A.

STRAIN=CT18;
MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;

Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Bashama D., Brooks K., Chillingworth T., Connerton P., Croin A., Davis P., Davise R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
Whitehead S., Barrell B.G.;
Whitehead S., Parry C., Quail W.A., Simmonds M., Skelton J., Stevens K., Whitehead S., Barry C., Quail W.A., Shimmonds S., Gaora P., Parry C., Martenead S., Barry C., Carl M., Simmonds M., Skelton J., Stevens K., Whitehead S., Barry C., Gaora Typhi CT18.";

SEQUENCE FROM N.A.
STRAIR=TY2 / Arcc 700931;
STRAIR=22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";

J. Bacteriol. 185:2330-2337(2003).
-!- FUNCTION: Toxin, which has some hemolytic activity towards mammalian cells. Acts by forming a pore-like structure upon contact with mammalian cells (By similarity).

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                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VGDIKVLLMDSQDKXFRATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRILD 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 VGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRILD 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 KLATE1AAIGEIKTETETTRFYUDYDDLMLSLLKGAAKKMINTCNEYQQRHGKKTLFEUP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DGVKKLNEAQKSLLTSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDRIRKEAYAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                            SUBCELLULAR LOCATION: Secreted. Exported from the cell by outer membrane vesicles. Also found in the periplasmic space (By
   it is present as
                                                                                                                                                                                                                                                                                                                                                                                                       ö
                       a pore structure that is active. Probably forms an octamer
                                                                                                                                                                                                                                                                                                                                                 In monomeric form (By similarity) 2BDFD835D044FDAE CRC64;
               it oligomerizes
                                                                                                                                                                                                                                                                                            InterPro; IPR010356; HlyE.

Pfam; PF06109; HlyE; 1.

Complete proteome; Cytolysis; Hemolysis; Toxin; Transmembrane.

INIT MET 0 0 By similarity.

PRANGNEM 178 198 Potential.
                                                                                                                                                                                                                                                                                                                                                                                Score 1498; DB 1; Length 302;
Pred. No. 3.1e-92;
0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-MAR-2004 (Rel. 43, Created)
29-MAR-2004 (Rel. 43, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Hemolysin E (Cytotoxin clyA) (Silent hemolysin sheA).
Salmonelhus, Synonyms=clyA, sheA;
     In periplasm,
   SUBUNIT: Monomer and oligomer. In periplasm
monomer, while in outer membrane vesicles,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 302
                                                                                                                                                                                                                                       EMBL; AJ313032; CAC38360.1; -.
EMBL; AJ313034; CAC38363.1; -.
EMBL; AL627270; CAD01758.1; ALT INIT.
EMBL; AG016839; AAO69115.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                               33658 MW;
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ilarity 99.7%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                               302 AA;
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Matches 301; Conserv
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                                                                        similarity)
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SEQUENCE
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Best Local &
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=22215712; PubMed=12228306;
MEDLINE=22215712; PubMed=12228306;
Mizunoe Y., Westermark M., Loefdahl S., Olsen B., Palmgren H.,
Mizunoe Y., Wai S.N., Uhlin B.E.;
Mizunoe Y., Wai S.N., Uhlin B.E.;
Mizunoe Y., Wai S.N., Which B.E.;
Infect. Immun. 70:5759-5769(2002).
Infect. Immun. 70:5759-5769(2002).
Infect. Immun. 70:5759-5769(2002).
Infect. Immun. 70:5759-5769(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity).

PTM: In periplasm, it forms a disulfide bond, which prevents the cligomerization. In outer membrane vesicles, the redox status prevents formation of the disulfide bond, leading to prevents formation of the disulfide bond, leading to oligomerization and pore formation (By similarity).

SIMILARITY: Belongs to the hemolysin E family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              outer
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity).
SUBCELLUJAR LOCATION: Secreted. Exported from the cell by membrane vesicles. Also found in the periplasmic space (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 302;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1461; DB 1;
Pred. No. 9.1e-90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96.4%; Scor.
97.0%; Pred. No. 9.1.
2; Mismatches
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By similarity.
Potential.
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HSSP; P77335; 1QOY.
InterPro; IPR010356; HlyE.
Pfam; PF06109; HlyE; 1.
                                                       Enterobacteriaceae; Salmonella
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                                                                                         NCBI_TaxID=54388;
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                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., SEQUENCE OF 1-12, SUBCELLULAR LOCATION, AND
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                                    HLYE ECOLI
PTANDARD;
P7735; Q47276; Q8VU70; Q9R3G4;
P77357; Q47276; Q8VU70; Q9R3G4;
D1-NOV-1997 (Rel. 35, Last sequence update)
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                                                                                                                                                                                  STRAIN=K12 / XL1-BLUE;
McNamara P.J., Iandolo
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                                                                                                                            Escherichia coli
                                                                                                                                                         NCBI_TaxID=562;
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A., Uhlin B.E.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-17, AND MUTAGENESIS OF 87-GLY--VAL-89; 142-ASN-ALA-143; 182-ALA-GLY-183; 186-ALA-GLY-183; 186-ALA-GLY-183; 186-ALA-GLY-183; 186-ALA-GLY-183; 186-ALA-GLY-183; 186-ALA-GLY-183; 186-ALA-GLY-183; 186-ALA-GLY-183; 186-ALA-GLY-183; 186-ALA-GLY-183; 186-ALA-GLY-183; 186-ALA-GLY-183; 186-ALA-GLY-183; 186-ALA-GLY-183; 186-ALA-GLY-183; 186-ALA-GLY-183; 186-ALA-GLY-183; 186-ALA-GLY-183; 186-ALA-GLY-183; 186-ALA-GLY-183; 186-ALA-GLY-183; 186-ALA-GLY-183; 186-ALA-GLY-183; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-ALA-GLY-184; 186-
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Uhlin B.E.;
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                                                                                                                                                                         EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE OF 1-295 FROM N.A. STRAIN=K12 / XL1-BLUE; King C.H., Shinnick T.M.; Submitted (MAR-1996) to the
                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-155 FROM N.A.
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                                                                                                                                                                        STANDARD;
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SEQUENCE FROM N.A.
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301 EV 302
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HLYE ECO57
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                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TSIFAEQTVEVVKSAIETADGALDLYNKYLDQVI PWKTFDETIKELSRFKQEYSQEASVL
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                                                                                                                                                                                                                                                                                                                                                                               Complete proteome; Cytolysis; Direct protein sequencing;
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    INDUCTION: During anaerobic growth. Weakly or not expressed in most strains. It is activated by slyA, while it is silenced by H-NS. Its expression is also regulated by CRP and FNR. PTM: In periplasm, it forms a disulfide bond between Cys-86 and Cys-284, which prevents the oligomerization. In outer membrane vesicles, the redox status prevents formation of the disulfide bond, leading to oligomerization and pore formation.
                                                                                                                                                                                                                                                                                                                                                                                                                 Potential.
In monomeric form.
K -> R (in strain CH9802).
G -> A (in strain CH9802).
GVA->DVD: Abolishes cytotoxic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NA->DD Abolishes cytotoxic activity. N->H: Strongly reduces cytotoxic
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Pred. No. 1.7e-85;
5; Mismatches 11; Indels (
nembrane vesicles. Also found in the periplasmic space.
                                                                                                     SIMILARITY: Belongs to the hemolysin E family.
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16; Mismatches
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                                                                                                                                                                                                                                             U73842; AAD04731.1; - ALT INIT. AE000216; AAC74266.1; ALT INIT. D90751; BAA36029.1; ALT INIT. D90752; BAA36029.1; ALT INIT. D90753; BAA36029.1; ALT INIT.
                                                                                                                                                                                                            EMBL; U57430; AAB07048.1; ALT INIT.
EMBL; X98615; CAA67204.1; ALT_INIT.
EMBL; AJ001829; CAA05035.1; --
                                                                                                                                                                                                                                                                                                          EMBL; U22466; AAA92081.1; -.
EMBL; U13610; -; NOT ANNOTATED_CDS.
PDB; 1QOY; X-ray; A=I-302.
ECHOBASE; EB3032; -.
                                                                                                                                                                                                                                                                                                                                                                                              Hemolysis; Toxin; Transmembrane.
                                                                                                                                                                                                                                                                                                  AF240780; AAL55667.1; -.
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InterPro; IPR010356; HlyE.
Pfam; PF06109; HlyE; 1.
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TRANSMEM
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EMBL;
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STRAIN-0157.H7 / RIMD 0508952 / EHEC;

STRAIN-0157.H7 / RIMD 0508952 / EHEC;

STRAIN-0157.H7 / RIMD 0508952 / EHEC;

MEDLINE-21156231; PubMed-11258796;

RA Hayashi T., Makino K., Ohishi M., Khurata T., Tanaka M., Tobe T.,

A Han C.-G., Ohtsubo B., Nakayama K., Murata T., Tanaka M., Tobe T.,

A Han C.-G., Ohtsubo B., Nakayama K., Murata T., Tanaka M., Tobe T.,

A Lida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,

A Kuhara S., Shiba T., Hattori M., Shinagawa H.;

Complete genome sequence of enterophemorrhagic Escherichia coli

"Complete genome sequence of enterophemorrhagic Escherichia coli

"Complete genome sequence of enterophemorrhagic activity towards

"Tol57:H7 and genomic comparison with a laboratory strain K-12.";

"DNA Res 8:11-22(2001).

"Un Na Res 8:11-22(2001).

"Un Na Res 8:11-22(2001).

"Ontact with mammalian cells (By similarity).

"Contact with mammalian cells (By similarity).

"Contact with mammalian cells (By similarity).

"Contact with mammalian cells (By similarity).

"Contact with la active. Probably forms an octamer (By emporitine that is active. Probably forms an octamer (By emporitine).
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PTM: In periplasm, it forms a disulfide bond, which prevents the prm: In opering membrane vesicles, the redox status oligomerization. In outer membrane vesicles, the redox status prevents formation of the disulfide bond, leading to oligomerization and pore formation (By similarity).
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MEDLINE=2032319; PubMed=10865950; DOI=10.1016/S0923-2508(00)00143-1;
MEDLINE=2032319; PubMed=10865950; DOI=10.1016/S0923-2508(00)00143-1;
del Castillo F.J., Moreno F., del Castillo I.;
"Characterization of the genes encoding the SheA haemolysin in
Recharacterization of the genes encoding the SheA haemolysin in
Recharichia coli O157:H7 and Shigella flexneri 2a.";
Res. Microbiol. 151:229-230(2000).
121 DGITKLINBAQKSLLVSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDKIRKBAYAGA
                                                                                                        AAGIVAGPFGLIISYSIAAGVIECKLIPELNNRLKTVQNFFTSLSATVKQANKDIDAAKL
                                                                                                                                                       KLATEIAAIGEIKTETETTRFYVDYDDLMLSLLKGAAKKMINTCNEYQQRHCKKTLFEVP
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SEQUENCE FROM N.A.
STRAIN=0157:H7 ( EDL933 / ATCC 700927 / EHEC;
STRAIN=0157:H7 ( EDL933 / ATCC 700927 / EHEC;
MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
Berna N.T., Plunkett G. III, Burland V., Mau B., Glasmer T.D.,
Fose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Kilnk S., Boutin A., Shao Y., Miller L.,
Grotbeck B.J., Davis N.W., Lim A., Dimalanta B.T., Potemousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-MAR-2004 (Rel. 43, Created)
29-MAR-2004 (Rel. 43, Last sequence update)
29-MAR-2004 (Rel. 44, Last annotation update)
05-JUL-2004 (Rel. 44, Last annotation update)
Hemolygin E (Cytotoxin clyA) (Silent hemolygin sheA).
Name=hlyE; Synonyms=clyA, sheA; OrderedLocusNames=z1344, ECs1677;
Name=hlyE; Synonyms=clyA, SheA; OrderedLocusNames=z1344, ECs1677;
Bacteria, Proteobacteria, Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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SUBCELLULAR LOCATION: Secreted. Exported from the cell by SUBCELLULAR LOCATION:
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us-09-993-292b-2.rup

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STANDARD;
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                                                                                                                                                                                                                                                                                                 Gaps
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"Identification of a new Escherichia coli She haemolysin homolog in
avian E. coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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0
                                                                                                                                                                                                                 By similarity.
Potential In monomeric form (By similarity); F261E29E1DE5FC87 CRC64;
                                                                                                          EMBL; AJ238954; CAB64962.1; ALT_INIT.
EMBL; AB00535; AAG56033.1; ALT_INIT.
EMBL; AP005255; BAB35100.1; ALT_INIT.
PIR; E85696; E85696.
PIR; E90838; E90638.
HSSP, P77335; IQOY.
InterPro; IPR010356; HIVE.
Pfan; PF06109; HIVE; I.
Complete proteome; Cytolysis; Hemolysis; Toxin; Transmembrane.
INIT_MET 0 0 0 By similarity.
                                                                                                                                                                                                                                                                        tch 91.2%; Score 1382; DB 1; Length 302; al Similarity 90.1%; Pred. No. 1.8e-84; 272; Conservative 18; Mismatches 12; Indels (
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Last annotation update)
SIMILARITY: Belongs to the hemolysin E family.
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MEDLINE=99242013; PubMed=10227474;
                                                                                                                                                                                                                                                  33585 MW;
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284
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                                                                                                                                                                                                                                                                                   Local Similarity
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01-NOV-1999
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DISULFID
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64 KSLLANNSQDRYFEATQVVYEWCGVTTQLLTAYLSLFNEYDEKKASAQKTILIKVLDDGII 123
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STRAIR=ATCC 12022 / Serotype 2b;
MEDLINE-20123445; PubMed=10660049;
Wallace A.J., Stillman T.J., Atkins A., Jamieson S.J., Bullough P.A., Green J., Artymiuk P.J.;
"E. coll hemolysin B (HlyE, ClyA, SheA): X-ray crystal structure of the toxin and observation of membrane pores by electron microscopy.";
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MEDLINE=20322319; PubMed=10865950; DOI=10.1016/S0923-2508(00)00143-1;
del Castillo F.J., Moreno F., del Castillo I.;
"Characterization of the genes encoding the SheA haemolysin in
Escherichia coli 0157:H7 and Shigella flexneri 2a.";
Res. Microbiol. 151:229-230(2000).
                                                                                                                                                                                                                                                                                                                                                                                   6 AEQTVEVVKSAIETADGALDLYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVLVGDI
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MEDLINE=22272406; PubMed=12384590;
Jin O., Yuana Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Jin O., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Shigella.
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                                                                                                                                                                                                                                                 Query Match 73.3%; Score 1110; DB 2; Length 3 Best Local Similarity 74.1%; Pred. No. 2.7e-66; Matches 215; Conservative 38; Mismatches 37; Indels
Vet. Microbiol. 66:125-134(1999).

EMBL; AF052225; AAD28079.1; -.
HSSP; P77335; LQOY.
InterProf. IPRO10356; HlyE.
Pfam; PF06109; HlyE; 1.
SEQUENCE 300 AA; 33555 MW; 6580B66C44A7B4BC CRC64;
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29-MAR-2004 (Rel. 43, Created)
29-MAR-2004 (Rel. 43, Last sequence update)
20-ULJ-2004 (Rel. 44, Last annotation update)
Hemolyain E-like protein.
OrderedLocusNames=SF1171, S1259;
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Oryza sativa (Rice).
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SEQUENCE 895 AA
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Best Local &
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                                           STRAIN=2457T, A.A.

STRAIN=2457T, A.A.

MEDLINE=22590274; PubMed=12704152;

MEDLINE=22590274; PubMed=12704152;

A Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,

A Wei J., Goldberg M.E., Pulmkett G. III, Rose D.J., Darling A.,

Pournier G., Maybew G.F., Plunkett G. III, Rose D.J., Darling A.,

A Schwartz D.C., Blathner F.R.;

A Schwartz D.C., Blathner F.R.;

T. Complete genome sequence and comparative genomics of Shigella

flexneri serotype 2a strain 2457T.";

Thecr. Immun. 71:275-2786(2003).

Thecr. Immun. 71:275-2786(2003).

Thecr. Immun. 71:275-2786(2003).

Thecr. Immun. 71:275-2786(2003).

Thecr. Immun. 71:275-2786(2003).

Thecr. Immun. 71:275-2786(2003).

Thecr. Immun. 71:275-2786(2003).

Thecr. Immun. 71:275-2786(2003).

Thecr. Immun. 71:275-2786(2003).

Thecr. Immun. 71:275-2786(2003).

Therefore not the hemolysin E family.

Therefore not functional May be a pseudogene.
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STRAIN-OS.HI / CFT073 / ATCC 700928 / UPEC;
STRAIN-OS.HI / CFT073 / ATCC 700928 / UPEC;
MEDLINE-2238824; PubMed=12471157; DOI=10.1073/pnas.252529799;
Welch R.A., Burland V., Plunkett G. III, Redford P., Roeech P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli.";
of uropathogenic Escherichia coli.";
Froc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
-; SIMILARITY: Belongs to the hemolysin E family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
34.3%; Score 519; DB 1; Length 11
Best Local Similarity 91.0%; Pred. No. 2.9e-27;
Matches 101; Conservative 5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF06109; H1yB; 1.
SEQUENCE 113 AA; 12879 MW; C328908D14C5C4EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-MAR-2004 (Rel. 43, Created)
29-MAR-2004 (Rel. 43, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Hemolysin E-like protein.
DracediocusNames-c1630;
Escherichia coli 06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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Q8FIZ7;
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------QSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGV-IEG-----KLIPE 210
                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             391 T-----TEBLGKIQSALQDRESBIEVLKGKTTALBIEVARLLADVNESNEQFD 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      274 EKVEILSSEVVRLKGLLDSTABSEBSKNRETEELV--KNLESEVSVLKGKLEFARIIEËR 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 QTVEVVKSAIETADGALD-----LYNKYLDQVIPWKTFDETIK-----ELSRFKQEY
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza
caurioN: Although it is strongly related to the hemolysin E tox from E.coli K-12 strain, it lacks all the N-terminal part of th protein, and it is therefore probably not functional. May be a pseudogene.
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Similar to an Arabidopsis thialiana chromosome BAC genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hsing Y.C., Chow T., Chen C., Wu H., Chu M., Chao Y., Liu submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AP001111; BAA90502.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 93;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 395; DB 1;
pred. No. 4.6e-19;
9; Mismatches 7;
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HSSP; P77335; 1QOY.
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1279 INNDINESVONLPEKT 1294
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es. 70; Conserv
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                                                                                                                                                                                                                                                                                                                                                  STRAIN=Toulouse;
PubMed=15210978;
                                                                                                                                                                                                                                                                                                           NCBI_TaxID=803;
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Matches
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Nature 0:0-0(2003).

ENBL/GenBank/DabJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QETEILRKOHQSRVGELESEIATIKEKYKKDLDELSRNNTSODAIKLKOHENELANFKAK 1215
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ASQQEVFGLQTTIDVLRNKLEAAEEAASEA-----LNNEKAANVKIEGLTEENVKLISE 492
                        LN------NRLKTVQNFFTSLSATVKQANKDIDAAKLKLATE-----IAAIGEIKTET 257
                                        QTVEVVKSAIETADGAL-----BLYNKYLDQVIPWKTFDETIK-----ELSRFKQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAQKDILIRILDDGVKKINEAQKSL------LTSSQSFNNASGKLLALDSQ-
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Neurospora.
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                                                                         ETTR----FYVDYDDLMLSLLKGAAKKMINTCNEYQQR-HGKKT
                                                                                        | :: | : | : | : | : | : | : | | KSTKESYEVMLDEANYDITCLRKNVDKLEAEVNKYREBCESKET
                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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21.3%; Pred. No. 27;
tive 65; Mismatches 141;
                                                                                                                                                                                                                                                       Neurospora crassa.
Eukaryota, Fungi, Ascomycota, Pezizomycotina,
Sordariomycetidae, Sordariales, Sordariaceae,
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INTERPO; IPR009638; Fez1.
INTERPO; IPR003909; KID_repeat.
INTERPO; IPR001898; SBP_bac_3.
Pfam; PF06818; Fez1; 1.
PFam; PF02524; KID; 5.
PROSITE; PS01039; SBP_BACTERIAL_3; UNKNOWN_1.
                                                                                                                                                                   4007 AA
                                                                                                                                                                                           Created)
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26,
26,
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01-MAR-2004 (TrEMBLrel.
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                                                                                                                                                                                                                               Hypothetical protein.
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Hes 75; Conserva
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                               NCBI_TaxID=5141;
                                                                                                                                                                                                                                            Name=NCU00658.1
                                                                                                                                                                                                                                                                                                                                   STRAIN=OR74A;
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Proc. Natl. Acad. Sci. U.S.A. 101:9716-9721(2004).

EMBL; EXBST700; CAPZ6028.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----KOEYSQE-ASVLVGDIKVLLMDSQDKYFEATQTV-----YEWCGV
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                                                                                                                                                                                             Westberg J., Persson A., Holmberg A., Goesmann A., Lundeberg J., Johansson K.-E., Pettersson B., Uhlen M.;
"The genome sequence of Mycoplasma mycoides subsp. mycoides SC type strain PGIT, the causative agent of contagious bovine pleuropneumonia (CBPP).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95;
                                                                                    ATP dependant protease ClpB.
Name=clpB; OrderedLocusNames=MSC 0613;
Mycoplasma mycoides (subsp. mycoides SC).
Bacteria; Firmicutes; Mollicutes; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00382; AAA; 2.
PROSITE; PS00871; CLPAB 2; 1.
ATP-binding; Complete proteome; Protease.
SEQUENCE 713 AA; 80782 MW; 1B5D204A9E29BE50 CRC64;
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CAE77235;
02-MAR-2004 (TrEMBLrel. 27, Created)
13-ARA-2004 (TrEMBLrel. 27, Last sequence update)
13-ARA-2004 (TrEMBLrel. 27, Last annotation update)
ATP dependant protease ClpB.
                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

8.2%; Score 123.5; DB 2;
Best Local Similarity 23.3%; Pred. No. 7.5;
Matches 79; Conservative 47; Mismatches 118;
                                                                                                                                                                                                                                                                     713 AA
                       713 AA
                                                  Created)
                       PRT;
                                                              -JUL-2004 (TrEMBLrel. 27, -JUL-2004 (TrEMBLrel. 27,
                                                   (TrEMBLrel. 27,
                         PRELIMINARY;
                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                           NCBI TaxID=44101;
                                                                                                                                                                                      STRAIN=PG1;
PubMed=14762060;
                                                    05-JUL-2004
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CAE77235
RESULT 11
Q6MT03
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572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-DSMZ 1740;
MEDINE-2882897; PubMed=14500908;
MEDINE-2882897; PubMed=14500908;
Baar C., Eppinger M., Raddatz G., Simon J., Lanz C., Klimmek O., Nandakumar R., Gross R., Rosinus A., Keller H., Jagtap P., Linke B., Meyer F., Lederer H., Schuster S.C.;
Meyer F., Lederer H., Schuster S.C.;
Meyer F., Lederer Begunec and analysis of Wolinella succinogenes.";
Proc. Natl. Acad. Sci. U.S.A. 100:11690-11695(2003).
EMBL: BXSTAIS59; CAE09993.1; -.
Complete protecome.
Complete protecome.
SEQUENCE 693 AA; 77641 MW; CBS7AIF23CFACCC2 CRC64;
                                                                                                     Westberg J., Persson A., Holmberg A., Goesmann A., Lundeberg J., Johansson K.-E., Pettersson B., Uhlen M.; "The genome sequence of Mycoplasma mycoides subsp. mycoides SC type strain PGIT, the causative agent of contagious bovine pleuropneumonia
                                                                                                                                                                                                                                                                                       Gaps
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Wolinella.
                                                                                                                                                                                                                                                                                       95;
   Mycoplasma mycoides (subsp. mycoides SC).
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
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                                                                                                                                                                                                                                                                                                                    TSIFAEQTVEVVKSAIETADGALDLYNKYLDQVIPWKTFDETI----
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                                                                                                                                                                                                                                                                                                                                                                                                                                        90 VIQLL--SAY-ILLFDEYNEKKASAQKDILIRILDDG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                           8.2%; Score 123.5; DB 2;
23.3%; Pred. No. 7.5;
Live 47; Mismatches 118;
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EMBL; BX842644; CAE77235.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OrderedLocusNames=WS0888;
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nes 79; Conservative
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                                                                    SEQUENCE FROM N.A.
                                         NCBI_TaxID=44101;
                                                                                  STRAIN=PG1;
PubMed=14762060;
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357 QYLLTSDDFVQIDDQKIQA---ELNQTFRPE---FLNRIDNI---VY------FN 396
                                                                                                                                   192 LIISYSIAAGVIEGKLIPELMNRLKTVQNFFTSLSATVKQANKDIDAAKLKLATEIAAIG 251
                                                                                                                                                                   397 ALSVOTI -- GEIVDKLLDELITRLODEONYFINFS------EEARNKIINE---- 439
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                 298 EAVRRNPYSIILFDEI-EKAHSDVFNILLQILDDGRLTDSLGKTIDFKNTIIVMTSNIAS 356
                                                                 KSLLISSOSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFG 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --YSQEASVLVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence and comparative analysis of the model rodent malaria parasite Plasmodium yoelii yoelii.";
Nature 419:512-519(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Silva J.C., Ermolaeva M.D., Allen J.B., Kooij T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.B., Selengut J.D., Koo H.L., Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Badwell S.L., Shallom S.J., van Aken S.B., Riedmiller S.B., Feldblyum T.V., Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M., Florens L., Yates F.R. III, Raine J.D., Sinden R.B., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., Van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 2723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
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19.4%; Pred. No. 54;
tive 54; Mismatches 102; Indels
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TIGRFAMS; TIGR01612; 235Kba-fam; 1.
SEQUENCE 2723 AA; 320451 MW; 08CD9C2EF7672ED2 CRC64;
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Last annotation update)
                                                                                                                                                                                                      252 EIKTETETTRFYVDYDDLM-LSLLKGAAKKMINT 284
                                                                                                                                                                                                                                      ------GYDRLFGARLLKDILKKIIET 460
 QLL--SAY-ILLFDEYNEKKASAQKDILIRILDDG
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InterPro; IPR011561; Pox I1 rel.
InterPro; IPR006499; RetTcuTocyteBP.
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01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
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ses 60; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=73239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=17XNL;
PubMed=12368865;
                                                                                                                                                                                                                                                                                                                                                                                                                             Name=PY01185
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                                                                                    SLREQLGEGANEVLSILQKSSQESSAFIL----EQEKMAKESTLVLFAKLKERFERLSEA 423
                                                                                                                                                                                                                                                                     SQVDRIRKEAYAGAAAGIVAGPF-GLIISYSIAAGVIEG--KLIPELN-----NRLKTVQ 219
                                                                                                                                                                                                                                                                                          NFFTSLSATVKQANKDIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDLMLSLLKGAAK 279
                                                                                                                                                                                                                                                                                                                                                               238 FGPTGVGKTEVARSLADILFNSPKKMIRLDMSEYMEKHSVAKLIGAPPGYVGYEEGGRLT 297
                                                                                                                                   71 DSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRILDDGVKKLNEA 130
                                                                                                                                                                                                      131 QKSLLTSS--------QFINDASGKLLALDSQLTNDFSEKSSYFQ 167
                                                                                                                                                                                                                                      ---FLTQNKGALEGMALDFRGFWEEYATRWRESSELTQGTLLETNQQVRASFAELSEGVL 480
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                                                                 11 EVVKSAIETADGALDLYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVLVGDIKVLLM
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24.6%; Pred. No. 6.1;
.ive 37; Mismatches 113; Indels 102; Gaps
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MEDLINE-97148974; PubMed=8995799;
MEDLINE-97148974; PubMed=8995799;
Palah M., Gupta R.S.
Phylogenetic analysis of mycoplasmas based on Hsp70 sequences:
cloning of the dnaK (hsp70) gene region of Mycoplasma capricolum.";
Int. J. Syst. Bacteriol. 47:38-45(1997).
EMBL; U51235; AAB09427.1; -
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:000166; F:nuclectide binding; IEA.
                                   77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria, Firmicutes, Mollicutes, Mycoplasmataceae, Mycoplasma.
NCBI_TaxID=2095;
Length 693;
8.1%; Score 122.5; DB 2; Length (21.7%; Pred. No. 8.4; tive 50; Mismatches 115; Indels
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Last annotation update)
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InterPro; IPR001270; Chaprnin clpA/B.
PRINTS; PR00300; CLPPROTEASEA.
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                                 67; Conservative
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82; Conservative
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                 Similarity
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01-OCT-2003 (TrEM
ClpB (Fragment).
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Query Match
Best Local
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79 ATQTYYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRILDDGVKKLNEAQKSLLTSS 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   135 LSAEDABALTARTVSELYPAIDPVSAKĖSSLVDDOLKIAKOEYDHSSGLYRASRTISLVA 194
195 IIVGVLIÄGTAGLLITRSITGPLAEG---VEVANRLAAGDLTVEVRAGGRDETGQLMAAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36 TANNGLD--TVYRDRVLR-----LKDLKIIADMY----AVNIVDVSHKVRNGNITWTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TADGALDLYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVLVGDIKVLLMDSQDKYFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C., Methe B.A., Nelson K.E., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J., Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S., Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J., Davidsen T.M., Zafaz N., White O., Tran B., Romero C., Forberger H.A., Weidman J., Khouri H.M., Feldblyum T.V., Utterback T.R., Weidman J., Khouri H.M., Feldblyum T.V., Iterback T.R., Genome of Geobacter sulfurreducens: metal reduction in subsurface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       220 -NFTSL-----SATVKQANKDIDAAKLKLAT---EIAA-IGBIKTETE 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Deltaproteobacteria; Desulfuromonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9SZK7;
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein F20D10.190 (Hypothetical protein AT4g38070).
Name=P20D10.190; Synonyms=AT4g38070;
                                                               -NFFTSL------SATVKQANKDIDAAKLKLAT---EIAA-IGEIKTETE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 GAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNNRLK----TVQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 302:1967-1969(2003).
EMBL; AB017211; ARX34750.1; -.
TIGR; GSU1374; -. 57093 MW; 3C9BEDABAF7C3812 CRC64;
                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1496 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.9%; Score 119; 23.5%; Pred. No. 1
                                                                                                                                                                                                               541
                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                             02-MAR-2004 (TrEMBLrel. 27, Last ann
Methyl-accepting chemotaxis protein.
HYLB OR GSU1374.
                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                     (TrEMBLrel. 27, (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                     Geobacter sulfurreducens.
Bacteria, Proteobacteria;
Geobacteraceae; Geobacter.
NCBI_TaxID=35554;
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les 69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=PCA / ATCC 51573;
PubMed=14671304;
                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  environments.";
                                                                                                                                                                                                                                    AAR34750;
02-MAR-2004
02-MAR-2004
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                                                                                                                                                                                                                     AAR34750
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Q9SZK7
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                                                                                                         ----ANKDIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDLMLSLLKG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36 TANNGLD--TVYRDRVLR-----LKDLKIIADMY----AVNIVDVSHKVRNGNITWTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79 ATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRILDDGVKKLNEAQKSLLTSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83 GRKSVEBAKKTIAEKLOAYLATNLAEEBKKHLEEAKPLİKVADATLER-----LASI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 TADGALDLYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVLVGDIKVLLMDSQDKYFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-PCA / ATCC 51573;
STRAIN-PCA / ATCC 51573;
STRAIN-PCA / ATCC 51573;
STRAIN-PCA / ATCC 51573;
Bubmed-14671304; DOI-10.1126/Science.1088727;
Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,
Heidelberg J.F., Wu D., Wu M., Ward N.L., Beanan M.J., Doddon R.J.,
Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,
Davidsen T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,
Weidman J.F., Khouri H.M., Fellblyum T.V., Utterback T.R.,
Van Aken S.E., Lovley D.R., Fraser C.M.;
"Genome of Geobacter sulfurreducens: metal reduction in subsurface
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
Geobacteraceae; Geobacter.
NCBI_TaxID=35554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QSFNNASGKLLALDSQLTNDFSEKSSYFOSQVD---RIRKEAY-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50111; CHEMOTAXIS_TRANSDUC_2; 1.
PROSITE; PS50885; HAMP; 1.
PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN 1.
SEQUENCE 541 AA; 57093 MW; 3C9BEDAEAF7C3B12 CRC64;
                                                                                                                                                                                                                                                                                                                                              05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Methyl-accepting chemclaxis protein.
Mame-hylb, ORFNames-GSU1374;
Geobacter sulfurreducens.
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                                                                                                                                                                                                                                                                                                              541 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR004090; Me chemotaxis.
InterPro; IPR005829; Sug_transporter.
InterPro; IPR010989; t-snare.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR004089; Chmtaxis_transd.
InterPro; IPR003660; HAMP.
                                                                                                                                                                                                                                                                                                              PRT;
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Pfam; PF00015; MCP8dignal; 1.
PRINTS; PR00260; CHEMTRNSDUCR: SMART; SN00304; HAMP; 1.
SWART; SM00283; MA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 302:1967-1969(2003).
EMBL; AE017180; AAR34750.1;
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                                                                                                                                                                         277 AAKKMINTCN
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Matches
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NCBI_TaxID=5888;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  317 KYENGKLEQENRELLGSLK------ELQEATIQGSGNSALSKLKNKFRNLEN 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     363 IHKNCSANLRSKEAEWSSQVEKMVEINDYKLQLQSKEAALKEVELELENCRSSTAKMRL 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EYSQEASVLVGDIKVL--LMDSQDKYFEATQTVYEWC-GVVTQLLSAYILLFDEYNEKKA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EWEEEKSKLLDEIYSLOTKLDSVTRISEDLOKKLOMCNGALTO------EETRRKHL 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAQKDILIRILDDGVKKLNEAQKSLLTSSQSFNNASGKLLALDSQLTNDFSEKSSYFQ-- 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----SQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEG----KLIPELNNRLKTVQN 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FFTSLSAT------TTRFYV 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 IFAEQTVEVVKSAIETADGALDLYNK--YLDQVIPWKT-----FDETIKELSRF----KQ
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
Spermatophyta; Prassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                    Mewes H.W.
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Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74;
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                                                                                                                                                                                    Kutzner M., Wambutt R., Bancroft I.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
SEQUENCE 1496 AA; 173346 MW; 03BBB75DCD2B03FB CRC64;
                                                                                                                                                           SEQUENCE FROM N.A.
Bevan M., Wedler H., Kutzner M., Wambutt R., Bancroft I.
Mayer K.F.X., Schueller C.;
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ALO35538; CAB37547.1; -.
EMBL; AL161592; CAB80472.1; -.
                                                                                                                                                                                                                                                                                           EU Arabidopsis sequencing project;
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                            Wedler H., Kutzner M., Wambutt R., Mewes H.W., Lemcke K.
Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.8%; Score 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OYEEISIMFL-----VLSRTVSEAOSR 444
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InterPro; IPR001092; HLH_basic.
Pfam; PF00010; HLH; 1.
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                                                                                                                            Zagulski M., Nowak J.K., Le Mouel A., Nowacki M., Migdalski A., Gromadka R., Noel B., Blanc I., Dessen P., Wincker P., Keller A.M., Cohen J., Meyer E., Sperling L.; "High coding density on the largest Paramecium tetraurelia somatic
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Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Photorhabdus,
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Nowak J.K., Migdalski A., Gromadka R., Zagulski M.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
BMBL; CR548612; CA1913635.1; -.
Hypothetical protein.
SEQUENCE 1877 AA; 220626 MW; F68260FE840D2796 CRC64;
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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OrderedLocusNames=plu1837;
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Curr. Biol. 0:0-0(2004)
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                         249 LYDAQATI---TSNIYDLESQYALAITSANELEADYKFAVESIPTDYLECPLCGTLHDNS 305
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                                                                                                                                                          129 LETPPPÄYYFLPFYIDQIKSWSSPWNSPENLGQYSNWKGPLIKYFTGYLKPEHFDIBENI 188
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                                                                                                                                                                                                                                          76 YFEATQIVYEWCGVVTQLLSAYILLFDEYNEKKA-----SAQKDIL-----
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                                                                                                         Gaps
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"Draft sequence of the diardia lamblia genome.";
"Draft sequence of the EMBL/GenBank/DDBJ databases.
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                        Indels 109;
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
GLP 227-22031 8359.
Glardia lamblia ATCC 50803.
Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
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                                                      577 AA; 65287 MW; B7F86EE4B34BEDE1 CRC64;
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19.2%; Pred. No. 36;
ive 57; Mismatches 126;
                                                                                DB 2;
                                                                                                           56; Mismatches 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1224 AA
                                                                                7.8%; Score 117.5; 19.2%; Pred. No. 15;
                                                                                                                                                                                          45 KELSRFKQEYSQEASVLVGDIKVL-----
                                                                                                                                      17 IETADGALDLYNKYLDQV----IPWKTF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00023; Ank; 5.
PROSITE; PS5008B; ANK_REPEAT; 3.
PROSITE; PS50297; ANK_REP_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
Nat. Biotechnol. 21:1307-1313(2003).
EMBL, BX571865; CAE14130.1; -.
PhotoList; plu1837; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   284 TCNEYQORHGKKTLFEVPDV 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           473 QLSVLQQIHGAKTCVVPPFV 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          preliminary data.
EMBL; AACB01000157; EAA37104.1;
InterPro; IPR002110; ANK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 65; Conserv
                                                                                    Query Match
Best Local Similarity
Matches 73; Conserv
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                                               Complete proteome
SEQUENCE 577 AA
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                                                                                                                                                                                                                                                                                                        117
                                                                                                                                                                                                                                                                                                                                                           173
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Q70004;
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2 TSIFAEQTVEVVKSAIETADGALDLYNKYL----DQV----

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                    130 ----AQKSLLTSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDRIRKEAYAGAAAGI 185
STRAIN=2001;
MEDULMS=68258115; PubMed=1894051;
Nicaud J.-M., Mackman N., Gray L., Holland I.B.;
Nicaud J.-M., Mackman N., Gray L., Holland I.B.;
"Characterisation of HlyC. and mechanism of activation and secretion of "Characterisation of HlyC."
                                                                         -----DILIRILDDGVKKLNE
                                                                                                                                                                                                                                                              186 VAGPFGLIISYSIAAGVIEGKLIPELNNRLKTVONFFTSLSATVKQANKDID-----
                                               KTFD------ETIKELSRFKQEYSQEASVLVGDIKVLLMDSQDKYFBATQTVYEWCGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MISCELLANEOUS: The hemolysin of E.coli is produced predominantly by strains causing extraintestinal infections, such as those of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-85234404; Pubmeda-3891743;
MEDLINE T., Pellett S., Welch R.A.;
"Nucleotide sequence of an Escherichia coli chromosomal hemolysin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: Secreted.
-!- DOMAIN: The Gly-rich region is probably involved in binding calcium, which is required for target cell-binding or cytolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- FUNCTION: Bacterial hemolysins are exotoxins that attack blood cell membranes and cause cell rupture by mechanisms not clearly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 activity.
DOMAIN: The three transmembrane domains are believed to be involved in pore formation by the cytocoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                the urinary tract.
SIMILARITY: Belongs to the RTX prokaryotic toxin family.
                                                                                                                                                                                                                                                                                                                                                                       1155 ERQQAETLKLSQRIPDKIASEYSDHVEKPRSVNESDDVM 1193
                                                                                                                                                                                                                                                                                                                                       238 ----AAKLKLATEI--AAIGEIKTETETTRFYVDYDDLM 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 10, Created)
(Rel. 10, Last sequence update)
(Rel. 44, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1023
                                                                                                                          90 VTQLLSAYILLFDEYNEKKASAQK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- PTM: Palmitoylated by hlyC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteriol. 163:94-105(1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  haemolysin from B. coli 2001
FEBS Lett. 187:339-344(1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-44 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Serotype 04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hemolysin, chromosomal Name=hlyA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SECUENCE FROM N.A.
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01-MAR-1989
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Created)
        01-OCT-2003 (TrEMBLrel. 25, C
01-OCT-2003 (TrEMBLrel. 25, I
01-MAR-2004 (TrEMBLrel. 26, I
Putative centromere protein.
ORFNames=OSJNBa0075H14.2;
                                                                                                                                                                   Science 300:1566-1569(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                       NCBI_TaxID=39947;
                                                                                                                                                                                                                                   Gramene; Q7XEH4;
                                                                                                                                                        chromosome 10
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agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54 YSQEASVL-----VGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILL-FDEY 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        208 LNKLGSVLSNTKHLNGVGN-KLONLPNLDNIGAGLDTV---SGILSAISASFILSNADAD 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NEKKASAQKDILIRILDD---GVKKLNEAQKSLLTSSQSFNNASGKLLALDSQLTNDFSE 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -------AAAAGLIASVVTLAISPLSFLSIADKFKRANKIEEYSQRFKK 344
                                             PIR, A24433; LEECA.
InterPro; IPR001943; Hemlysn_Ca_bind.
InterPro; IPR001949; REAA.
InterPro; IPR011049; Serralysn_like_C.
Pfam; PF00353; HemolysinCabind; 6.
Pfam; PF003183; RTX; I.O.
PRINTS; PR00313; CABNDNORPT.
PRINTS; PR01488; RTXTOXINA.
PROSITE; PS00330; HEMOLYSIN_CALCIUM; 4.
Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIIS----YSIAAGVIEGKLIPELNNRLKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TSIFAEQTVEVVK-----SAIETADGALDLYNKYLDQVIPWKTFDETIKELSRFKQE
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                                                                                                                                                                                                                                                                                                                                                                              N(6)-palmitoyl lysine (By similarity)
N(6)-palmitoyl lysine (By similarity)
A -> T (in strain 2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 1023;
                                                                                                                                                                                                                                                                                                                                                                                                                                  7.7%; Score 116; DB 1; Length 10
20.5%; Pred. No. 36;
tive 59; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               MW; 196D5C0A9A28B54D CRC64;
                                                                                                                                                                                                  16 X REPEATS, GLY-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VTGIISGILEASKQAMFEHVASKMADVIAEWEKKHGK 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------AKKMINTCNEYQQRHGK 294
 ities requires a license agreement (send an email to license@isb-sib.ch)
                                                                                                                                                                             Potential.
Potential.
                                                                                                                                                                    Potential.
                             EMBL; M10133; AAA23975.1; -. EMBL; X02768; CAA26546.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 20.5
hes 69; Conservative
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TRANSMEM
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Matches
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PRELIMINARY;

Q7XEH4

Q7XEH4 ID Q

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114 DILIRILDDGVKKLNEAQKSLLTSSQSFNNASGKLLALDSQLT------NDFS 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EK------SSYFQSQ--VDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGK 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           477 EQKVQMLMQDLEQKRQEADSAHAQLQDECNRH------TQTEADLHRFKNLHSQ-- 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      207 LIPELNNRLKTVQNFFTSLSATVKQANKDIDAAKLKLATEIAAIGEIKTETETTRFYV-- 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | | : | | : | | : | | | IBGKVQMLEQELKHKKKEEVDSLQISIQDEAHKRSEGEAALLAMTNLNSESQEEVNRLTL 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 EQTVEVVKSAIE----TADGA----LDLYNKYLDQVIPWKTFDETIKELSRFKQEYSQEA 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------DYDDLMLSLLKGAAKK------MINTCNEYQORHGKKTL 297
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2004 (Rel. 44, Last sequence update)
Probable signal recognition particle 68 kDa protein (SRP68).
ORYMANGE=PS55C.8;
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                   Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 124;
                                                                                                                                                                                                                                                                                  The Rice Chromosome 10 Sequencing Consortium; "In-depth view of structure, activity, and evolution of rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 2033;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gramento, 1745H9; -.
INTECPTO; IPRO1991; AA TRANSFER CLASS 2; UNKNOWN 1.
SEQUENCE 2033 AA; 231439 MW; ACFD716945B5C462 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AE017095; AAP53815.1; -.
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 7.7%; Score 116; DB 2; L. Local Similarity 18.7%; Pred. No. 82; es 67; Conservative 62; Mismatches 106;
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NCBI_TaxID=6239;
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61;
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                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its work by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 AAAGIVAGPFGLIISYSIAAGVI------EGKLIPBLNNRLKTVQNFFTSLSATVK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --ILLFDEYNEKKASAQKDILIRILDDGVKKLNE-AQKSLLTSSQSF-----NNASGKL 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LALDSQLTNDFSEKSSYFQS------0vDRIRKEAYAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAI---IDNITKSEKKSKPQDLLRLYDSVIEIYKEVAEIPGADHDKNLIQAFEVKVEYYRA 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: Signal-recognition-particle assembly has a crucial role in targeting secretory proteins to the rough endoplasmic reticulum membrane. SRP68 binds the 7S RNA, SRP72 binds to this complex subsequently. This ribonucleoprotein complex might interact directly with the docking protein in the ER membrane and possibly participate in the elongation arrest function (By similarity). SUBUNIT: Signal recognition particle consists of a 7S RNA molecule of 30 nucleotides and six protein subunits: SRP72, SRP68, SRP54, SUBCELLUAR LOCATION: Cytoplasmic (By similarity). SIMILARITY: Belongs to the SRP68 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRCFYMASSYSALHKYSEAAALFDRTVSRVQDAEGKL----KKLKSSSFITNETOSSLN
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Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87;
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7.6%; Score 115.5; DB 1; Length
Best Local Similarity 21.2%; Pred. No. 22;
Matches 68; Conservative 56; Mismatches 109; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WormPep; F55C5.8; CE20875.
InterPro; IPR008941; TPR-like.
Hypothetical protein; Ribonucleoprotein; RNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-2001 (TrEMBLrel. 18, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
BPS2 protein homolog (Bps2).
Name=bps2; OrderedLocusNames=SSO2241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : :::|| :: | ::|| ::|| ::|| ELRSEVESAKVTVRAARLASAAGDVKTDSELAKI-ID-
       (AUG-1996) to the EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal recognition particle.
SEQUENCE 622 AA; 70574 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z78198; CAB01573.1; -. PIR; T22716; T22716.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                239 AKLKLATBIAAIGBIKTETETTRFYVDYDD-----LMLSLLKGAAKKM------INTCN 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 LLMDSQDKYFEATQTVYEWCGVVTQLLSA-----YILLFDEYNEKKASAQKDILIRILD 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146 AEINARDELOK-----KYNNIRELQAKIRAID-------BEIDKLEKE-- 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42 ISLLTSSIK----AEDLIAVFADSGYVEAELDNKLYYRRIKRIRNGLGEEKNLIMDDRRA 97
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STRAIN=ATCC 35092 / DSM 1617 / P2;

MEDLINE=21332296; PubMed=11427726;

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Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 RESSSNIVAK----TTYTIT--LTRONKINEILNKIKVKKDELANLEFALKKIEBEIQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179 AGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNNRLKTVQNFFTSLSATVKQANKDIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98 LLL----TYPSPENR-----LVTQILSGDGNVEWPISTTSKINEIK--AKKEELQKLLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 VEVVKSAIETADGALDLYNKYLDQVIPWKTFDETI--KELSRFKQEYSQEASVLVGDIKV
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NCBI_TaxID=66797;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Length 587;
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                                                                                                                                                                                                                                                                                                                                                                                                                     7.6%; Score 115; DB 2; Length 58° 20.3%; Pred. No. 22; tive 66; Mismatches 103; Indels
                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).

EMBL; AE006828; AAK42408.1; -.

PIR; A90394; A90394.

CCOMplete Protecome.

SEQUENCE 587 AA; 68436 MW; B90DBC1E19C05E86 CRC64;
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22.6%; Pred. No. 19;
ive 41; Mismatches
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(TrEMBLrel. 07, I
(TrEMBLrel. 25, I
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316 RNWEEVVPEPIQSQL------NQKDEQIK---DLTKQVNQINKDKVGIEQQFNT 360
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Last annotation update)
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Shirekas S., Scaller-F
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"The genome sequence of Drosophila melanogaster.";
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Eukaryota, Metazoa; Arthropoda, Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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"The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                   :
                                                                                             Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Claniker S.E., Wheeler D.A., Kronmiller B., Frise E., Hodgson A., Patel S., Adams M., Chamer M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Paciele J.M., Park S., Pfeiffer B.D., Richards S., Sodergren B.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C. Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; Finishing a whole-genome shotqun: release 3 of the Drosophila melanogaster euchromatic genome sequence."; Genome Biol. 3:RESEARCH0079-RESERARCH0079 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=2242669; PubMed=12537572; Matthews B.B., Campbell K.S., Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.B., Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P. Bettencourt B.R., Celniker S.B., de Grey A.D., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Annotation of the Drosophila melanogaster euchromatic genome: a
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EMBL; AE003695; AAF54775.1; -.
IntAct; Q9YGA8; ..
FlyBase; FBGM03801; CG4066.
SEQUENCE 588 AA; 63663 MW; OCF2D6D093880B32 CRC64;
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Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).
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7.6%; Score 114.5; Dest Local Similarity 21.1%; Pred. No. 24;
Matches 67; Conservative 38; Mismatches
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MEDLINE=22426070; Pubmed=12537573;
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                   Science 287:2185-2195(2000).
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171 DRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNNRLKTVONFFTSLSATVK 230
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                                                                                                                                                                                                                                                                                           MEDLINE=22061436; PubMed=12004073;
Read T.D., Salzberg S.L., Pop M., Shumway M., Umayam L., Jiang I Holtzapple E., Busch J.D., Smith K.L., Schupp J.M., Solomon D., Keim P., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 652;
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                                                                                                                                                                                     Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
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Last annotation update)
                                                          Last sequence update)
Last annotation update)
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652
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PROSITE; PS01072; SLH_DOMAIN; UNKNOWN_1.
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EMBL, AE011190; AAM26077.1; -.
InterPro; IPR0101119; SLH.
InterPro; IPR010989; t-snare.
InterPro; IPR010978; tRNA_binding_arm.
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  PRT;
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                                                                                                                                                Bacillus anthracis str. A2012.
Plasmid pXO1.
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01-NOV-1999 (TrEMBLrel. 12,
01-OCT-2004 (TrEMBLrel. 28,
PXO1-90 (S-layer protein,).
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                                                               05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, S-layer protein, (PXO1-90).
                                               (TremBLrel. 27,
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  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          652 AA;
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SEQUENCE FROM N.A.
                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LNEAQK-----SLLTSSQSFNNASGKLLALDSQLTNDFSEKSSYFQ---SQV 170
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                                                                                                                                                                                                                     Federova N.B.,
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                                                                    SEQUENCE FROM N.A.
STRAIN=Sterne; PLASMID=virulence plasmid PX01;
MEDLINE=99445483; PubMed=10515943;
MEDLINE=99445483; PubMed=10515943.
MEDLINE=99445483; PubMed=10515943.
Keim P., Koehler T.M., Lamke G., Kumano S., Mahillon J., Manter D., Martinez Y., Ricke D., Svensson R., Jackson P.J.;
"Sequence and organization of pX01, the large Bacillus anthracis plasmid harboring the anthrax toxin genes.";
J. Bacteriol. 181:6509-6515(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                               81;
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18.6%; Pred. No. 27;
                                                                                                                                                                                          SEQUENCE FROM N.A.

STRAIN=Ames / isolate 0581; PLASMID=DX01;

Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Ferental Milson M., Stanley S., Decker S., Read T.D., Salzberg S.L.

Fraser C.M.;

"Bacillus anthracis comparative genomics.";

"Bucillus anthracis comparative genomics.";

EMBL; AF055404; AAD32394-1;

EMBL; AE01736; AAT28865.2;

PIR; B59102; B59102.
                                                                                                                                                                                                                                                                                                                                                                                                                              66; Mismatches 106; Indels
                       Plasmid virulence plasmid PX01, and Plasmid pX01.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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Last sequence update)
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PROSITE; PS01072; SLH DOMAIN; UNKNOWN_1.
Complete proteome; Plasmid.
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Backl PXO1. 0124.
Bacillus anthracis str. Ames 0581.
Plasmid pXO1.
 OrderedLocusNames=GBAA_pXO1_0124;
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InterPro; IPR001119; SLH.
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             Bacillus anthracis.
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58; Conserv
                                              NCBI_TaxID=1392
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AAT28865;
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Matches
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DE S-1a
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127 LNEAQK-----SLLTSSQSFNNASGKLLALDSQLTNDFSEKSSYFQ---SQV 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              171 DRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNNRLKTVQNFFTSLSATVK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 436 ECNKKIDNTKKOLAFFDKSNKKQQELESELVQLNKKIDELGKRHKHRQELEASQKKALDE 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79 ATQ-----TVYEWCGVVTQLLSAYILLFDBYNB--KKASAQKDILIRILDDGVKK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  231 QANKDIDAAKLKLAT-EIAAIGEIKTETETTRFYVDYDDL-----MLSLLKGAAKKMINT 284
                                                                                                                                                                STRAIN=Ames 0581;
Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B., Wilson M., Stanley S., Decker S., Read T.D., Salzberg S., Fraser C.M.; "Bacillus anthracis comparative genomics.";
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AR017336; AAT28865.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25 DLYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVL-----VGDIKVLLMDSQDKYFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome sequence and comparative analysis of the model rodent malaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carlton J.M., Angluoli S.V., Suh B.B., Kooij T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.B., Selengut J.D., Koo H.L., Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bladwell S.L., Shallom S.J., van Aken S.B., Riedmuller S.B., Feldblyum T.V., Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M., Florens L., Yates F.R. III, Raine J.D., Sinden R.B., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., Van Lih L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmodium yoelii yoelii.
Bukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=73239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   parasite Plasmodium yoelii yoelii.";
Nature 419:512-519(2002).
-!- CAUTION: The sequence shown here is derived from an
                                                                                                                                                                                                                                                                                                                                                                                                     652 AA; 76210 MW; 723F5FBE03516355 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 7.6%; Score 114.5; DB 2; Best Local Similarity 18.6%; Pred. No. 27; Matches 58; Conservative 66; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        779 AA
                           Bacillus cereus group, Bacillus anthracis
NCBI_TaxID=261594;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              414 SRLKNH-----
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NCBI_TaxID=9606;
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                                    Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     303 QMFANVKIENKNLLIKGEEYDTNDGGLKLEKGEEVISNYNNEDEGTELFLKNNVSVLELF 362
                                                                                                                                                                                                                                                                                                                                     RIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELN------NRLKTVQNFFT 223
                                                                                                                                                                                                                                                                                                                                                                                                      254 EINKPGDAENA-----LEFYKKGSNKENKLIEEVNFFKPOKGYAEEKRISTFSD 302
                                                                                                                                                                                                                                                                                                                 123 --GVKKINBAQKSLLTSSQSFNNASGKLLALDSQLTND----FSEKSSYF----QSQVD 171
                                                                                                                                                                                                                                                                            146 ME-----KSY---KSEYEKKEBEEDSKISHDVHENLKVTFVMKKNIDNFLFTQY
                                                                                                                                                                                                   24 IDLYNKYLDQVIPWKTPDETIKELSRFKQEYSQEASVLVGDIKVLLMDSQDKYFEATQTV
                                                                                                                                                                                                                    92 LGKYGKEVENIEFPQTFDEYFN--SRSKEDYEQ---LEAGKLKI-LTENTUTYKDEIRKI
                                                                                                                                                                                                                                                        84 YEWCGVVTQLLSAYILLFDEYNEKKASAQKD-------ILIRILDD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=9835934; PubMed=9693369;
de Hostos E.L., McZaffrey G., Sucgang R., Pierce D.W., Vale R.D.;
de Hostos E.L., McZaffrey G, Sucgang R., Pierce D.W., Vale R.D.;
de Hostos E.L., mcZaffrey G, Sucgang R., Pierce D.W., Vale R.D.;
de Hostos E.L., McZaffrey G, Sucgang R., Pierce D.W., Vale R.D.;
Mol. Alexandra discolution (1998).
 18
                                                                                                                                                                         97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KGAAKKMI-----NTCNE-----YQQRHGKKTLFEVPD 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | | : ::|| | KENVKASLKYKKENIIKNNLNENLLCGRVKVHWFPKFMKRIIMKIPD 409
                                                                                                                                             DB 2; Length 779;
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                           ch 1.6%; Score 114.5; DB 2; Length 1 Similarity 20.5%; Pred. No. 33; 71; Conservative 51; Mismatches 128; Indels
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SUDMITTED (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AB102780; BAC56912.1; -.
HSSP; P33173; 1161.
HSSP; P33173; 1161.
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                  EMBL; AABLO100631; EAA21743.1; -.
EMBL; AABLO100631; EAA21743.1; -.
GO; GO:005525; F:GTP binding; IEA.
InterPro; IPR005289; GTP-binding.
InterPro; IPR002917; MWR HSR1.
Pfam; PF01926; MWR HSR1; 1.
TIGRPAMS; TIGR00650; MG442; 1.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MR-2004 (TrEMBLrel. 26, Last annotation update)
11-MR-2004 (TrEMBLrel. 26, Last annotation update)
01-MR-2004 (TrEMBLrel. 86, Last annotation update)
Dictyostellum discoideum (Slime mold).
Eukaryota, Mycetozoa, Dictyostellum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=44689;
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                                                                                                                                                     Query Match
Best Local &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRILDDGVKKLNEAQKSLLTSSQSF 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1059 LERSLKSENDNLLQQSSLLKSQLESIEKQKQDQLIPIQLELESKKCELSKLSSQFSEQTK 1118
                                                                                                                                                                                                                                                                                                                                                                                                                 1223 QSLEREIKDLKRSHISTET-----ELDKLKKTHLAADVKSKDFIALNKSVEILIKSQEQL 1277
                                                                                               14;
                                                                                                                                                                  942 FDQSQQDNQSIKQSYNQLBSTLTLAQSENQRLTTENKQFITSLNBIKSLFNSIQQQK-ET 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 LKLATEIAAIGEIKTETETTRFYUDYDDLMLSLLKG------AAKKMINTCNEYOORH 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 LYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVLVGD----IKVLLMDSQDKYFEATQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           513 ILAENSRKITUL-------QVNEKSLIRQYTTLVB-LERQLRKENBKQKM------
                                                                                                                                                                                                                      80 TQTVYEWCGVVTQ---LLSAYILLFDEYNEKKASAQKDILIRILDDGVKKLNEAQKSLLT
                                                                                                                                                                                                                                                                                                        214 -----REPARTYONFFTSLSATVKOANKD---IDAAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70; Gaps
                                                                                                                                                                                                                                                1001 IQLEFEFQEKENQFDSLLTNYNQLFSKXNDLATSNESNRL--EFDQFKKDSNQSIQSLES
                                                                                                                                        --VGDIKVLLMDSQDKYFEA
                                                                                               Gaps
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SEQUENCE FROM N.A.

Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto N., Hikiji T., Suzuki Y., Obayashi M., Nishi T., Shibahara T. Okitani R., Ota T., Suzuki Y., Sugano S.;

Tanaka T., Nakamura Y., Isogai T., Sugano S.;

Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AK025632; BABJS196-1; -.

NON TER.

NON TER.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                  Indels 132;
                                                     Length 1885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 720;
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                                                                                                                                                                                                                                                                                                                                                                                           172 RIRKEAYAGAAAGIVAGPFGLIIS---YSIAAGVIEGKLI---PELNN-
                 15686AED3B007EC7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          720 AA; 84029 MW; A86586FEAA953D0B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.5%; Score 114; DB 2; Lv
20.7%; Pred. No. 33;
Live 56; Mismatches 111;
                                                            DB 2;
                                                                                                    109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     720 AA.
                                                                                                      51; Mismatches
                                                            Score 114.5;
pred. No. 95;
ATP-binding; Microtubule; Motor protein.
SEQUENCE 1885 AA; 218215 MW; 15686AE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                40 FDETIKELSRFKQEYSQEASVL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein FLJ21979.
Homo sapiens (Human).
                                                            7.6%;
Local Similarity 20.7%;
Les 76; Conservative 5.
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nes 62; Conserv
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us-09-993-292b-2.rup

Oy 217 TVQNFFTSLSATVKQANKDIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDLMLSLLKG 276	PRESULT 36 OTRD43 DY CYBD43 DY CYBD43 DY CYBD45 DY CYBD45 DY CYBD45 DY CYBD45 DY CYBD45 DY CYBD46 DY	Qy 71 -DSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIR-ILDDGVKKLN 128 : : :	177 AYAGAAGIVAGPFGLIISYSIAAGVIEGKLIPELNNRLKTVQNFFTSLSATVK
QY 202 VIEGKLIPELNNRLKTVQNFFTSLSATVKQANKDIDAAKLK 242 : : :	RESULT 35 QUECTIO AC QUECTIO AC QUECTIO AC QUECTIO AC QUECTIO AC QUECTIO TO 1-MAR-2003 (TERBALE-12, Created) TO 1-MAR-2003 (TERBALE-12, Last sequence update) DT 01-MAR-2003 (TERBALE-12, Last sequence update) Chromosome segregation SMC protein. GN Graphylococcus epidermidis. Staphylococcus epidermidis. CC STRAIN-ATCC 12228; RA Zhang YO. Ren SX., Li HL., Wang YX., Pu G., Yang J., RA Zhang YO. Ren SX., Li HL., Wang YX., Pu G., Yang J., RA Zhang YO. Ren SX., Li HL., Wang YX., Pu G., Yang J., RA Zhang YO. Ren SX., Li HL., Wang YX., Pu G., Yang J., RA Zhang YO. Ren SX., Li HL., Wang YX., Pu G., Yang J., RA Zhang YO. Ren SX., Li HL., Wang YX., Pu G., Yang J., RA Chang YO. Ren SX., Li HL., Wang YX., Pu G., Yang J., RA Chang YO. Ren SX., Li HL., Wang YX., Pu G., Yang J., RA Chang YO. Ren SX., Li HL., Wang YX., Pu G., Yang J., RA Chang YO. Ren SX., Li HL., Wang YX., Pu G., Yang J., RA Chang YO. Ren SX., Li HL., Wang YX., Pu G., Yang J., RA Chang YO. Ren SX., Li HL., Wang YX., Pu G., Yang J., RA Chang YO. Ren SX., Li HL., Wang YX., Pu G., Yang J., RA Chang YO. Ren SX., Li HL., Wang YX., Pu G., Yang J., RA Chang YO. Ren SX., Li HL., Wang YX., Pu G., Yang J., RA Chang YO. Ren SX., Li HL., Wang YX., Pu G., Yang J., RA Chang YO. Ren SX., Li HL., Wang YX., Pu G., Yang J., RA CONOONS STAIN AND CONOO	Query Match Best Local Similarity 18.6%; Score 114; DB 2; Length 1189; Best Local Similarity 18.6%; Pred. No. 59; Matches 62; Conservative 59; Mismatches 130; Indels 82; Gaps 9; Qy 7 EQTVEVVKSAIETADGALDLYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASV 60 :: : : : :	61 LVGDIKVLLMDSQDKYFEATQTVYEWC

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:|: : : ||
SEKLQKEKEEKKNIINDVK 1016
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INFDSLKKEFEKSFDEVQI 1073
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RFLEHTINENEAKKSRLDS 419
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/LVKLCKKIFLLKYYTTKD 852
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ZENNININMMLSDELKKLQ 903
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                                                                                                                                                                                                                                                                                                                                                                                                                     del rodent malaria
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J.D., Koo H.L.,
Bidwell S.L.,
Cummings L.M.,
E., Harris M.A.,
ya A.B.,
White O.R.,
S.L., Gardner M.J.,
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ntry which is
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                                                                                                                                                                                                                   lasmodium.
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RESULT 39
                                                   RESULT 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             168 VEB-SKRÁYDBÁVVLYDSSRTMLALLLEGÍLICGGVFATRLIRSÍIHPLTTLKDBÁARVA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGKLIPEL----NNRLKTVQNFFTSLSATVKQANKDIDAAKLKLATEIAAIGEIKTETET 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         227 LGDLSQSIQVSGRNEVIDVQQSVQAMQANLRNTLQDIQGSAAQLA---AAAREELQTATES 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLMDSQDK-----YFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQK---DILI 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ::|| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62
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"Nahy, a catabolic plasmid-encoded receptor required for chemotaxis of Pseudomonas putida to the aromatic hydrocarbon naphthalene.";
J. Bacteriol. 181:3310-3316(1999).
EMBL; AF1003302; AAD13223.1;
HSSP; P02942; 1QU7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 TVEVVK-SAIETADGALDLYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVLVGDIKV
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                                                                                                                                                                                                                             Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
Pseudomonadaceae; Pseudomonas.
NCBI_raxID=303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 538;
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GO; GO:0016620; Cimembrane; IEA.

GO; GO:0016871; F:signal transducer activity; IEA.

GO; GO:0006935; P:chemotaxis; IEA.

GO; GO:0007165; P:chemotaxis; IEA.

GO; GO:0007165; P:chemotaxis; IEA.

InterPro; IPRO04089; Chutaxis transd.

InterPro; IPRO04089; Me chemotaxis.

InterPro; IPRO04099; Me chemotaxis.

InterPro; IPRO04099; Me chemotaxis.

InterPro; IPRO0107; TSNARE.

Pfam; PFO0672; HAMP; 1.

Pfam; PFO0672; HAMP; 1.

PRINTS; PRO0260; CHEMTRNSDUCR.

SNART; SM00304; HAMP; 1.
                                                                                                  01-MAY-1999 (TrEMBLrel. 10, Last sequence update) 01-UNN-2003 (TrEMBLrel. 24, Last annotation update) Methyl-accepting chemotaxis protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 7.5%; Score 113.5; DB 2; Local Similarity 21.9%; Pred. No. 25; les 84; Conservative 56; Mismatches 118;
                                       538 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50111; CHEMOTAXIS_TRANSDUC_2; PROSITE; PS50885; HAMP; 1. PROSITE; PS50192; T_SNARE; 1.
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                                                                                        Created)
                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                              STRAIN=G7;
MEDLINE=99255564; PubMed=10322041;
                                                                                        (TrEMBLrel. 10, (TrEMBLrel. 10,
                                         PRELIMINARY;
                                                                                                                                                                                                            Pseudomonas putida.
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                                                                                           01-MAY-1999
                                                                                                                                                                                      Name=nahY;
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Matches
                                              Q9Z4Z9
RESULT 37
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AC 092421
DT 01-MAD
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122 DG--VKKINEAQKSLLT-SSQSFNNASG------KLLALDSQLTNDF----- 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  160 ----SEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELMNRL
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KEDLINE-2195285; PubMed=11759840;

KEDLINE-2195285; PubMed=11759840;

KEDLINE-2195285; PubMed=11759840;

KEDLINE-2195285; PubMed=11759840;

A Wachardo T., Nakamura Y., Wolk C.P., Kuritz T., Kawashima K., Kimura T., Kimida Y., Kohara M., Mateumoto M., Mateumo A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Ayanda M., Tabata S.; Sugimoto M., Takazawa M., Yamada M., Tabata S.; Sugimoto M., Takazawa M., Yamada M., Tabata S.; Sugimoto M., Takazawa M., Yamada M., Tabata S.; Sugimoto M., Takazawa M., Yamada M., Tabata S.; Sugimoto M., Takazawa M., Yamada M., Diande S., Sugimoto M., Takazawa M., Yamada M., Masaka S., Sugimoto M., Takazawa M., Yamada M., Masaka S., Sugimoto M., Takazawa M., Yamada M., Tabata S., Sugimoto M., Takazawa M., Yamada M., Diande S., Sugimoto M., Takazawa M., Yamada M., Yamada M., Tabata S., Sugimoto M., Takazawa M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yama
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        All0059 protein.
OrderedLocusNames=all0059;
Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBI_TaxID=103690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B893994D1F4656D8 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      461 LGVVLALIWGMRHRIIHSAQDLQKVSNLRLLGTVPKLA 498
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein MSV156.
                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                           727 AA.
: || :||| 344 IDRLSGKINETTRTVFRLAEEAS 366
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01-MAR-2002 (TrEMBLrel. 20,
01-JUN-2003 (TrEMBLrel. 24,
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SEQUENCE 727 AA
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01-MAR-2002
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252 64

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82 TVYEWCGVVTQLLSAYILLFDEYN------EKKASAQKDILIRILDDGVKKLNEAQK 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 SLLTSSQSFNNASGKLLALDSQLTNDFSBKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGL 192
EWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRILDDGVKKLNEAQKSLLTSSQSFNNA 144
                                                                                                     145 SGKILALDSQLTNDFSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIE 204
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                                                                                                                                                                                                        205 GKLIPELNNRLKTVQNFFTSLSATVKQANKDIDAA-KLKLATEIAAIGEIKTETETTRFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence and comparative analysis of the model rodent malaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carlton J.M., Angluoli S.V., Suh B.B., Kooij T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.B., Selengut J.D., Koo H.L., Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L., Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V., Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M., Plorens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., Van Lih L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        parasite Plasmodium yoelii yoelii.";
Nature 413:512-519(2002).
-1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmodium yoelii yoelii.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
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                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1489 AA
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01-MAR-2004 (TrEMBLrel. 26, Last seg
01-MAR-2004 (TrEMBLrel. 26, Last ann
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InterPro, IPR011591; Botulinum.
InterPro, IPR006499; ReticulocyteBP.
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TIGRFAMs; TIGR01612; 235kDa-fam; 1.
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503 KEFDELRMQL 512
                                                                                                                                                                                                                                                                                                          264 VDYDDLMLSL 273
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PubMed=12368865;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  269 NSKINTLNENIKGVMNLYTETKAKISNLONEILNKDSTIKSLDEKOKLLDELDKNINNIT 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 YEWCGVVTQLLSAYILLFDEYNEKKASAQKDIL----IRILDDGVKKLNEAQKSLLTSS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------KLDT 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   246 EIAAIGEIKTET-----ETTRFY-----VDYDDLM-----LSLLKGAAKKMI 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DLKDKVTE-----FEEKLKETQRRMLEMBEKAK------DSDRLHEAKDTIE 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EYKKIDDIKNNNLQKLEESYKKIDEQTEYYKNKINKEYNDIIELKNNNLQKLEEENKKID 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  214 DELNYLLDE--SKKEFIKKQEELNXTIDKXQEELIKKLNDKEINFNIDEKQKLLD---QI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           329 SLYNKSNTKITNIQQLLESSLTDFNNANININELKSKIKLFDNDIQKLNND------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DLYNKYLDQVI PWKTFDETIKELSRFKQEYSQEASVLVGDIKV-LLMDSQDKYFEATQTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186 VAGPFGLIISYSIAAGVIEGKLIPELMNRLKTVQNFFTSLSATVKQANKDIDAAKLKLAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                Melanoplus sanguinipes entomopoxvirus (MSEPV).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
Entomopoxvirus B.
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Similar to spindle pole body protein pcpl from Schizosaccharomyces
                                                                                                                                                                                                        Kutish G.F., Rock D.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177;
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                                                                                                                                                                                                                                                                                                                                                                                                                Length 1127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Pungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Lasiosphaeriaceae; Podospora.
NCBI_TaxID=5145;
                                                                                                                                                                                                                                                                                                                                                                                                          7.5%; Score 113.5; DB 2; Length 1
19.2%; Pred. No. 60;
Live 56; Mismatches 106; Indels
                                                                                                                                                                                                Afonso C.L., Tulman E.R., Lu Z., Oma E., Kutish G.F., Roc "The genome of Melanoplus sanguinipes entomopoxvirus."; J. Virol. 73:533-552(1999).
BMBL; AF063866; AAC97677.1; -. PIR; T28317; T28317.
Hypothetical protein.
SEQUENCE 1127 AA, 134265 MW; F185DA1D5A3FE7D1 CRC64;
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SEQUENCE 1363 AA; 156746 MW; C40D66C6189F0F2A CRC64;
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Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-99102612; PubMed-9847359;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             60; Conservative
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53; Conservative
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                                                                                                  NCBI_TaxID=83191;
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R HSSP; PD2468; INPE.

R WOXTMPEP; PD2468; INPE.

R WOXTMPEP; T22A3.8; CE31067.

R GO; GO:0005578; C:extracellular matrix; IEA.

DR GO; GO:0005578; C:extracellular matrix; IEA.

DR GO; GO:0005198; F:erceptor binding; IEA.

DR GO; GO:0005198; F:erceptor binding; IEA.

DR GO; GO:0003034; P:regulation of cell adhesion; IEA.

DR GO; GO:0030334; P:regulation of cell migration; IEA.

DR GO; GO:004595; P:regulation of embryonic development; IEA.

DR InterPro; IPR00980; Gold like.

DR InterPro; IPR00930; Gal bind like.

DR InterPro; IPR00930; Grow fac_recept.

DR InterPro; IPR00930; Laminin B.

DR InterPro; IPR00199; Laminin G.

DR InterPro; IPR00199; Laminin G.

DR InterPro; IPR00199; Laminin G.

InterPro; IPR00199; Laminin G.

DR InterPro; IPR00191; Laminin I.

DR InterPro; IPR00191; Laminin I.

TherPro; IPR0010307; Laminin II.
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Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
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EMBL; Z81125; CAA15432.3; JOINED.
EMBL; AL008585; CAB03385.3; JOINED.
EMBL; Z81125; CAB03385.3; -.
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-Bristol N2;
MEDLINE-99069613; PubMed=9851916;
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F87908; F87908.
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Science 282:2012-2018(1998).
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Dujon B., Sherman D., Fischer G., Neuveglise C., Talla E.,
Lafottaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
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A Goffard N., Frangeul L., Cattolico I., Confanioleri F., de Daruvar A.,
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Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
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Nicaud J.M., Nikolski M., Oztas S., Ozier-Kadogeropoulos O.,
Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Seniou-Meyer M., Zivanovic I., Bolctin-Pukuhara M., Thierry A.,
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Mincker P., Souciet J.L.;
"Genome evolution in yeasts.";
-----SATVKQANKD 235
                                    492
                                                                        IDAAK----LKLATEIAAIGEI-KTETETTRFYVDYDDLMLSLLKGAAKKMINTCNEYQQ 290
                                                                                                   493 VNQSKRNYEIGIVEKINEIAEANKKRIESTK------ELIQPTIQNLISTQEELLK 542
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                     01-0CT-2004 (TrEMBLrel. 28, Created)
01-0CT-2004 (TrEMBLrel. 28, Last sequence update)
01-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to DEHAOCO95589 Debaryomyces hansenii IPF 1836.1.
ORFNames=YALIOFO23879;
Yarrowia lipolytica (Candida lipolytica).
Bukaryota; Fungi; Ascomycota; Saccharomyceties; Saccharomycetales; Dipodascaceae; Yarrowia.
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Submitrace (JUL-2004) to the EMBL/GenBank/DDBJ databases.
SUBMITRACE RASA132; CAG77705.1; -.
SEQUENCE 1906 AA; 210346 MW; FGED7D1AF7B7562B CRC64;
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22.1%; Pred. No. 1.1e+02;
tive 48; Mismatches 116;
  193 IISYSIAAGVIEGKLIPELNNRLKTVQNFFTSL-----
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Matches 66; Conservative
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233 NKDIDAAKLKLATBIAAIGBIKTETTRFYVDYDDLMLSLLKGAAKKMINTCNEYQQR 291
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MEDLINE-2266894; PubMed=12783803; MEDLINE-2266894; PubMed=12783803; MEDLINE-2266894; PubMed=12783803; Musper C.C., Hall D.H., Hedgecock B.M., Kao G., Karantza V., Madsworth W.G.; Vogel B.E., Hutter H., Chisholm A.D., Yurchenco P.D., Wadsworth W.G.; "Laminin alpha subunits and their role in C. elegans development."; Development 130:3343-3358 (2003).
rkblimlnARY; PRT; 3102 AA.

045614; P91824; O972R4;
01-UW-1998 (TrEMBLrel. 06, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
01-OCT-2007 (TrEMBLrel. 28, Last annotation update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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02-WAR-2004 (TrEMBLrel. 27, Last sequence update)
04-WAY-2004 (TrEMBLrel. 27, Last annotation update)
Flagellin.
BCB1780.
Bacilius Cereus (strain ATCC 10987).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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TIGR; BCE1780; -.
SEQUENCE 465 AA; 49855 MW; E4C307E7717381D5 CRC64;
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                                       Pfam; PF00700; Flagellin_C; 1.
Pfam; PF00669; Flagellin_N; 1.
PRINTS; PR00207; FLAGELLIN.
Complete protocome; Flagellin_C; 1.
Complete proteome; Flagellin_C; 3.
SEQUENCE 465 AA; 49855 MW; E4C307E7717381D5
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        InterPro, IPR001492;
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Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L., Shores K.A., Ravel J., Oekstad O.A., Angluoli S.V., Kolonay J.F., Shores R.A., Kolstoe A.-B., Tourase N.G., Read T.D.;
"The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic adaptations and a large plasmid related to Bacillus anthracis pXOl.";
Nucleic Acids Res. 32:977-988(2004).
EMBL; AE017289; AAS40708.1; -.
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20.8%; Pred. No. 2e+02;
tive 57; Mismatches 96; Indels 121;
                          R Pfam; PF00052; Laminin B; 2.

R Pfam; PF00052; Laminin BGF; 17.

Pfam; PF00053; Laminin G2; 3.

R Pfam; PF06009; Laminin I; 1.

R Pfam; PF06009; Laminin I; 1.

R Pfam; PF06005; Laminin I; 1.

R PRINTS; PR00011; Laminin B; 2.

SWART; SW00018; Lami; 2.

R SWART; SW00282; Lami; 2.

R SWART; SW00186; EGF Lam; 17.

R SWART; SW00186; EGF Lam; 17.

R SWART; SW00186; EGF Lam; 17.

R PROSITE; PS01022; EGF I: 12.

R PROSITE; PS01048; LAMININ TYPE EGF; 14.

R PROSITE; PS01048; LAMININ TYPE EGF; 14.

R PROSITE; PS01048; LAMININ TYPE EGF; 14.

R PROSITE; PS01048; LAMININ TYPE EGF; 14.

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R PROSITE; PS01048; LAMININ TYPE EGF; 14.
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=222523;
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InterPro; IPR003129; TSP_N.
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                                                                                                                                                         214 RLKTVQNFFTSLSATVKQANKDIDAAKLKLATBIAAIGBI-----KTETETTRFYVDYD 267
                                                                                                                                                                             107 KKASAQKDILIRILDDGVKKLNEAQKSLLISSQSF-NNASGKLLA---LDSQLT----N 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=S286C / AB972;
STRAIN=S286C / AB972;
MEDLINE=97313264; PubMed=9169868;
MEDLINE=97313264; PubMed=9169868;
MEDLINE=97313264; PubMed=9169868;
Araujo R., Awiles E., Berno A., Brennan T., Carpenter J., Chen E., Araujo R., Aviles E., Duncan M., Guzman E., Hartzell G., Cherry J.M., Chung E., Duncan M., Komp C., Lashkari D., Lew H. Hunicke-Smith S., Hyman N.W., Ksyser A., Komp C., Lashkari D., Lew H. Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C., Petell F.X., Roberts D., Sehl P., Schamm S., Shogren T., Smith V., Taylor P., Wei Y., Botstein D., Davis R.W.;
With nucleotide sequence of Saccharomyces cerevisiae chromosome V.";
Nature 387:78-81(1997).
                                            DFSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIA--AGVIEGKL--IPELNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bateman A., Chothia C.; "Fibronectin type III domains in yeast detected by a hidden Markov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomycetes;
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01-077-1993 (Rel. 27, Last sequence update)
05-071-2004 (Rel. 44, Last amotation update)
Hypothetical 106.1 kDa protein in GLY1-GDA1 intergenic region.
OrderedLocusNames=YEL043W; ORFNames=SYGP-ORF14;
Saccharomyces cerevisiae (Baker's yeast).
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956 AA; 106132 MW; 3F78B99A0FCA03AF CRC64;
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Saccharomycetales; Saccharomycetaceae; Saccharomyces
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SGD, S0000769; YEL043W.
SGD, G0:0005793; C:endoplasmic reticulum; IDA.
GO; G0:0005793; C:endoplasmic reticulum; IDA.
InterPro; IPR008957; FW_III.
InterPro; IPR008957; FW_III-like.
SMART; SM00066; FN3; 1.
DOMAIN
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MEDLINE=97148176; PubMed=8994808;
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Science 273:1058-1073(1996).
-!- FUNCTION: Involved in DNA double-strand break repair (DSBR). The rad50/mrell complex possesses single-strand endonuclease and ATP-dependent double-strand-specific 3'-5' exonuclease activity. Rad50 provides an ATP-dependent control of mrell by activity. Rad50 provides an ATP-dependent control of mrell by unwinding and/or repositioning DNA ends into the mrell active site
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WEDLINES-6537999; PubMed=8688087;

Bult C.J., White O., Olson G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Glodek C.I.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Kerlavage A.R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Scott J.L., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                     180 GAAAGIVAGPFGLIISYSIAA------GVIEGKLIP-ELNNR-LKT-----V
                                                                                                                                                             93 LLS-----AYILLFDEYNEKKASAQKDI-----LIRILDDGVKKLNEAQKSLLTS---S
                                                                         KTFDETIKELSRFKQEYSQEASVLVGDIKVLLMD-----SQDKYFEATQTVYEWCGVVTQ
                                                                                                                 KSLKSNİKSL------ENSKLLTDLKIEKLNKKIDKSKEKISKMRNDMQKWSQEDTE
                                                                                                                                                                                        (By similarity).
-!- COFACTOR: Binds 1 zinc ion per heterotetramer (By similarity).
-!- SUBUNIT: Heterotetramer composed of two mrell subunits and two rad50 subunits (By similarity).
-!- SIMILARITY: Belongs to the SMC family. RAD50 subfamily.
                                    Gaps
                                       88;
                                       78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Methanococcus jannaschii.
Archaea; Buryarchaeota; Methanococci; Methanococales;
Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                               219 QNFFTSLSAT----VKQANKDIDAAKLKLATBIAAIGBI 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       487 KNNGDSLAATNSNNSAEKNRSSGSIQLPLSNNMSRTGSI
                                                                                                                                                                                                                                                    139 QSFNN----ASGKLLALDSQLTNDFS-EKSSYF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Last sequence update) 05-UTL-2004 (Rel. 44, Last annotation update) DNA double-strand break repair rad50 ATPase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1005 AA.
7.5%; Score 113; DB
4.4%; Pred. No. 53;
ve 45; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=rad50; OrderedLocusNames=MJ1322;
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                         24.48;
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                                           Conservative
                           Similarity
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                                                  68;
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Mol. Gen. Genet. 243:215-224(1994)
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                                                                                                                                                                                                                                                                                                                                                          662 ELNKLREDEREINRLKDKLNELKNKEKE------LIEIENRRSLKFDKYKEYLGL 710
                                                                                                                                                                                                                                                                                                                                              111 AQKDILIRILDDGVKKLNEAQKSLLTSSQSFNNASGKLLALD------- 152
                                                                                                                                                                                                                                                                                                                                                                                                                           PEL--NNR--LKTVQNFFTSLSATVKQANKDIDAAKLKLATEIAAIGEIKTETETTRFYV 264
                                                                                                                                                                                                                                                                                    DEILEDIKSQLNKFK----NFYNQYLSAVSYLNSVDEEGIRNRIKEIENIVSGWNKEKCRE 661
                                                                                                                                                                                                                                                                 7 EQTVEVVKSAIETADGALDLYNKYLDQVIPWKTFDE-----TIKELSRF-----KQEYSQ 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Canard B., Garnier T., Saint-Joanis B., Cole S.T.; "Molecular genetic analysis of the nagH gene encoding a hyaluronidase of Clostridium perfringens.";
                                                                                                                                                                                                                                                                                                                                                                                   ----SQLTNDFSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLI
                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1992 (Rel. 23, Created)
28-FRB-2003 (Rel. 41, Last sequence update)
01-CT-2004 (Rel. 45, Last annotation update)
Hyaluronoglucosaminidase precursor (EC 3.2.1.35) (Hyaluronidase) (Mu
                                                                                                                          SMART; SM00382; AAA; 1.
TIGRFAMs; TIGR01725; phge HK97 gp10; 1.
ATP-binding; Coiled coil; Complete proteome; DNA repair; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clostridium perfringens.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
                                                                                                                                                                                                                                              98;
                                                                                                                                                                                                                           DB 1; Length 1005;
                                                                                                                                                                                                                                              91; Indels
                                                                                                                                                                                   Zinc (By similarity).
Zinc (By similarity).
MW, 9BBBB48173E788F3 CRC64;
                                                                                                                                                                  ATP (By similarity).
Coiled coil (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1628 AA.
                                                                                                                                                                                                                          7.5%; Score 113; DB
19.7%; Pred. No. 57;
tive 55; Mismatches
                         HAMAP, MF 00449; -; 1.
InterPro; IRR00353; AAA ATPase.
InterPro; IRR003439; ABC transporter.
InterPro; IRR003439; ABC transporter.
InterPro; IRR003405; SMC C.
InterPro; IRR003395; SMC N.
Pfam; PP04423; Rad50_zn_hook; 1.
Pfam; PP02463; SMC C; 1.
Pfam; PP02463; SMC N; 1.
Pfam; PP02463; SMC N; 1.
ProDom; PD000006; ABC_transporter; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=nagH; OrderedLocusNames=CPE0191;
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158 849
502 502
505 505
1005 AA; 119387 M
                                                                                                                                                                                                                                    Local Similarity 19.7
nes 60; Conservative
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 PIR; A64465; A64465.
HSSP; P58301; 1F2T.
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DOMAIN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
-!- FUNCTION: Putative virulence factor which is likely to act on connective tissue during gas gangere.
-!- CATALYTIC ACTIVITY: Random Mydrolysis of 1-34-linkages between N-acetyl-beta-D-glucosamine and D-glucuronate residues in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIE, S4390, S4300.

PIR, S430, S4300.

InterPro; IPR0004210; Dockerin 1.

InterPro; IPR000421; FASB C.

Pram; PR00146; Dockerin 1; 2.

Pram; PR00754; FS F8 type C; 3.

SMART; SM00231; FASBC; 1.

PROSITE; PS50022; FASBC 3; 1.

PROSITE; PS50022; FASBC 3; 1.

SAGMAL 1.

SAGMAL 1.

PROSIMAL 1.
                                                                                                                                                          Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
"Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- SÜBCELLULAR LOCATION: Secreted.
-1- SIMILARITY: Contains 1 Fs/8 type c domain.
-1- GAUTION: The partially purified protein from strain CPN50 is approximately 70 kDa smaller than the sequence indicated here.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84;
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KIGS -> BIRN (in strain CPN50).

V -> M (in strain CPN50).

A -> E (in strain CPN50).

D -> E (in strain CPN50).

G -> S (in strain CPN50).

I -> V (in strain CPN50).

I -> I (in strain CPN50).

I -> I (in strain CPN50).

I -> F (in strain CPN50).

I -> F (in strain CPN50).

I -> F (in strain CPN50).

Missing (in strain CPN50).

Missing (in strain CPN50).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hyaluronoglucosaminidase.
F5/8 type C.
                                           STRAIN=13 / Type A;
PubMed=11792842; DOI=10.1073/pnag.022493799;
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EMBL; AP003185; BAB79897.1; -.
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1628 AA; 182474
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SEQUENCE FROM N.A.
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1483 LDASIKALVKETPEVDKTNLGELINQGKSLLDESVEGFNVGEYHKGAKDGLTVEINKAEE 1542
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                                                       221 FFTSLSATVKQANKDIDAAKLKLATEIAAIGEIKTETETTRF----YVDYDDLMLSILKG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=15115801; DOI=10.1093/nar/gkh562; Navel J., DeBoy R.T., Nelson K.E., Foute D.E., Mongodin E.F., Ravel J., DeBoy R.T., Kolonay J.F., Rasko D.A., Angiuoli S.V., Gill S.R., Paulsen I.T., Peterson J.D., White O., Nelson W.C., Nierman W.C., Beanan M.J., Brinkac L.M., Daugherty S.C., Dodeon R.J., Durkin A.S., Madupu R., Haft D.H., Selengut J., Van Aken S.E., Khouri H.M., Fedorova N., Forberger H.A., Tran B., Kathariou S., Wonderling L.D., Unlich G.A., Bayles D.O., Luchansky J.B., Fraser C.M.; Whole genome comparisons of serotype 4b and 1/2a strains of the foodborne pathogen Listeria moncytogenes reveal new insights into the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MTSIFAEQTVEVVKSAIETADGALDLYNKYLDQVIPW----KTFDETIKELSRFKQEYSQ
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                                                                                                Indels 121;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Membrane protein, putative.
OrderedlocusNames=LMOC1365 2330;
Listeria monocytogenes (serotype 4b / strain F2365).
Bacteria, Firmicutes; Bacillales; Listeria.
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7.4%; Score 112.5;
Best Local Similarity 20.7%; Pred. No. 56;
Matches 78; Conservative 43; Mismatches
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Nucleic Acids Res. 32:2386-2395(2004)
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InterPro; IPR004089; Chmtaxia transd.
InterPro; IPR001809; Outrsurface.
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ProDom; PD001127; Outrsurface; 1.
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1594 VSKNIGSTIN 1603
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SEQUENCE 927 AA;
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280 YTSGVDTL---AĞGINQAYTGSTALSDGLNKANGS-----VPTLASĞITQLNNGQKSLA 330
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10-MAY-2004 (TrEMBLrel. 27, Last sequence update)
10-MAY-2004 (TrEMBLrel. 27, Last sequence update)
Membrane protein, putative.
LMOF2365_2330.
Listeria monocytogenes str. 4b F2365.
Listeria, Firmicutes; Bacillales; Listeriaceae; Listeria;
Listeria monocytogenes.
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SEQUENCE 927 AA; 97232 MW; 9AE73C67B14685CA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                          927 AA.
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QI		US-09-993-292A-2	US-10-128-714-3039	US-10-128-714-8039	US-10-369-493-10918	US-10-087-192-222	US-10-437-963-197045	US-10-080-608A-66	US-10-370-685-155	US-10-767-701-43815	US-10-282-122A-70920	US-10-467-421-37	US-10-282-122A-58016	US-10-369-493-22080
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19	111		794	12	-257-377-2	Sequence 2, Appli
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of Essential Genes in Aspergillus fumigatus and
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                              4 IVADKTVEVVKNAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASV--L
      225 -LSNTVKQANKDIDAAKLK---LTTEIAAIGEIKTETETTRFYVDYDDLMLSLLKEA---
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8.4%; Score 126; DB 14;
Best Local Similarity 21.4%; Pred. No. 0.32;
Matches 73; Conservative 49; Mismatches 73;
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GENERAL INFORMATION:
APPLICANT: Jiang, Bo.
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APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 197045
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                                                  13;
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                                                                                                                                                                                                                                                                             111 -----AQKDILIKVLDDGITKLNEAQKSLLVS---SQSFNNASGKLLALDSQLTNDFSE 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        378 KGESLASTTEE-----LGKIQSALQDRESEIEVLKGKTTALEIEVARLLADVN 425
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                                                                                                                                                                                                                 162 KSSYFQSQVDKIRKEAYAGAAAGVVAGPFGLIISYSIAAGVVEGKL-----IPELKNKL
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                                                                                                                                    535 DKKEEBVKKTLEQHDNIVTHYKNMIREQDLQLEELRQQVSTLKCQNEQLQTAVTQQVSQI
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  Length 962;
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8.0%; Score 120.5; DB 13; Length larity 23.7%; Pred. No. 0.62; Conservative 51; Mismatches 136; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: PAT_MRT4530_92840C.1.pep
US-10-437-963-197045
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             276 EAAKKMINTCNE 287
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ORGANISM: Oryza sativa
  Query Match
Best Local Similarity
Matches 74; Conserva
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT PILING DATE: 2002-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 10918
LENGTH: 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 633 TEVERSREMKSKLESIKDEIENRKKSIEGLRIEMENKQSAMHQY----DGIDEQ---- 682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 AAGVVAGPFGLIISYSIAAGVVEGKLIPELKNKLKS----VQNFFTTLSNTVKQA-NKDID 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DIKTLLMD--SQDKYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQKDILIKVLD 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KTVEVVK----NAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASVLVG
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Publication No. US20020182586A1

GENERAL INFORMATION:
APPLICANT: Mortis, David W.
TILLE OF INVENTION: CANCER
TITLE OF INVENTION: CANCER
TITLE OF INVENTION: CANCER
TITLE OF INVENTION: CANCER
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377

PRIOR PILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: US 09/747,377

PRIOR PILING DATE: 2000-12-22

PRIOR PILING DATE: 2000-12-22
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SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 222
LENGTH: 962
                                           Sequence 10918, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Ferroplasma acidarmanus
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US-10-087-192-222
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Best Local 8
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Matches
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Sequence 43815, Application US/10767701
Sequence 43815, US2040172684A1
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yinhua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21 [33535] B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 43815
LENGTH: 496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       748 ILOSQLABKOSLIENIKSSQLSPGTNEQSSATAGDŠEQIAELKQELATLKŠQL-NSQŠVE 806
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  865 ALSERRTAIKEQLDSSNS-----TIAILQNEKNKLEVDITDSKKEQDDLLV-LLAD
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                                                                                                                                                                                                                                                                                                                                                                                               7 DKTVEVVKNAIETADGALDLY-NKYLDQVIPWQTFDETIKELSRFKQEYSQAASVLVGDI
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                                                                                                                                                                                                                                                    Length 961;
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US-10-767-701-43815
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20.2%; Pred. No. 0.45;
tive 49; Mismatches 134;
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PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 159
SOFTWARE: Patentin version 3.2
SEQ ID NO 155
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915 QDQKIFSLKNKLKE 928
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Matches 68; Conservative
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                                                                                                                                                   TYPE: PRT
ORGANISM: BOS taurus
US-10-370-685-155
                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 72; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-767-701-43815
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99
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                                                                                                                                                                                                                                                                      Query Match
                                                                                                                              LENGTH:
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APPLICANT: Hyman, Paul
APPLICANT: Goldberg, Edward
TITLE OF INVENTION: Nanostructures Containing PNA Joining and Functional Elements
FILE REFERENCE: NNNF.P-004
CURRENT APPLICATION NUMBER: US/10/370,685
CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: 10/080,608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVONFFITLSNIVKQANKDIDAAKLKLTTEIAAIGEIKTETETTRFYVDYDDLMLSLLKE 276
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                  536
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                                                                                                                                       --KLIPEL-----KNKLKSVQNFFTTLSNTVKQANKDIDAAKLKLTTE-----IAAI
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                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 66, Application US/10080608A
Publication No. US20030198956A1
GENERAL INFORMATION:
APPLICANT: Makowski, Lee
APPLICANT: Hyman, Paul
APPLICANT: Williams, Mark
TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
FILE REFERENCE: 8471-010-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/080,608A CURRENT FILING DATE: 2002-02-21 NUMBER OF SEQ ID NOS: 180 SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 155, Application US/10370685 Publication No. US20030215903A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       277 AAKKMINTCNEYOK 290
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US-10-370-685-155
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US-10-080-608A-66
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Matches
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| Sequence 22080, Application US/10369493
| Sequence 22080, Application US/10369493
| Publication No. US20030233675A1
| GENERAL INFORMATION:
| APPLICANT: Caco, Yongwei
| APPLICANT: Blater, Steven C.
| APPLICANT: Goldman, Barry S.
| APPLICANT: Chen, Xianfeng TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS WITH IMPROVED PROPERTIES | FILE REPRESENCE: 38-10(52052)B | CURRENT APPLICATION NUMBER: US/10/369,493 | CURRENT FILING DATE: 2003-02-28 | PRIOR FILING DATE: 2002-02-28 | PRIOR FILING DATE: 2002-02-21 | NUMBER OF SEQ ID NOS: 47374 | SEQ ID NO 22080 | LENGTH: 1679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   populocation 00. US20030333675A1

genence 22285, Application US/10369493

genence 22285, Application No. US20030333675A1

general information:

APPLICANT: Gao, Yongwei

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF ITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

TILLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

TILLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

THIS REPERENCE: 38-10(52052)B

CURRENT APPLICATION NUMBER: US/10/369,493
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                                  354 OKAEANLIKTQOBLEKYQKSTKELLAELRDQYVDLMQEQA--AVGNELKYLERQYIQETA 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39 TPDETIKELSR----FKQEYSQAASVLVGDIKTLLMDSQDKYFEATQTVYEWCGVATQLL
-TTRPYVDYDDLMLSLLKEAAKKMINTCNEYQKRH-----
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7.5%; Score 112.5; DB 14;
Best Local Similarity 20.6%; Pred. No. 6;
Matches 51; Conservative 44; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Saccharomyces cerevisiae US-10-369-493-22080
                                                                                                                        293 -GKKTLFEVPEV 303
                                                                                                                                                                           412 KSKOTLAKOSEV 423
                    248 --AAIGEIKTETE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1316 AİKDKLE 1322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: ELITRA.034A
CURRENT FILING DATE: 2003-02-20
PRIOR PAPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2000-02-20
PRIOR PAPLICATION NUMBER: 60/191,078
PRIOR PLING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/203,727
PRIOR PLING DATE: 2000-05-26
PRIOR PAPLICATION NUMBER: 60/203,727
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-10-23
PRIOR PAPLICATION NUMBER: 60/233,625
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-11-22
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2000-12-22
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PRIOR PLING DATE: 2001-02-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Xu, H. TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 15; Length 1020;
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Pest Local Similarity 20.5%; Pred. No. 3.1;
Matches 64; Conservative 46; Mismatches 105;
     || |: KEEAQALQTNAQESLQAAKAAGEEYDATHEDKGL 399
                                                                                                                                                          Sequence 58016, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Enterococcus faecium US-10-282-122A-58016
                                                                                                                                                                                                                                                      APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                              Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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SOFTWARE: Patent
SEQ ID NO 58016
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85; Gaps

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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Ghen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPERSION OF MICROBIAL PROPERTIES
FILE REPERENCE: 38-10(52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 5221
LENGTH: 2823
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1997 DEEYVQTAGRHAEKLEVQAQ----KIVDRFVDTRTETENPLKASHAYENIVEALKNATEAV 2053
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   1940 EDQIAYSRNSIEKARSEELMNMFEDKEKINMTLAELPDLVEQCQNITLL---YSQLIDEY 1996
                                                                                                                                                                                                                                                                                                               YSIAAGVVEGKLIPELKUKLKSVQNFFTTLSNTVKQANKDIDAAKLKLTTEIAAIGEIKT 255
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                                                               105 NE-----KKASAQKDILIKVLDDGITKLNEAQKSLLVSS-----QSFNNAS--- 145
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                                                                                                                                                                                       -----GKLLALDSQLTNDFSEKSSYFQSQVDKIRKEAYAGAAGVVAGPFGLIIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 113; Gaps
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Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5221
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Sequence 5220, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

CURRENT PPLICATION NUMBER: US/10/369,493

CURRENT FILING DATE: 2003-02-28

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 5220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             805 COK-------KIDELEDALSELKKETSÖKDHHİKOLEEDNNSNIEWYÖNKIEA 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           137 SSQSFNNASGKLLALDSQLTN----DFSEKSSYFQSQVDKIRKEAYAGAAAGVVAGPFGL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              851 LKKDYESV---ITSVDSKQTDIEKLQYKVKSLEKEIEEDKIRLHTY-----NVMD---ET 899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83 VYEWCGVATQLLAAYILLFDEYNE----KKASAQKDILIKVL-DDGITKLNEAQKSLLV 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IISYSIAAGVVEGKL-IPELKNKLKSVQNFFTTLSNTVKQANKDIDAAKLKLTTEIAAIG 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 TEIVADKTVEVVKNAIETADGALDLYNK---YLDQVI-----PWQTFDETIK-----
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7.4%; Score 112; DB 14; Length 18
1 Similarity 19.7%; Pred. No. 7.6;
68; Conservative 66; Mismatches 122; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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larity 21.3%; Pred. No. 15;
Conservative 56; Mismatches
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 22285
                                                                                                                                                                                                                         ORGANISM: Saccharomyces cerevisiae US-10-369-493-22285
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Best Local Similarity
Matches 73; Conserv
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US-10-369-493-5220
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178 YAGAAAGVVAGPFGLIISYSIAAGVVBGKLIPELKNK-----LKSVONFF----TTLS 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 IVGDIKTLIMDSQDKYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQKDILIKVI, 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 DDGITKLINBAQKSLL-VSSQSFNNASGKLLAL-DSQLTN-DFSEKSSYFQSQVDKIRKEA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 DDGITKLNEAQKSLL-VSSQSFNNASGKLLAL-DSQLTN-DFSEKSSYFQSQVDKIRKEA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               205 ESVQEKYNDTAQSLRDVSAQLESYKSSTLKEIEDLKLENLTLQEKVAMAEKSVEDVQQQI 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                178 YAGAAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNK-----LKSVQNFF----TTLS 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              265 LTAESTNQ------EXA------RAVQDLQNRSTLKEEBIKEITSSFLEKITDLK 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MTEIVADKTVEVVKNALETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASV
                                                                                                                                                                                                                                                                                                                                                                 LVGDIKTLLMDSQDKYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQKDILIKVL
                                                                                                                                                                                                                                                                 1 MTEIVADKTVEVVKONAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASV
                                                                                                                                                                                                                                                                                                                98 LDNLLREKEVELEKHIAAHAQAILIAQEKYNDTA---ÖSLRDVTAQLESVQEKYNDTAQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               227 NTVKQANKDI------DAAKLKLTTEIAAIGBIKTETETTRFYVDYDDL 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
7.4%; Score 111; DB 15; Length 794;
Best Local Similarity 20.5%; Pred. No. 2.9;
Matches 60; Conservative 63; Mismatches 108; Indels 6;
                                                                                                                                                                     7.4%; Score 111; DB 10; Length 4 20.5%; Pred. No. 1.5; tive 63; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/10257377; Sequence 2, Application No. US20040037834A1
GENERAL INPORMATION:
APPLICANT: B. Michel R. Woloski,
APPLICANT: Ashley M. Williams,
TOTICANT: Deanna J. Sereda,
TITLE OF INVENTION: RHAMM Peptide Conjugates;
TITLE OF INVENTION: RHAMM Peptide Conjugates;
TITLE OF INVENTION: NUMBER: US/10/257,377;
CURRENT FILING DATE: 2001-04-20
CURRENT FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.1
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 77. LENGTH: 476
                                                                                                                                                                                                   Best Local Similarity 20.5
Matches 60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Mus musculus
US-10-257-377-2
                                                                                                         musculus
                                                                             ; TYPE: PRT
; ORGANISM: Mus
US-09-978-309A-77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 2
LENGTH: 794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-257-377-2
                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                    Query Match
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Sequence 77, Application US/09978309A

Publication No. US20030100490A1

GENERAL INFORMATION:

APPLICANT: CTUZ, TON.

APPLICANT: TUTLEY, Eva A.

TITLE OF INVENTION: Compositions and Methods for Treating Cellular Response to TITLE OF INVENTION: Hyaladherin and Hyaluronans

TITLE OF INVENTION: Hyaladherin and Hyaluronans

FILE REFERENCE: 033352-010

CURRENT APPLICATION NUMBER: US/09/978,309A

CURRENT APPLICATION NUMBER: US 09/685,010

PRIOR APPLICATION NUMBER: US 09/541,522

PRIOR PILING DATE: 2000-04-03

PRIOR FILING DATE: 2000-04-03

PRIOR PILING DATE: 1999-04-01

NUMBER OF SEQ ID NOS: 84
                                                                                                              APPLICANT: Cruz, Tony
APPLICANT: Pastrak, Aleksandra
APPLICANT: Cruz, Tony
APPLICANT: Turley, Eva A.
TITLE OF INVENTION: Compositions and Methods for Treating Cellular Response to
TITLE OF INVENTION: Injury and Other Proliferating Cell Disorders Regulated by
TITLE OF INVENTION: Injury and Other Proliferating Cell Disorders Regulated by
TITLE OF INVENTION: Hyaladherin and Hyaluronans
FILE REPERBYCE: 03352-010
CURRENT APPLICATION NUMBER: US 09/685,010
PRIOR PILING DATE: 2000-10-05
PRIOR PILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: US 60/127,457
PRIOR PILING DATE: 1999-04-01
PRIOR FILING DATE: 1999-04-01
NUMBER OF SEC ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NOS: 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LVGDIKTLLMDSQDKYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQKDILIKVL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 DDGITKLNEAQKSLL-VSSQSFNNASGKLLAL-DSQLTN-DFSEKSSYFQSQVDKIRKEA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         206 ESVQEKYNDTAQSLRDVSAQLESYKSSTLKEIEDLKLENLTLQEKVAMAEKSVEDVQQQI 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 YAGAAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNK-----LKSVQNFF----TTLS 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        266 LIAESTNQ------EYA-----RMVQDLQNRSTLKEEEIKEITSSFLEKITDLK 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MTEIVADKTVEVVKNAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         227 NIVKQANKDI------DAAKLKLTIBIAAIGBIKTETETTRFYVDYDDL 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
7.4%; Score 111; DB 10; Length 435;
Best Local Similarity 20.5%; Pred. No. 1.3;
Matches 60; Conservative 63; Mismatches 108; Indels 62
                                      Sequence 80, Application US/09978309A Publication No. US20030100490A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
CORGANISM: Mus musculus
US-09-978-309A-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 18
US-09-978-309A-77
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Sequence 5, Application US/09884696;
Publication No. US20030035809A1
| General Information:
| APPLICANT: GENEGE, JOHN A |
| APPLICANT: ARGELOS, JOHN A |
| APPLICANT: HESY JOHN A |
| APPLICANT: HESY JOHN A |
| APPLICANT: HESY JOHN A |
| APPLICANT: HESY JOHN A |
| TITLE OF INVENTION: MORAKELLA BOVIS CYTOTOXIN GENE, ANTIBODIES |
| TITLE OF INVENTION: BOVIS INFECTIONS |
| TITLE OF INVENTION: BOVIS INFECTIONS |
| FILE REPERENCE: 481.06 |
| CURRENT APPLICATION NUMBER: US/09/884,696 |
| CURRENT FILING DATE: 2001-06-19 |
| SOFTWARE: PARCHIN Ver. 2.1 |
| SOFTWARE: PARCHIN Ver. 2.1 |
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| SOFTWA
                                                                                                                                                                                                                                                        380 NDVKSMYSALAEALLTLSSNSDNQAKATQSDIKALKDISYGVIGSNRPTEFNDMLRNLKŤ 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            218 VQNFFTTLSNTVKQANKDIDAAKLKLTTELAAIGEIKTETETTRF-----YVDYDDLM 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54 YSQAASVL-----VGDIKTLIMDSQDKYFEATQTVYEWCGVATQLLAAYILL-FDEY 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              105 NEKKASAQKDILIKVLDD---GITKLNEAQKSLLVSSQSFNNASGKLLALDSQLTNDFSE 161
167 QSQVDKIRKEAYAGAAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNKLKSVQNFFTTLS 226
                                                                                                  915 NSVIONDNVINDNOIVSN 379
                                                                                                                                                                                               227 NIVKQANKDIDAAKLKLT------TEIAAIGEIKTETETTRFYVDYDDLMLSL-- 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 TEIVADKTVEVVK------NAISTADGALDLYNKYLDQVIPWQTFDETIKELSRFKQE
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7.4%; Score 111; DB 10;
Best Local Similarity 21.3%; Pred. No. 4.1;
Matches 71; Conservative 56; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        271 LSLLKEAAK-----KMINTCNEYOKRHGK 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                405 ISGILEASKQAMFEHVASKWADVIAEWEKKHGK 437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             |: ::| ::| 440 RLENSSKSNQQLIDVLKELEKR 461
                                                                                                                                                                                                                                                                                                                                                                                                    274 -LKEAAK---KMINTCNEYQKR 291
                                                                                                  356 QYQIQKLSTD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Terry, Roemer D. APPLICANT: Bo, Jiang APPLICANT: Charles, Boone APPLICANT: Howard, Bussey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-032-585-7519
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                                                                                                                                                           227 NTVKQANKDI------DAAKLKLTTEIAAIGEIKTETETTRFYVDYDDL 269
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                                                                                                                                                                TITLE DOF INVENTION: IGGENTIAL CALLON OF ESSENTIAL REPRESENCE: 11TRA, 034A
CURRENT APPLICATION NUMBER: 05/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR PELING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/200, 335
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230, 335
PRIOR PILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 60/230, 347
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-110-23
PRIOR PILING DATE: 2000-110-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-02
PRIOR PILING DATE: 2000-12-02
PRIOR PILING DATE: 2000-12-02
PRIOR PILING DATE: 2001-02-09
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PELING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PELING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/22,578
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/25,931
PRIOR PLING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PLING DATE: 2001-12-22
PRIOR PLING DATE: 2001-12-22
PRIOR PLING DATE: 2001-12-22
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-16
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PRIOR PLING DATE: 2010-02-16
PRIOR PLING DATE: 2010-02-16
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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Forsyth, R.
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Wall, Daniel
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Carr, Grant
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LTAESTNO-
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5 VADKTVEVVKNAIETAD---GALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASVL
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data:
NUMBER OF SEQ ID NOS: 78614
SCPTWARE: PatentIn version 3.1
SEQ ID NO 51864
LENGTH: 1163
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ilarity 17.9%;
Conservative 6
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ORGANISM: Zea mays
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR PELICATION NUMBER: 60/191,078
PRIOR PLILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PLILING DATE: 2000-05-3
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR PLILOR DATE: 2000-10-29
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/257,931
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PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-10-29
PRIOR FILING DATE: 2000-10-29
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PRIOR FILING DATE: 2000-10-29
PRIOR FILING DATE: 2000-10-29
PRIOR FILING DATE: 2000-10-29
PRIOR FILING DATE: 2000-10-29
         TITLE OF INVENTION: Gene Distuption Methodologies for Drug Target Discovery File Reference: 10182-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: Patentin version 3.1
SEQ ID NO 7519
LENGTH: 1171
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                                                                                                                                                                                                                                                                                                                                                                    103 EYNEKKASAQKDILIK--VLDDGITKLNEAQKSLLVSSQSFNNASGKLLALDSQLTNDFS
                                                                                                                                                                                                                                                                                                                                                                                             289 EENLKTDGSMKELEIKENQLSNDLTRLNTARDIAMDNLTEEKNKHTKLIEQLEQLKQQLA
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18.3%; Pred. No. 4.9;
tive 53; Mismatches 87; Indels 38;
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Publication No. US20040029129A1
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Wall, Daniel
Trawick, John
Garr, Grant
Yamamoco, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                   TYPE: PRT Candida albicans US-10-032-585-7519
                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 18.3
Matches 40; Conservative
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APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: NUMBER: US/10/425,114
CURRENT APPLICATION NUMBER: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NOS: 73128
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                                                                                                                                                                                                                                                                                 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 DKYFEATQTVYEWCGVATQLLAAYILLFDEYN-------EKKASAQKDILIKV-- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       272 IDLKEKRARLGESSSKVKPYIDNYENTLKQIDILKEQILSRENTWKAISLEKEDMEKKLS 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             224
                                                                                                                                                                                                                                                                                                                                                                109 IVDITGDE-VEVLEEGAKSVNEKCOEIIGLSLDDFTRTV--VLPQGKFSEFLKLEGKERR 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 226 DFFNEASK------EYLKABEBYNBGKEVWGLQIBIBEKNRVRKDLMEKKDB 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 --IDDGITKLNBAQKSLLVSSQSFNNASGKLLALDSQLTN-------DFSEKSS 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          165 YFQSQVDKIRKEAYAGAAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNKLKSVONFFTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              332 IAKDNKEK------ALPKFMIKHHIILDAIKEKDLLDNIKLEKKKLQGKIEK
                                                                                                                                                                                                                                                                                                                                                                                                                                   -----TLLMDSQ
                                                                                                                                                                                                                                                                                    Gaps
removed - See File Wrapper or PALM
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                                                                                                                                                                                                                                                                              69; Mismatches 114; Indels 152;
                                                                                                                                                                                                                                                                                                                               1 MTBIVADKTVEVVKNALETADG------ALDLYNKYLDQVIPWQTFDETIK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----TTRFYVDYD-----DLMLSLLKEAAKKMINTCNEYQKR 291
                                                                                                                                                                                                                                Length 1163;
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US-10-425-114-60225
                                                                                                                                                                                                                                      DB 15;
                                                                                                                                                                                                                                      Score 110;
Pred. No. 5
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US-10-425-114-60225

Sequence 60225, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:
                                                                                                                                          TYPE: PRT ; ORGANISM: Clostridium acetobutylicum US-10-282-122A-51864
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DB 13; Length 660;

Indels

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273 NNSPDNIAATKEL----IDAAETKVNELKQ------EHTG---LTDSPLVKKAEEQ 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      372 MAAIALQGF----RSMIEQFNVNNPATAKELQAMEAQUTAMSDQLVGADGELPAEIQAIK 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43 TIKELSRFKQEYSQAASVLVGDIKTLLMDSQDKYFEATQTVYEWCGVATQLLAAYILLFD 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103 EYNEKKASAQKDILIKVLDDGITKLNEAQKSLLVSSQSFNNASGKLLALDSQLTNDFSEK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163 SSYFQSQVDKIRKEAYAGAAAGVVAGPFGLIISYSIAAGVVEGK-----LIPELKOK 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     215 LKSV--QNFFTTLSNTVKQAN-----KDIDAAKLKLTTE----IAAIGEIKTETETTR 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 VEVVKNAIETADGALDLYNKYL------IPWQTFDE
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Publication No. US20040137007A1
GENERAL INFORMATION:
APPLICANT: Bhatia, Ajay
APPLICANT: Brobst, Peter
APPLICANT: Stromberg, Erika Jean
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND DIAGNOSIS;
TITLE OF INVENTION: OF CHLAMYDIAL INFECTION
TITLE OF INVENTION: OF CHLAMYDIAL INFECTION
CURRENT APPLICATION NUMBER: US/10/762,058
CURRENT FILING DATE: 2004-01-15
NUMBER OF SEQ ID NOS: 140
                                                                                                                                                   APPLICANT: Bhatia, Ajay
APPLICANT: Probet, Peter
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT
TITLE OF INVENTION: COMPOUNDS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.515C2
CURRENT PELLING DATE: 2001-12-05
NUMBER OF SEQ ID NOS: 157
SEQ ID NO 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.3%; Score 109.5; DB 13; 20.6%; Pred. No. 3; ive 56; Mismatches 111;
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                                                                Sequence 139, Application US/10007693
Publication No. US20020146776A1
GENERAL INFORMATION:
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; ORGANISM: Chlamydia trachomatis
US-10-762-058-139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               262 FYVDYDDLMLSLLKE 276
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nes 65; Conserv
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Best Local Similarity
Matches 65; Conserv
      RESULT 26
US-10-007-693-139
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                                                                                                                                   I-----LIKVLDDGITKLN-----EAQ-KSLLVSSOSFNNASGKLLA-----LDSQL 155
                                                                                                                                                                                                                                                                                                                                             TNDFSEKSSYFQ--SQVDKIRKEAYAGAAAGVVAGPFGLIISYSIAAGVVEGKLIPELKN 213
                                                                                                                                                                                                                                                                                                                                                                                                    ENDSNEKSVLEERAMELEQVRRQLEDSRAEASME----LOTTIKNLNOVLQEK--AELEN 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KLKSVQNFFTTLSNTVKQANKDIDAAKLKLTTEIAAIGEIKTETETTRFYVDYDDLMLSL 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 EYNEKKASAQKDILIKVLDDGITKLNEAQKSLLVSSQSFNNASGKLLALDSQLTNDFSEK 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSYFQSQVDKIRKEAYAGAAAGVVAGPFGLIISYSIAAGVVEGK-----LIPELKNK 214
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                                                                                             VGDIKTLIMD--SQDKYFEATQTVY----EWCGVATQLLAAYILLFDEYNEKKASAQKD 114
14 ISDERIABLEDBLQCBARQQIEALEVKONMHCQ----CEKLEESLKQVSNEKEDLVAAILAS 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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| Publication No. US20030175700A1
| GENERAL INFORMATION:
| APPLICANT: Bhatia. Ajay
| APPLICANT: Brocher, Peter
| APPLICANT: Stromberg, Erika Jean
| TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TRE
| TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TRE
| TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TRE
| CURRENT APPLICATION NUMBER: US/09/841,260
| CURRENT FILING DATE: 2001-04-23
| NUMBER OF SEQ ID NOS: 140
| SEQ ID NO 139
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20.6%; Pred. No. 3;
tive 56; Mismatches
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ORGANISM: Chlamydia trachomatis
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----SEKQVSELNQ 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          274 LKEAAKKMINTCNE 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 20.6
Matches 65, Conservative
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US-09-841-260-139
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APPLICANT: Cruz, Tony
APPLICANT: Cruz, Tony
APPLICANT: Cruz, Tony
APPLICANT: Turley, Eva A.
APPLICANT: Turley, Eva A.
APPLICANT: Turley, Eva A.
APPLICANT: Turley, Eva A.
APPLICANT: Turley, Eva A.
APPLICANT: Compositions and Methods for Treating Cellular Response to
TITLE OF INVENTION: Injury and Other Proliferating Cell Disorders Regulated by
TITLE OF INVENTION: Hyaladherin and Hyaluronans
TITLE OF INVENTION: Hyaladherin and Hyaluronans
FILE REFERENCE: 033352-010
CURRENT FILING DATE: 2000-10-05
PRIOR PELING DATE: 2000-10-05
PRIOR PELING DATE: 2000-04-03
PRIOR PELING DATE: 2000-04-03
PRIOR PELING DATE: 1999-04-01
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 79
LEGTH: 476
LENGTH: 476
LENGTH: 476
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Sequence 6691, Application US/20040216190A1

Publication No. US20040216190A1

Sedication No. US20040216190A1

GENERAL INFORMATION:
APPLICANT: KOVAIIC, David K.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
TITLE OF INVENTION NUMBER: US/10/739,930

CURRENT APPLICATION NUMBER: US/10/739,930

CURRENT FILING DATE: 2003-12-18

NUMBER OF SEQ ID NOS: 11088

SEQUENCE OF SEQ ID NOS: 11088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 DDGITKLNBAQKSLL-VSSQSFNNASGKLLAL-DSQLTN-DFSEKSSYFQSQVDKIRKEA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               206 ESVQEKYNDTAQSLRDVTAQLESYKSSTLKEIEDLKLENLTLQEKVAMAEKSVEDVQQQI 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    266 LTAESTNQ-----EYA------RWVQDLQNRSTLKBEBIKETSSFLBKITDLKN 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 LVGDIKTLLMDSQDKYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQKDILIKVL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MTEIVADKTVEVVKNAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSOAASV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99 LDNLLREKEVELEKHIAAHAQAILIAQEKYNDTA---QSLRDVTAQLESVQEKYNDTAQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             228 TVKQANKDI-----DAAKLKLTTEIAAIGEIKTETETTRFYVDYDDL 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      309 QLRQQDEDFRKQLEEKGKRTAEKENVMTELT-----MEINKWRLLYEEL 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 476;
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7.2%; Score 108.5; DB 10;
Best Local Similarity 20.2%; Pred. No. 2.3;
Matches 59; Conservative 63; Mismatches 109;
                                                                                                                    Sequence 79, Application US/09978309A Publication No. US20030100490A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
CRGANISM: Mus musculus
US-09-978-309A-79
                    852
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US-10-739-930-6691
: | |
849 EYLD
                                                                                      RESULT 29
US-09-978-309A-79
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; Sequence 1061, Application US20030233675A1
; Publication No. US20030233675A1
; GENERAL INPORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeny
; APPLICANT: Chen, Xianfeny
; APPLICANT: Chen, Xianfeny
; APPLICANT: Chen, Xianfeny
; TITLE OF INVENTION: BLANTS WITH IMPROVED PROPERTIES
; TITLE OF INVENTION: BLANTS WITH IMPROVED PROPERTIES
; TITLE OF INVENTION: BLANTS WITH IMPROVED PROPERTIES
; TITLE OF INVENTION: BLANTS WITH IMPROVED
; TITLE OF INVENTION: BLANTS WITH IMPROVED
; TITLE OF INVENTION: BLANTS WITH IMPROVED
; TITLE OF INVENTION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR PILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 1061
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                                                                                                                                                                                                                                          163 SSYFQSQVDKIRKEAYAGAAAGVVAGPFGLIISYSIAAGVVEGK------LIPELKNK 214
                                                                                                                                                                                                                                                                                                                               LKSV--QNFFTTLSNTVKQAN-----KDIDAAKLKLTTE----IAAIGEIKTETTTR 261
                                                                                                                                                                                                                                                                                                                                                        ::: | | : : | | : : | | :: : | 372 MAAIALGGF----RSMIEGFNVNNPATAKELQAMEAQLTAMSDQLVGADGELPAEIQAIK 427
      TIKELSRFKQEYSQAASVLVGDIKTLLMDSQDKYFEATQTVYEWCGVATQLLAAYILLFD 102
                                                                                               103 EYNEKKASAQKDILIKVLDDGITKLNEAQKSLLVSSQSFNNASGKLLALDSQLTNDFSEK 162
                                                                                                                                                                                        ----SQLTNDFSEKSSYFQSQVDKIRKEAYAGAAAGVVAGPFGLIISYSIAAGVVECKLI
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7.2%; Score 109; DB 14;
Best Local Similarity 19.1%; Pred. No. 5.8;
Matches 58; Conservative 55; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Methanococcus jannaschii
                                                                                                                                                                                                                                                                                                                                                                                                                            FYVDYDDLMLSLLKE 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     428 ----- DALAQALKQ 436
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPENSION OF MICROBIAL PROPERTIES
FILE REFERENCE: 38-10 ($2052) B
CURRENT PELLOR DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360, 039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
EBRGTH: 886
                                                                                                                                                    293 LRLKLHTVEEEKI-EALNSDKSTSLEIETLNEQKNQLADKLEANKDELEKTKKAMEGLAS 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LL---MDSQDKYFBATQTVYEWCGVATQLLAAYILLFDBYNEKKASAQKDILIKVLD--D 122
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                                                   196 YSIAAGVVEGKLIPELKNKLKSVQNFFTTLSNTVKQ-----ANKD-IDAAKLKLTTEIA 248
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                       KILALDSQLTNDFSE-----KSSYFQSQVDKIRKEAY----AGAAAGVVAGPFGLIIS 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        476 KLKERLEKVEKALEKQETVLKYRQMVDELKALENEL-SSHDAEKLSAESEEYRKVKERLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 14; Length 886;
                                                                                                                                                                                                                                                 249 AIGBIKTETETTR--FYVDYDDL--MLSLLKEAAKKMINTCNEYQ 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 7.2%; Score 108.5; DB 14; Best Local Similarity 21.0%; Pred. No. 5.4; Matches 74; Conservative 59; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              233 NK---DIDAAKLKL-------
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; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: LA ROSA, Thomas J.
                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 1016, Application US/10369493; Publication No. US20030233675A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Archaeoglobus fulgidus US-10-369-493-1016
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US-10-437-963-107270
                                                                                                                                                                                                                                                                                                                                             RESULT 32
US-10-369-493-1016
                       147
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APPLICANT: Liu, Jingdong

APPLICANT: Exou, Yihua

APPLICANT: Soren, Steven E

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Co., Yongul

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof For Plant Concent of TITLE OF INVENTION: 105/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

LENGTH: 647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :: : | | : | : | | : | | 13
173 RLERMIDELQSDVDDARNFGSKSKQLADEWQKKAQLLEVRLEBADQSNILKGESLNSAME 232
                                                                                                                                                                                                                                                                                               57 AASVLVGDIKTLLMDSQDKYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQKDI- 115
                                                                                                                                                                                                                                                                                                                                                                                                                               324 GKKKKYEKTLED-----LKSFKEMGDPFD---GKVLTTQFERIKKQQESLLEEVSET 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163 SSYFQSQVDKIRKEAYA----GAAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNKLKS 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           373 RKKIODEISNLEKKTLITNVVFGAAFAIVAVASIALIATGVGAAAGFGALAAPL--LAAG 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----TKLNEAQKSLLVSSQSFNNASG 146
                                                                                                                                                                                                                                            238 DAHMELSKHLVEVTQGVADFITEIEDDV--WDNQALKYLVLAYFENTKKTLEIFKTIENC 295
                                                                                                                                                                                                                                                                                                                                             296 VENAEMGOL-----EKESAEKÖVG 323
                                                                                                                                                                                                                                                                                                                                                                                              ----LIKVLDDGITKLNBAQKSLLVSSQSPNNASGKLLAL-----DSQLTNDFSEK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              218 VQNFFTTLSNTVKQANKDIDAAKLKLTTEIAAIGEIKTE---TETTRFYVD-YDDLMLSL 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 EIVADKTVEVVKNAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASVLV 62
                                                                                                                                                                                                7 DKTVEVVKNAIETADGALDLYNKYLDQVIPWQT------FDETIKELSRFKQEYSQ 56
                                                                                                                                               Gaps
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                                                                                              Length 552;
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                                                                                                                                               42; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LK------EAAKKMINTCNEYOKRHGK--KTLFEVPE 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: ARATH-23APR03-C7198_1.p
US-10-739-930-6691
                                                                                                    DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , OTHER INFORMATION: Clone ID: 700221631_FLI.pep
US-10-425-114-51665
                                                                                              Query Match 7.2%; Score 108.5; I Best Local Similarity 21.9%; Pred. No. 2.9; Matches 75; Conservative 42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-425-114-51665
; Sequence 51665, Application US/10425114
; Publication No. US20040034888A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 LIKVLDDGI-----
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FEATURE:
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Sequence 48, Application US/09978309A

; Bublication No. US2030100490A1

; GENERAL INFORMATION:

; APPLICANT: CTUZ, TON:

; APPLICANT: CTUZ, TON:

; APPLICANT: CTUZ, TON:

; APPLICANT: TUTLEY, Eva A.

; TITLE OF INVENTION: Compositions and Methods for Treating Cellular Response to
; TITLE OF INVENTION: Hyaladherin and Hyaluronans

; TITLE OF INVENTION: Hyaladherin and Hyaluronans

; TITLE OF INVENTION: Hyaladherin and Hyaluronans

; TITLE OF INVENTION: Hyaladherin and Hyaluronans

; TITLE OF INVENTION: Hyaladherin and Hyaluronans

; TITLE OF INVENTION: Hyaladherin and Hyaluronans

; TITLE OF INVENTION: Hyaladherin and Hyaluronans

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; TITLE OF INVENTION: Hyaladherin and Hyaluronans

; TITLE OF INVENTION: Hyaladherin and Hyaluronans

; TITLE OF INVENTION: Hyaladherin and Hyaluronans

; TITLE OF INVENTION: Hyaladherin and Hyaluronans

; TITLE OF INVENTION: Hyaladherin and Hyaluronans

; RICK APPLICATION NUMBER: US 09/541,522

; RICK APPLICATION NUMBER: US 60/127,457

; RICK APPLICATION NUMBER: US 60/127,457

; RICK FILING DATE: 1999-04-01

; NUMBER: OF SEQ ID NOS: 84

; SOFTWARE: FastSEQ for Windows Version 4.0

; LENGTH: 631

; WADDEL OF TOTAL HYALDHERICATION HYALURONS USED ID NOS: HAWARD HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADEN HAMADE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 LVGDIKTLLMDSQDKYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQKDILIKVL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 DDGITKLNEAQKSLL-VSSQSFNNASGKLLAL-DSQLTN-DFSEKSSYFQSQVDKIRKEA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  360 -ESQEKYNDTAQSLRDVTAQLESYKSSTLKEIEDLKLENLTLQEKVAMAEKSVEDVQQQI 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178 YAGAAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNK------LKSVQNFF----TTLS 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MTBIVADKTVEVVKNAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
7.1%; Score 107.5; DB 15; Length
Best Local Similarity 19.8%; Pred. No. 4.1;
Matches 58; Conservative 65; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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7.1%; Score 107.5; DB 10;
Best Local Similarity 19.8%; Pred. No. 4.1;
Matches 58; Conservative 65; Mismatches 107;
                                                                                                             WO PCT/CA97/00240
US/10/205,647A
                                    FILING DATE: 23-JULY-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/CA97/(
FILING DATE: 10-APR-1996
APPLICATION NUMBER: GB 9607441.4
FILING DATE: 10
                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 630 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapien
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                    TITLE OF INVENTION: Brad Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement; PILE REFERENCE: 38-21(53221)B CURRENT PILICATION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966 SEQ ID NOS: 204966 LYPP: "TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE: TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KELGALEEAKEI-----TTKAFBVEKTEILKELBDLKRKVVEIQTNKDLVEVGND 464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               465 KIRLDVLSAQQKQSILEVEANNIKM--ELGALVEAK-EVATKAF--DAEKAKITKELEDV 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             249 LVAEQKLNICEAEIERLKMELGALTEANEAARAFDTQN-EEITKELEDLKTKLEEIKTN 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 ILIKVLDDGITKLNEAQKSLLVSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDKIR 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEAYAGAAAGVVAGPFGLIISYSIAAGVVEG----KLIPELKNKLKSVQN------ 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 --AASVLVGDIKTLLMDSQDKYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQKD 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 IVADKTVEVVKNAIETAD---GALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQ----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.2%; Score 108; DB 16; Length 7
22.0%; Pred. No. 4.6;
tive 63; Mismatches 126; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: PAT_MRT4530_11638C.1.pep
US-10-437-963-107270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            278 AKKMINTCNEYOKRHGKKTLFE 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 22.0*
The Conservative 71; Conservative
            Kovalic, David K
Zhou, Yihua
Cao, Yongwei
Wu, Wei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Oryza sativa
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CURRENT APPLICATION NUMBER: US/10/028,246A
CURRENT PILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/256619
PRIOR APPLICATION NUMBER: 60/265619
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2001-01-19
PRIOR FILING DATE: 2001-01-19
PRIOR FILING DATE: 2001-04-20
PRIOR APPLICATION NUMBER: 60/285189
PRIOR APPLICATION NUMBER: 60/285189
PRIOR APPLICATION NUMBER: 60/38819
PRIOR PILING DATE: 2001-04-20
PRIOR PILING DATE: 2001-04-20
PRIOR FILING DATE: 2001-04-20
PRIOR FILING DATE: 2001-04-20
PRIOR FILING DATE: 2001-04-20
PRIOR FILING DATE: 2001-07-26
PRIOR FILING DATE: 2001-08-09
NUMBER OF SEQ ID NOS: 211
                                                                                                                                                                  Application US/10028248A
5. US20030235882A1
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Vernet, Corine
Casman, Stacie
Malyankar, Uriel
Shenoy, Suresh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Smithson, Glennda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ichernev, Velizar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sciore, Paul
Millet, Isabelle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-028-248A-107
                                                                                                                                                                                                                                APPLICANT: Shimkets, Richard
                                                                                                                                                                                                                                                                                                                                                         Spytek, Kimberly
Gangollí, Esha
Miller, Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Si, Jingsheng
Edinger, Shlomit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bryan
                                                                                                                                                                                                                                                                                                                                                                                                                           Boldog, Ferenc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ramesh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Colman, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liu, Xiaohong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stone, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zerhusen
                                                             KEL 347
                     KTL 297
                                                                                                                                                 -10-028-248A-107
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                     295
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                                                    셤
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Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Screen, Steven E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

SEQ ID NO 68086

LENGTH: 680
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                                                                                                           : | | :: : | :: | ERLLADVIDSNEHLDASQQEVFGLQTIDVLRNKLEAAELAASEA----LDNERTATTK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          203 VEG-----KLIPELKNKLKSVQNFFTTLSNTVKQANKDIDAAKLKLTTE------ 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        285 KEDDYEHALAQIGDLKMALKSMEETYEVMLDESEQDITGLRETVEKLEAEVNKYREECES 344
                                                                                                                                                                  121 DDGITKLNEAQKSLL-VSSQSFNNASGKLLAL-DSQLTN-DFSEKSSYFQSQVDKIRKEA 177
                                                                                                                                                                                                                                                    178 YAGAAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNK-----LKSVQNFF----TTLS 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96 AYILLFDEYNEKKASAQKDILIKVLDDGITKLNEAQKSLLVSSQSFNNASGKLLALD--- 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       153 SQLTNDFSEKSSY-----FQSQVDKIRKEAYAGAAAGVVAGPFGLIISYSIAAGV 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              247 -----IAAIGE----IKTETETTRFYVDYDDLMLSLLKEAAKKMINTCNEYQKRHGK 294
                                     254 LDNLLREKEVELEKHIAAHAQAILIAQEKYNDTA---QSLRDVTAQLESVQEKYNDTAQS 310
                                                                                   LVGDIKTLLMDSQDKYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQXDILIKVL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MTEIVADKTVEVVKNAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---LYNKYLDQVIPWQTFDETIKE 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47 LSRFKQEYSQA-----ASVLVGDIKTLLMDSQDKYFEATQTVYEW--CGVATQLLA 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 IAEVNAEK-VEILSNEVVRLKGLLDSSAASEESKSREAELLVKNLE-----SE 68
                                                                                                                                                                                                                                                                                                                                     227 NTVKQANKDI------DAAKLKLTTBIAAIGBIKTETETTRFYVDYDDL 269
                                                                                                                                                                                                                                                                                                                                                               | ::| ::| ::| | ::| | 463 NQLRQQDEDFRKQLEEKGKRTAEKENVMTELT------MEINKWRLLYEEL 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.1%; Score 106.5; DB 15; Length 680;
19.3%; Pred. No. 5.5;
tive 68; Mismatches 122; Indels 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Clone ID: UC-ZMROTEOSINTE068G03_FLI.pep
US-10-425-114-68086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MTEIVADKTVEVVKNAIETADGALD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Zea mays subsp. mexicana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 19.34
Matches 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-425-114-68086
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APPLICANT: Rothenberg, Mark
TITLE OF INVENTION: No. US20030235882A1el Nucleic Acids and Polypeptides and Methods
TITLE OF INVENTION: Thereof
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104 YNEKKASAQKDILIKVLDDGITKLNEAQKSLLVSSQSFNNASGKLLALD---SQLTNDFS 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 14; Length 1999;
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Qy 44 IKELSRPKQEYSQAASVLVGDIKTLLMDSQDKYFEATQTVYEWCGVATQLLAAXILLFDE 103	QY 104 YNEKKASAQKDILIKVLDDGITKLNEAQKSLLVSSQSFNNASGKLLALDSQLTNDFS 160 :	QY 161 EKSSYFQSQVDKIRKEAYAGAAAGVVAGPFGLIISYSIAAGVVEGK 206	Qy 207LIPELKNKLKSVQNFFTTLSNTVKQANKDIDAAKLKLTTEIAAIGE 252 : :: :: :: :: : :	QY 253 IKTETETTRFYUDYDDLMLSLLKEAAKKOMINTCNEYQKR 291 	RESULT 39 US-10-408-765A-1635 ; Sequence 1635, Application US/10408765A ; Publication No. US20040101874A1	; GENERAL INFORMATION: ; APPLICANT: Ghosh, Sounitra S. ; APPLICANT: Fahy, Boin D. ; APPLICANT: Zhang, Bing	; APPLICANT: Glbson, Bradtord W. ; APPLICANT: Taylor, Steven W. ; APPLICANT: Glenn, Gary M.	; APPLICANT: Warnock, Daie E. ; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION ; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME	CURRENT APPLICATION NUMBER: US/10/408,765A CURRENT FILING DATE: 2003-04-04 NUMBER OF SEQ ID NOS: 3077 SOFTWARE: PEACSEQ for Windows Version 4.0 SOFTWARE: PEACSEQ for Windows Version 4.0	;	Query Match 7.0%; Score 106; DB 16; Length 1583; Best Local Similarity 20.2%; Pred. No. 19; Matches 72; Conservative 61; Mismatches 108; Indels 116; Gaps 17;	Qy 7 DKTVEVVKNAIETADGALDLYNKYLDQVIEWQTFDETI 44	QY 45 KELSRFKQEYSQAASVLVGDIKTLLMDSQDKYFEATQTVYEWCGVATQLLAAYI-LLFDE 103	135 LVSSQSFNNASGKILALDSQLTNDFSEKSSYFOSQVDKIRKBAYAGAAAGVVAGPFGL	QY 193 IISYSIAAGVVEGKLIPELKNYLKSVQNFFTTLSNTVKQANKDIDAAKLKLTTEIAAIG- 251 QY : 193 IISYSIAAGVVEGKLIPELKNYLKSVQNFFTTLSNTVKQANKDIDAAKLKLTTEIAAIG- 251 A : : : :	252 752
Db 1304 AlbsQlQDTQBLLQBENRQKLSLSTKLKQVBDEKNSFRBQLEEBEBE 1350	Qy 207LIPELKNKLKSVQNFFTTLSNTVKQANKDIDAAKLKLTTEIAAIGE 252	Qy 253 IKTETETTRFYUDYDDLMLSLLKEAAKKMINTCNEYQKR 291	RESULT 38 US-10-107-782-107	- Z & m	: Colman, : Edinger : Gangoll : Kekuda, : Li, Li,			; APPLICANT: Shamets, suresh, ; APPLICANT: Shimkets, richard, ; APPLICANT: Si, Jingsheng, ; APPLICANT: Si, Jingsheng, ; APPLICANT: Smithson, Glennda,	CANT: Spytek, Ki CANT: Stone, Dav CANT: Taupier, I CANT: Tchernev, CANT: Vernet, C	APPLICANT: Zerhusen, Brian ; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES AND METHODS OF USE THEREOF ; FILE REFERENCE: 21402-222CLF ; FILE REFERENCE: 21402-222CLF ; CURRENT APPLICATION NUMBER: US10/107,782	; CURRENT FILING DAILS: 2002-03-2, ; PRIOR APPLICATION NUMBER: 10/028,248 ; PRIOR FILING DATE: 2001-12-19 ; PRIOR APPLICATION NUMBER: 60/256,619			FRIOK AFFLICHION NOTEDEN: 00/2/2/2/2/2/2/2/2/2/2/2/2/2/2/2/2/2/2/	;	Query Match 7.1%; Score 106.5; DB 15; Length 1999; Best Local Similarity 18.3%; Pred. No. 24; Matches 51; Conservative 39; Mismatches 112; Indels 77; Gaps 6;

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APPLICANT: Zerhusen, Brian
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES AND METHODS OF USE THEREOF
CURRENT APPLICATION NUMBER: US/10/107,782
CURRENT FILING DATE: 2002-03-27
                                                                                                   16;
                                                                     194 ISYSIAAGVVEGKLIPELKNKLKSVQNFFTTLSNTVKQANKDIDAAKLKLTTEIAAIGEI 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Indele
                                                                                                                                                                                       254 KTETETTRFYVDYDDLMLSLLKEAAKKMINTCNEYQKR 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.0%; Score 106; DB 15;
20.4%; Pred. No. 25;
iive 69; Mismatches 120;
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PRIOR APPLICATION NUMBER: 10/028,248
PRIOR APPLICATION NUMBER: 60/256,619
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2001-01-19
PRIOR FILING DATE: 2001-01-19
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-04-20
PRIOR FILING DATE: 2001-04-20
PRIOR FILING DATE: 2001-04-20
PRIOR FILING DATE: 2001-04-20
PRIOR FILING DATE: 2001-04-20
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PRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 215
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 105
LENGTH: 1961
                                                                                                                                                                                                                                                                                                           Sequence 105, Application US/10107782 Publication No. US20040018970A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: 60/311,266
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chernev, Velizar,
ernet, Corine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patturajan, Meera,
Rothenberg, Mark,
Sciore, Paul,
Shenoy, Suresh,
Shimkets, Richard,
Si, Jingsheng,
Sii, Lhson, Glennda,
Spytek, Kimberly,
Stone, David,
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Malyankar, Uriel,
Miller, Charles,
Millet, Isabelle,
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Gangolli, Esha,
Kekuda, Ramesh,
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Best Local Similarity 20.44
Matches .69; Conservative
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Boldog, Ferenc,
APPLICANT: Casman, Stacie
APPLICANT: Colman, Steve,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                               JS-10-107-782-105
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TITLE OF INVENTION: No. US20030235882A1el Nucleic Acids and Polypeptides and Methods
TITLE OF INVENTION: Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1198 VEBLAEQLE-----QTKRVKATLEKAKQTLENERGELANBVKA---LLQGKGDSEHKRK 1248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1249 KVEAQLQELQVKFSEGERVRTELADKVSKLQVELDSVTGLLNQSDSKSSKLTKDFSALES 1308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 ASVLVGDIKTLLMDSQDKYFEAT----QTVYEWCG-VATQLLAAYILL----FDEYNEK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 KASAQ-KDILIKV-----LDDGITKLNEAQKSLLVSSQSFNNASGKIL----ALDS 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------DFSEKSSYFQSQVDKIRKEAYAGAAAGVVAGPFGLI 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 BIVADKTVEVVKNAIETADGALDLYNKYLDQV-IPWQTFDETIK----ELSRFKQEYSQA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 7.0%; Score 106; DB 14; Length 19
Best Local Similarity 20.4%; Pred. No. 25;
Matches 69; Conservative 69; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 21402-222
CURRENT APPLICATION NUMBER: US/10/028,248A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/256619
PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/262959
PRIOR FILING DATE: 2001-01-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/262959
PRIOR PILING DATE: 2001-01-19
PRIOR PILING DATE: 2001-01-19
PRIOR PRILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-04-20
PRIOR FILING DATE: 2001-04-20
PRIOR FILING DATE: 2001-04-20
PRIOR FILING DATE: 2001-06-28
PRIOR FILING DATE: 2001-06-30
PRIOR FILING DATE: 2001-06-09
NUMBER OF SEQ ID NOS: 211
SEQ ID NO 105
LENGTH: 1961
                                                                                     Application US/10028248A
o. US20030235882A1
                                                                                                                                                                                                                                                                                                                                                                                                        faupier Jr, Raymond J
                                                                                                                                                    APPLICANT: Shinkets, Richard APPLICANT: Patturajan, Meera APPLICANT: Vernet, Corine APPLICANT: Casman, Stacie APPLICANT: Malyankar, Uriel APPLICANT: Shenoy, Suresh
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Zerhusen, Bryan
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Edinger, Shlomit
Stone, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sciore, Paul
Millet, Isabelle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-028-248A-105
                                                                                                                                                                                                                                                                                             Spytek, Kimberly
Gangolli, Esha
Miller, Charles
                                                                                                                                                                                                                                                                                                                                                              Boldog, Ferenc
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                                                                                                                                                                                                                                                                                                                                                                                                                               Kekuda, Ramesh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu, Xiaohong
                                                                                          Sequence 105, Applic Publication No. US20 GENERAL INFORMATION:
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63 GDIKTLLMDSQD------KYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQK 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                264 TITQYNNAİHNAQQQINTAKTEAQQVINNERATPQQVSDALTK------VRAAQTKI 314
                                                                                                                          1782 OINHADKTAQVNQDSINAQNIISKIKPATTVKATALQQIQNIATNKINLIKANNEATDEE 1841
                                                                                                                                                                                                      163 SSYFQSQVDKIRKEAYAGAAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNKLKSVQNFF 222
66 KILLMDSQDKYFBATQTVYEWCGVATQLLAAYILLFDBYNBKKASAQKDILIKVLDDGIT 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TVEVVKNAIBTAADGALDLYNKYLDQVI-----PWQTFDETIKELSRFKQEYSQAASVLV
                                                                                                                                                                                                                                                              TTLSNIVKQANKDIDAAKLKLTTE------IAAIGEIKTE-----TETTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 116;
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                                                                                       126 KINEAQKSLIVSSQSFN--NASGK-----LLALDSQLTNDFS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Ohlsen, Kari L.
APPLICANT: Oylsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Gart, J.
APPLICANT: Gart, J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
CONRENT: Yamamoto, John D.
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICANTON NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
7.0%; Score 106; DB 9; L
Best Local Similarity 21.9%; Pred. No. 28;
Matches 75; Conservative 37; Mismatches 115;
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PRIOR PRICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR PRILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
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PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: PASESEQ FOR WINDOWS VERSION 4.0
SOFTWARE: 2006
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5639, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                        262 FYVDYDDLMLSLLKEAAKKMIN 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , ORGANISM: Staphylococcus aureus
US-09-815-242-5639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
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                                                                                                                                               1198 VEELAEQLE-----QTKRVKATLEKAKQTLENERGELANEVKA---LLQGKGDSEHKRK 1248
                                                                                                                                                                                                                         194 ISYSIAAGVVEGKLIPELKNKLKSVQNFFTTLSNTVKQANKDIDAAKLKLTTEIAAIGEI 253
                                                                                                                                                                                                                                                                                  ---DFSEKSSYFQSQVDKIRKEAYAGAAAGVVAGPFGLI 193
                                                                                                       58 ASVLVGDIKTLLMDSQDKXPEAT----QTVYEWCG-VATQLLAAYILL----FDEYNEK 107
                                                                                                                                                                                             108 KASAQ-KDILIKV-----LDDGITKLNEAQKSLLVSSQSFNNASGKLL----ALDS 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 VEVVKNAIETA----DGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASVLVGDI
                    3 BIVADKIVEVVKNALETADGALDLYNKYLDQV-IPWQTFDETIK----ELSRFKQEYSQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68;
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7.0%; Score 106; DB 9; Length 20
Best Local Similarity 22.4%; Pred. No. 27;
Matches 72; Conservative 56; Mismatches 126; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Essential Genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           254 KTETETTRFYVDYDDLMLSLLKEAAKKMINTCNEYOKR 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: HABELDEAN, KOUELL
APPLICANT: Chisen, KAULL
APPLICANT: 2yskind, Judith W.
APPLICANT: 2yskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Annamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essent:
TITLE OF INVENTION: PROKARYOTES
TITLE OF INVENTION: PROKARYOTES
TITLE OF INVENTION: PROKARYOTES
TITLE OF INVENTION: PROKARYOTES
TITLE OF INVENTION: PROKARYOTES
TITLE OF INVENTION NUMBER: 60/204, 915, 9210 PRIOR PELING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/205, 488
PRIOR PLING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/205, 625
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
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PRIOR PLING DATE: 2000-11-27
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5015, Application US/09815242 Sequence 5015, Application US/09815242 Patent No. US20020061569A1 GENERAL INFORMATION: APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , ORGANISM: Staphylococcus aureus
US-09-815-242-5815
                                                                                                                                                                                                                                                                                                154 QLTN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastS
SEQ ID NO 5815
LENGTH: 2076
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Qy 163 SSYPQSQVDKIRKEAYAGAAAGVVAGPFGLIISYSIAAGVVBGKLIPELKNKLKSVQNFF 222	Qy 223 TTLSNTVKQANKDIDAAKLKITTEIAAIGEIKTETETTR 261	Qy 262 FYVDYDDLMLSLLKEAAKKMIN 283 DD 1954 LQTHDLDVHPIKKPDAEKTIN 1975	RESULT 45 US-09-815-12610 . Seminare 12610 Application US/09815242	GENERAL INFORMATION: APPLICANT: Haselbeck, Robert APPLICANT: Applicant: Ageind, Judith W. APPLICANT: Zyskind, Judith W. APPLICANT: Zyskind, Judith W. APPLICANT: Trawick, John D. APPLICANT: Trawick, John D. APPLICANT: Tawick, Abbert T. APPLICANT: Yamamoto, Robert T. APPLICANT: Xu, H. Howard ITILE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A. FILE REFERENCE: ELITRA.011A.01A. FILE REFERENCE: ELITRA.011A.01A. FILE REFERENCE: 2001-03-21 FRICH FILING DATE: 2001-03-21 FRICH FILING DATE: 2000-03-21 FRICH FILING DATE: 2000-03-21 FRICH FILING DATE: 2000-03-21 FRICH FILING DATE: 2000-03-21 FRICH FILING DATE: 2000-03-21	PRIOR APPLICATION NUMBER: 60/207,727	Query Match 7.0%; Score 106; DB 9; Length 5795; Best Local Similarity 21.9%; Pred. No. 1.1e+02; Matches 75; Conservative 37; Mismatches 115; Indels 116; Gaps 17	Qy 9 TVEVVKNAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASVLV 62 	Qy 63 GDIKTLAMDSQDKYPEATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQK 113	Qy 114 DILIKVLDDGTKLNEAQKSLLVSSQSFNNASGKLLA 150 ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;	Db 2703GNLQTAINDKSGTLASQNFLDADEQKRNAYNQAVSNAETILNKQTGPNTAK 2753
Qy 114 DILIKVLDDGITKLNEAQKSLLVSSQSFNNASGKLLA 150 	QY 151 LDSQLTNDFSEKSSYFQSQVDKIRKEAYAGAAAGVVAGPFGLIISYSIAA 200	Qy 201 GVVEGKLIPELKNKLKSVQNFFTTLSNTVKQANKDIDAAKLKL 243	Oy 244TTEI-AAIGEIKTETETTRFYUDYD 267 DD 532 QRVSNAQDVQRNATELNTAMGTLKHAIADKTNTLASSKYVNAD 574	RESULT 44 US-09-815-12913 US-09-815-12913 US-09-815-12913 Sequence 12913, Application US/09815242 Patent No. US20020061569A1 GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Haselbeck, Ravi L. APPLICANT: Wall, Daidh W. APPLICANT: Trawick, John D. APPLICANT: Trawick, John D. APPLICANT: Trawick, John D. APPLICANT: Trawick, John D. APPLICANT: Trawick, John D. APPLICANT: The World Carn, H. APPLICANT: Wall, Howard TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Probaryotes FILE REFERENCE: ELITRA.011A CURRENT APPLICANTON WUMBER: US/09/815,242	6060606060606060 " r	; LEWELH: 2.180 ; TYPE: PRT ; ORGANISM: Staphylococcus aureus US-09-815-242-12913	Query Match 7.0%; Score 106; DB 9; Length 2186; Best Local Similarity 22.4%; Pred. No. 29; Matches 72; Conservative 56; Mismatches 126; Indels 68; Gaps 11;	Qy 10 VEVVKNAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASVLVGDI 65 1:	Oy 66 KTLIMDSQDKYFEATQTVYEWCGVATQLIAAYILLFDEXNEKKASAQKDILIKVLDDGIT 125	:: : :

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APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---DAAKLK-----LITTEIAAIGEIKTETETTRFYVD-----YDDLMLSLLK----EA 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EATQTV-----YEWCGVATQLLAAYI-----LLFDEYNEKKASAQKDILIKV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 LDDGITKLNEAQKSLLVSSQSFNNASGKLLALDSQLTN--DFSEKSSYFQSQVDKIRKEA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         347 LVDFLTKINQL-----TSNN-----RLDDVIDNLEDSSNKIDSSISTINDIKNKV 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 53523
LENGTH: 742
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                       PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-66
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
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PRIOR PILING DATE: 2000-11-27
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PRIOR PILING DATE: 2001-12-29
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PRIOR PILING DATE: 2001-12-29
PRIOR PILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Buckharov, Andrey A.
APPLICANT: Barbazuk, Brad
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MKKLVS 512
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Publication No. US20040031072A1
GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
Cao Yongwei
TITLE OF INVENTION:
Plants and Uses Thereof for Plant Improvement
FILE OF INVENTION:
Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE:
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                                                                                     2754 TAVEQALINNVNSAKHALNGTONL----NNAKOAAITAINGASDINOKOKDALKAQANGA 2808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146 GKL-----LALDSQLTNDFSEKSSYFQSQVDKIRKEAYAGAAAGVVAGPFGLIISYSIAA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104 YNEKKASAQ------KDILIKVLDDGITKLNEA---QKSLL------VSSQSFNNAS 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :: |||: | :: || : | : || : || : || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201 GVVEGKLI--PELKNKLKSVQNFFTTLSNTVKQANKDIDAAKLKLT----TEIAAIGEI 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190 BIIKSKSİFYDAIKGKGRSLSQPSAVLSTT-----NAGQISITLDHKDTEVAACVAD 241
---NKDIDAAKLKL--- 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A CURRENT APPLICATION NUMBER: US/10/282,122A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77; Indels
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                                                                                                                                                                                                                                         ---TIEI-AAIGEI-----KTETETTRFYVDYD 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_66432C.1.pep
US-10-424-599-248508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 7.0%; Score 105.5; Best Local Similarity 21.9%; Pred. No. 3.9; Matches 49; Conservative 43; Mismatches
    201 GVVEGKL -- IPELKNKLKSVQNFFTTLSNTVKQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 53523, Application US/10282122A
Publication No. US20040029129A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Robert
APPLICANT: Ohleen, Roxit
APPLICANT: Cydkind, Judith
APPLICANT: Wall, paniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trawick, John
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98 ILLFDEYNEKKASAQKDILIKVLDDGITKLNEAQKS--LLVSSQSF-----NNASGKLLA 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | | | | | | | | : | : | | : | | 354 VAEGLIDKETAVTRVKAEHIDLLLHPRIDPNAKLEVVAKGLPASPGAAVGKVVFTAEVAE 413
                                                                                                                                                                                                                                                                                                                                                                             ---- DVVAGIRTPDFIDT 293
                                                                                                                                                                                                                                                                                                                                                                                                                                   211 LKNKLKSVQNFFTTLSNTVKQANKDID-------AAKLKLTTEI 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                294 LGNKIPEAYNOLVDICRKLEAHFKDMQDIEFTIQEGKLYMLQTRTGKRTAAAAVKLATDM 353
                                                              248 AAIGEIKTETETTRFYVDYDDLML-----SLLKEAAK------KMINTCN--E 287
                                                                                                                             -----SRFKQEYSQAASVLVGDIKTLLMDSQDKYFEATQTVYEWCGVATQLLAAY 97
                               VADKTVEVVKNAIETADGALDLYNKYLDQV----IPWQTFDETI----KEL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Encoding Immunomodulatory
                                                                                                                                                                              172 LDAKALKDLABRPK------GVIKL-----BKGPEPPQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/592,126
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/10/393,602
FILIAG DATE: 19-Mar-2003
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                               257 F---TRNPSTGERKFFGEYLINAOGE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT. 50
US-10-393-602-148
US-10-393-602-148
Sequence 148, Application US/10393602
Publication No. US20030170714A1
GENERAL INFORMATION:
APPLICANT: Gregory Dolganov
ITLE OF INVENTION: Transcripts E
Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION
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SEQUENCE CHARACTERISTICS:
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TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (415)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   414 EMAEKGEKTI 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       288 YOKRHGKKTL 297
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APPLICANT: Cac, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Seeven C.
APPLICANT: Slater, Serven C.
APPLICANT: Gldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REPERENCE: 38-10(52052)8
FURRENT APPLICATION NUMBER: US/10/369,493
CURRENT PILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                : :| |: :: || : : || :| 324 KLGDVNILQEKVSLLSQEIDNKGIRIRELSSLLSSKEADYRNLCSFSDQTKESLELAEAK 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       384 IQQLEEEVHRTRNDLSSKI ----SSIDLINBELQALNSAKNBAEBKLSELTKDYTDLKAS 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GDIKTLIMDSQDKYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQKDILIKVLDD 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     274 STKKTVTSLSEE--FRREKTLABELREEIRRL------BSSLAQAGDDKDVLEAKLKE 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GITKLNEAQKSLLVSSQSFNNASGKLLALDSQLT------156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------NDFSEKSSYFQSQVDKIRKEAYAGAAA------GVVAGPFGLIISY 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIAAGVVEGKLIPELKNKLKSVQNFFT-TLSNTVKQ-----ANKDIDAAKLKLTTEIAA 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       440 SEARESRNSELLLEKDNMIKQLDGKLSDALSDSSKDRENIAALNKELDATKAMLENEVAA 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           250 IGEIK-----TETETTRFYVDYD-----DLMLSLLKEAAKKMINTCNEYQK 290
                                                                                                                                                                                                                                                                                                                                                                                                                                   8 KTVEVVRNAIETA----DGALDLYNK-YLDQVIPWQTFDETIKELSRFKQEYSQAASVLV 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38 21 (53221)8
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 191043
LENGTH: 815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41; Mismatches 117; Indels 135;
                                                                                                                                                                                                                                                                                                                                   Length 815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.0%; Score 105.5; DB 14; Length 873; 20.8%; Pred. No. 9.3;
                                                                                                                                                                                                                                                                                                                              7.0%; Score 105.5; DB 16; Length
20.1%; Pred. No. 8.5;
tive 68; Mismatches 131; Indels
                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: PAT_MRT4530_8739C.1.pep
US-10-437-963-191043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 11332, Application US/10369493; Publication No. US20030233675A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Methanosarcina mazei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           291 RHGKKTLFEVPEV 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             555 GLTNK-LGEVESV 566
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Best Local Similarity 20.1*
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                                                                                                                                                                            TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-369-493-11332
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LENGTH: 873
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Matches
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us-09-993-292b-28.rapb

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Query Match 7.0%; Score 105.5; DB 14; Length 1312; Best Local Similarity 18.8%; Pred. No. 16; Matches 75; Conservative 58; Mismatches 96; Indels 171; Gaps 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55 SQAASVLVGDIKTLLMDSQDKYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQKD 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :|::::|
641 DLDRLKEEIEKSSKQRAMLAGATA--VYSQFITQLTDENQSCCPVCQRVFQTEAELQEVI 698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            757 V------NRDIQRLKNDIBEGETLIGTIMPEEESAKVCLTDVTIMERPQMEL 802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : | | | | | : | | | : | | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       169 QVDKIRKE-----AYAGAAAGVVAGPF-----190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----GLI-ISYSIAAGVVEGKLIPELKNKLKS 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---ELSRFKQEY 54
; SEQUENCE DESCRIPTION: SEQ ID NO: 148:
US-10-393-602-148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 VEVVKNAIETADGALDLYNKYLDQVIPWQTFDETIK------
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Search completed: January 5, 2005, 11:08:51 Job time : 66.2944 Becs

Sequence 2, Appli Sequence 2080, Ap Sequence 1358, Ap Sequence 4284, Ap Sequence 2178, Ap Sequence 3159, Ap Sequence 3159, Ap Sequence 4, Appli Sequence 4, Appli Sequence 5, Appli Sequence 6, Appli Sequence 1154, Ap Sequence 1154, Ap

Sequence 52, Appl Sequence 701, App Sequence 701, Appl Sequence 1154, Ap Sequence 1, Appli Sequence 1, Appli Sequence 20284, Ap Sequence 20284, Ap

Sequence Sequence Sequence Sequence

Sequence:

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APPLICANT: King Harold C.
APPLICANT: King Harold C.
APPLICANT: Sathish, Mundayoor
APPLICANT: Sathish, Mundayoor
APPLICANT: Shinnick, Thomas M.
TITLE OF INVENTION: Regulator of Contact-Mediated Hemolysin
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS: 3
ADDRESSES: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgian
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.4%; Score 1499; DB 1; Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,115
FILING DATE: 26-UN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Green, Jamie L.
REGISTRATION NUMBER: 32,467
REGISTRATION NUMBER: 32,467
REGISTRATION NUMBER: 33,467
RETERRENCE/DOCKET NUMBER: 03063-0171US
TELEFRAK: (404) 818-3799
                  US-09-710-279-1358
US-09-710-279-1358
US-09-248-795A-20613
US-09-248-796A-20613
US-09-134-001C-3159
US-09-134-000A-4
US-09-312-157-4
US-09-312-157-4
US-09-312-157-4
US-09-312-157-4
US-09-538-092-701
US-09-538-092-1154
US-08-353-700-1
US-08-353-700-1
US-08-353-700-1
US-08-134-000C-3870
US-09-134-000C-3870
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                                                                                                                                                                                                                         US-09-447-497-15
US-09-447-497-14
US-09-447-497-12
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                                                                                                                                                                                                                                                                                                                                        US/08557115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 309 amino acida
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
pplication
                                                                                                                                                                                                                                                                                                                                        Sequence 3, Applicati
Patent No. 5731151
GENRRAL INFORMATION:
ANTI-SENSE:
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22266666666666644444444444468
80012646666666444444444466
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Sequence 3, Appli
Sequence 7736, Ap
Sequence 66, Appl
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3, Appli
3, Appli
18798, A
1873, Ap
807, Ap
807, Ap
115, Ap
148, Ap
1148, Appl
1148, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2, Appli
11, Appl
                                                                          ; Search time 15.9474 Seconds (without alignments) 1260.042 Million cell updates/sec
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1 MTEIVADKTVEVVKNAIETA.....TCNEYQKRHGKKTLFEVPEV 303
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Sequence 2
Sequence 5
Sequence 3
Sequence 2
Sequence 1
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Sequence 4
Sequence 1
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Sequence 3
Sequence 3
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Sequence
Sequence
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Sequence 5
Sequence 1
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/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RB_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
         GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                    478139 segs, 66318000 residues
                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries
                                                      OM protein - protein search, using sw model
                                                                            2005, 10:51:49
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Maximum DB seq
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112
111.5
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116
115.5
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Database

Result

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GENERAL INFORMATION:
APPLICANT: GARY BREION
TITLE OF INVENTION:
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TITLE OF INVENTION:
TITLE OF INVENTION UNMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
INVENTION OF SEQ ID NOS: 8344
SEQ ID NO 7736
LENGTH: 1036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---YAGAAAGVVAGPFGL 192
                                                                                                                                                                                                                                                                                                                                                 241 LKLTTEIAAIGEIKTETETTRFYVDYDDIMLSLLKEAAKKMINTCNEYQKRHGKKTLFEV 300
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                                                                                                                                                                                DDGITKLNEAQKSLLVSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDKIRKEAYAG 180
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                                                                                                                                                                                                     241 LKLTTEIAAIGEIKTETETTRFYUDYDDLMLSILKEAAKKMINTCNEYQKRHGKKTLFEV
                                                                       1 MTEIVADKTVEVVKNAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASV
                                                                                                           LVGDIKTLLMDSQDKYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQKDILIKVL
                                                                                                                                            61 LVGDIKTILMDSQDKYPEATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQKDILIKVL
                                                                                                                                                                                                                                                         181 AAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNKLKSVQNFFTTLSNTVKQANKDIDAAK
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Gaps
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 Indels
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Mismatches
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Best Local Similarity 21.5%
Matches 82, Conservative
 301; Conservative
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                                                                                                                                                                   61 LVGDÍKTLÍMDSQDKYFEATQTVYEWCGVATQLÍLAAYÍLLFDEYNEKKASAQKDÍLÍKVL 120
                                                                                              1 MTBIVADKTVEVVKNAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASV 60
                                                           1 MTEIVADKTVEVVKNAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASV
                        Gaps
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APPLICANT: Sathish, Mundayoor
APPLICANT: Shinnick, Thomas
TITLE OF INVENTION: REGULATOR OF CONTACT-MEDIATED HEMOLYSIN
TITLE OF INVENTION: OF MYCOBACTERIUM TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.4%; Score 1499; DB 5; Length 309; 100.0%; Pred. No. 2.3e-134;
                     0; Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05869
     Pred. No. 2.3e-134;
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                       0; Mismatches
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REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 141
TELECOMMUNICATION INFORMATION:
     100.08;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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NAME: Perryman, David G.
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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amino acid
   al Similarity 100.
301; Conservative
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Suite 120
STREET: 127 Peachtre
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Best Local Similarity
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STATE: Georgia
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PCT-US94-05869-3
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Matches 30
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TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REPERENCE: PUJ48018.
CURRENT REPERENCE: PUJ48018.
CURRENT PILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR PILING DATE: 1999-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        245 TEIAAIGEIKTETETTRFYVDYDDLMLSLLKEAAKKMINTCNEYQKRHGKKTLFEVPE 302
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                                                                                                                                                                                                                                7.8%; Score 118; DB 3; Length 1211;
19.3%; Pred. No. 0.041;
tive 53; Mismatches 112; Indels 12:
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20.0%; Pred. No. 0.04;
tive 42; Mismatches
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GENERAL INFORMATION:
; LENGTH: 1211
; TYPE: RRT
; CRANISM: Staphylococcus epidermidis
US-09-134-001C-4820
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SOFTWARE: Patentin Ver. 2.
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Best Local Similarity
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Matches
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Sequence 4820, Application US/09134001C

Sequence 4820, Application US/09134001C

Sequence 4820, Application US/09134001C

GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
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APPLICANT: 
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    AFLEDNFKLLSQYNKEYSVERSVLITQQHWDELIGELASVTKNGAKTLSGKSYIDY----
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22.9%; Pred. No. 0.029;
ive 54; Mismatches 138; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hyman, Paul
APPLICANT: Williams, Mark
TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
FILE REPERENCE: 8471-010-999
CURRENT APPLICATION NUMBER: US/09/914,259
CURRENT FILING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 180
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 66
                                                                                                      271 LSLLKEAAKKMINTCNEYQKR 291
                                                                                                                                                           Sequence 66, Application US/09914259
Patent No. 6495336
GENERAL INFORMATION:
APPLICANT: Makowski, Lee
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915 QDQKIFSLKNKLKE 928
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ORGANISM: Bos taurus
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Matches 72; Conserv
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APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                            12;
                                                                                                                                                                                                                                                 AS---DKVETTKAEAQSLKDDATQT-FESAKQAVEGKVEAIKEQVLDQVDSLKDDTDQDN 205
                                                                                                                                                                                                                                                                                                                     103 ATEKLEVAKEATQ-------DKVEKTQSLVEDİKDKAQSLQEDAADTVEALKQA 149
                                                                                                                                                                                                               58 ASVLVGDIKTLLMDSQDKYFEATQTVYEWC-----GVATQLLAAYILLFDEYN--- 105
                                                                                                                                                                                                                                                                                          ---EKKASAQKDILIKVLDDGITKLNEAQKSLLVSSQSF-NNASGKL----LALD--SQ 154
                                                                                                                                                                                                                                                                                                                                                                        LTNDFSEKSSYFQSQVDKIRKEAYAGAAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNK 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                  215 LKSVQNFFTTLSNTVKQANKDIDAAKLKLTTEIAAIGEIKTETTRFYVDYDDLMLSLL 274
                                                                                                                                   57
                                                                                              Gaps
                                                                                            77;
                                                       Length 718;
                                                                                                                                   6 ADKTVEVVKNAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQE
                                                                                            Indels
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                     Query Match 7.7%; Score 115.5; DB 4; Best Local Similarity 21.0%; Pred. No. 0.033; Matches 70; Conservative 57; Mismatches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  275 KEAAKKMINTC------NEYQKRHGKKTL 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMÁTION:
NAME: Afiniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5317, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
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OPERATING SYSTEM: <Unknown>
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TYPE: amino acid
TOPOLOGY: linear
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, ORGANISM: M.catarrhalis
US-09-540-236-2753
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Patent No. 660709

GENERAL INFORMATION:

APPLICANT: GARY BREYON:

APPLICANT: GARY BREYON:

TITLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL TITLE OF INVENTION: UNMER: US/09/543,681A

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT FILING DATE: 2000-04-05

PRIOR PELING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 8019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2753, Application US/09540236

Patent No. 673910

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 2709.2005-001
CURRENT PEPLING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 2753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDIKTLLMDSQDKYFEATQTVYEWCGVATQL--LAAYILLFDEYNEKKASAQKDILIKVL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DDGITKINEAQKS--LIVSSQSFNNASGKILLALDSQLTNDFSEKSSYFQSQVDKIRKEAY 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGA---AAGVVAGPFGLIISYSIAAGVVEGK-----LIPE--LKNKLKSVQNFFTTL 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAADDIVNKIIGAPSGIVPSELIPDGLVKRAGFIKDRILNIPDERIKDYLESDVNY--VM 658
--KLKSVQNFFTTLSNTVKQANKDI- 236
                                                                           237 -----DAAKLKLTTEIAAIGEIKTETETTRFYVDYDDLMLSLLKEAAKKMINTCNE 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 EIVADKTVEVVKNAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASVLV 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    226 SNTVKQANKDIDAAKLKLTTEIAAI---GEIKTETETTRFYVDYDDLM 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | ::| : | : : | : : | : : | ENYIRQV-----EYNQLI 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 1129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.7%; Score 116; DB 4; Length 112
23.3%; Pred. No. 0.057;
ive 55; Mismatches 120; Indels
                                                                                                          :| | : : :
200 FLEHTINENEAKKSRLDSRLVE-
                                                                                                                                                         288 YOKRHGKKTLFEVPE 302
                                                                                                                                                                                240 YQS--SKKSMEKVEQ 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67; Conservative
  203 VEGKLIPELKN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-543-681A-8019
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US-09-540-236-2753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63
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334 KVKHPEKLOESLMKAAAEKETEIQKAEANLIKTQQELEKYQKSTKELLAELRDQYVDLMQ 393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 AQKDILIKVLDDGITKLNEAQKSLLVSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQV 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     171 DKIRKEAYAGAAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNKLKSVQNFFTTLSNTVK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   231 QA-----NKDIDAAKLKLTTEI--AAIGEIKTETE-----TTRFYVDYDDLMLSLLK 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 ETLTÓTDVSLMVAEIKTAKKD----- 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    252 AKFNLELGKLSESI----QEQESILAKQRKENAQADRLIEKNQOVLLDLSEKLKQTEGQK 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 VADKTVEVVK-----NAIBTADG---ALDLYNKYLDQVIPWQTFDETIKELSRFK 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 7.5%; Score 113.5; DB 4; Length 1196; Best Local Similarity 20.0%; Pred. No. 0.11; Matches 67; Conservative 50; Mismatches 111; Indels 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: TURLEY, EVA A.
APPLICANT: SHUWEN, ZHANG
APPLICANT: ENTWISTLE, JOYCELYN
TITLE OF INVENTION: HYALURONAN RECEPTOR PROTEIN
NUMBER OF SEQUENCES: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              276 BAAKKMINTCNEYQKRH-----GKKTLFEVPEV 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EQA--AVGNELKYLERQYIQETAKSKQTLAKQSEV 426
                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...1196
SEQUENCE DESCRIPTION: SEQ ID NO: 3944:
                                                 REFERENCE/DOCKET NUMBER: GTC-012
    Pamela Deneke
                                                                                                                                                                                                                                                                                                                                     ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1251 ATRIVE OF THE AMERICAS CITY: NEW YORK STATE: NEW YORK COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC_compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Rel. #1.0, ASCII
CURRENT APPLICATION DATA:
  NAME: Ariniello, Pamela Den
REGISTRATION NUMBER: 40,489
                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3944:
SEQUENCE CHARACTERISTICS:
LENGTH: 1196 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 2, Application US/08477831C; Patent No. 6429291
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10020-1104
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                                                                                                                                                                                                                                                                                                                                                           FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52
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Matches
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                         21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            94 LAAYILLFDEYNEKKASAQKDILIKVLDDGITKINEA-----QKSLLVSSQSF--- 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 SFGFVLGLDSFDKK-----EDGTIERSIDKÍKALNEISVVTVPAYDSSNVQVNKRSYESF 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --NNASGKLLALDSQLTNDFSEKSSYFQSQVDKIRK------EAYAGAAAGVV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        192 MSNN-----QAKQTNNSLESTSKAQKESNNMEKTLIDNEKTELRGYEEYIRSQGEVR 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187 AGPFGLIISYSIAAGVVEGKLIPELKNKLKSVQNF----FTTLSN-----TVKQAN 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----DDLMLSLLKEA 277
                                                                                                                                                                                                                                                                                                                                                                   3 EIVADKTVEVVKNAIETADG------ALDLYNKYLDQVIPWQTFDETIKELS- 48
                                                                                                                                                                                                                                                                                                                                                                                                                                ----RFKQBYSQ-AASVLVGDIKTLLMDSQDKYFBATQT-----VYEWC--GVATQL 93
                                                                                                                                                                                                                                     Query Match 7.6%; Score 114; DB 4; Length 515;
Best Local Similarity 23.3%; Pred. No. 0.027;
Matches 90; Conservative 58; Mismatches 111; Indels 128; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234 KDIDAAKLKLTTEIAAIGEIKTETETTRFYVDY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 MAY 1998
APPLICATION NUMBER: 60/051571
                                                                                           ) NAME/KEY: misc feature
; LOCATION: (B) LÖCATION 1...515
; SEQUENCE DESCRIPTION: SEQ ID NO: 5317:
US-09-107-532A-5317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              278 ----AKKMINTCNEY----QKRHGKKT 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGIAL SOURCE:
ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3944, Application US/09107532A
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 7310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Massachusetts
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 6583275
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-107-532A-3944
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STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGIH: 808
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 DDGITKLNEAQKSLL-VSSQSFNNASGKLLAL-DSQLTN-DFSEKSSYFQSQVDKIRKEA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        335 ESVQEKYNDTAQSLRDVTAQLESYKSSTLKEIEDLKLENLTLQEKVAMAEKSVEDVQQQI 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 YAGAAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNK-----LKSVQNFF----TTLS 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          228 LDNLLREKEVELEKHIAAHAQAILIAQEKYNDTA---QSLRDVTAQLESVQEKYNDTAQS 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MTEIVADKTVEVVKNALETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       227 NTVKQANKDI------DAAKLKLTTEIAAIGEIKTETETTRFYVDYDDL 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | :: | :: | :: | | | | : | | | 438 NQLRQQDEDFRKQLEEKGKRTAEKENVMTELT------MEINKWRLLYDEL 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch
1. Similarity 20.5%; Pred. No. 0.054;
60; Conservative 63; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11, Application US/08477831C
| Sequence 11, Application US/08477831C
| Patent No. 6429291
| GENERAL INFORMATION:
| APPLICANT: TURLEY, EVA A. |
| APPLICANT: SHUWEN, ZHANG APPLICANT: SHUWEN, ZHANG APPLICANT: ENTWISTLE, JOYCELYN TITLE OF INVENTION: HYALURONAN RECEPTOR PROTEIN TOTALE OF INVENTION: HYALURONAN RECEPTOR PROTEIN NUMBER OF SEQUENCES: 60
| CORRESPONDENCE ADDRESS: ADDRESSEE: FISH & NEAVE STREET: 1251 AVENUE OF THE AMERICAS CITY: NEW YORK COUNTRY: US.A. |
| COMPUTER READABLE FORM: COMPUTER READABLE FORM: COMPUTER READABLE FORM: COMPUTER PROTEIN TOWN COMPUTER PROTEIN TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOWN COMPUTER TOW
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                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: /desc = "RHAMM I protein"
US-08-477-831C-2
APPLICALLA...
FILING DATE: 07-JUN-122.
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: PIERKI, MARGARET A.
REGISTRATION NUMBER: 30,709
REFERENCE/DOCKET NUMBER: SIM-10
TELECPMUNICATION INFORMATION:
TELEPHONE: 212-596-9090
TELEPAX: 212-596-9000
TELEPAX: 212-596-9000
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   APPLICATION NUMBER: US/08/477,831C
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NAME: PIERRI, MARGARET A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
US-08-477-831C-11
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Sequence 4995, Application US/09543681A

Sequence 4995, Application US/09543681A

Sequence 4995, Application US/09543681A

GENERAL INFORMATION:
APPLICANT: GARY BRETON

IITLE OF INVENTION: UOLUBIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL

TILLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

FILE REPERENCE: 2709.1002-001

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT FILING DATE: 2000-04-05

DELOR ADDITIONAL OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE TOWN OF THE T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 DDGITKLINBAQKSLL-VSSQSFNNASGKLLAL-DSQLTN-DFSEKSSYFQSQVDKIRKBA 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 YAGAAAGWVAGPFGLIISYSIAAGWVEGKLIPELKNK-----LKSVQNFF----TTLS 226
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420 LTAESINQ------BYA------RWQDLQNRSTLKEBEIKEITSSFLEKITDLK 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         253 LDNILREKEVELEKHIAAHAQAILIAQEKYNDTA---QSLRDVTAQLESVQEKYNDTAQS 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 LVGDIKTLLMDSQDKYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQKDILIKVL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MTEIVADKTVEVVKNAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASV 60
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7.4%; Score 111.5; DB 4; Length 808;
Best Local Similarity 22.0%; Pred. No. 0.093;
Matches 66; Conservative 55; Mismatches 108; Indels 71; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 IVADKTVEVVKNAIBTADGALDLYNKYLDQVIPWQTFDETIKELSRFKQE-YSQAASVLV
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PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 4995
LENGEN 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
DESCRIPTION: /desc = "RHAMM I-2a"
                                        SIM-10
                                   REFERENCE/DOCKET NUMBER: SIM-
TELECOMUNICATION INFORMATION:
TELEPHONE: 212-596-900
TELEPAX: 212-596-900
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 631 amino acids
REGISTRATION NUMBER: 30,709
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Best Local Similarity 20.5%;
Matches 60; Conservative 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         single
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61 LVGDIKTLIAMDSQDKYPEATQTVYEWCGVATQLLAAYILLFDBYNEKKASAQKDILIKVL 120
                                                                   266 LTAESTNQ-----EYA-----RMVQDLQNRSTLKEEEIKEITSFLEKITDLK 308
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                                                                                                                  227 NTVKQANKDI------DAAKLKLTTEIAAIGEIKTETETTRFYVDYDDL 269
                                                                                                                                          | :: : |::|
----MEINKWRLLYEEL 353
                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hawkins, Phillip R.
APPLICANT: Wilde, Craig G.
APPLICANT: Wilde, Craig G.
APPLICANT: Seilhamer. Jeffrey J.
TITLE OF INVENTION: HYLLICAL VEIN ENDOTHELIAL CELLS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 7.4%; Score 111; DB 1; Length 477; Best Local Similarity 20.5%; Pred. No. 0.047; Matches 60; Conservative 63; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,178 FILING DATE: August 20, 1996
CLASSIFICATION: 435
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/402,217
FILING DATE: March 10, 1995
ATTORNEY/AGENT INFORMATION:
                         178 YAGAAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNK---
                                                                                                                                       NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REPERENCE JOCKET NUMBER: PF-0028-1 DIV
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                        Sequence 3, Application US/08700178
Patent No. 5783669
Patent No. 5783669 5700912
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            477 amino acids
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LENGTH: 477 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLALLIBRARY: MOLLLIBRARY: GI 53979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94304
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                                                                                                                                                                                                                                                 US-08-700-178-3
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343 ELLKIPNLLK--IKTIDFYSNPANDLNTLNDDLSKLSIDYSKSLSLIKEQIEKRKSDIFT 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 DDGITKLNEAQKSLL-VSSQSFNNASGKLLAL-DSQLTN-DFSEKSSYFQSQVDKIRKEA 177
                                                                      180 GAAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNKLKSVQNFFTTLSNT--VKQANKDID 237
                                                                                                              ------PLEFHSSVSVEDSINELRYSYE---KIRSKSNDFTKSLNTEQVKARN---- 444
                                                                                                                                                            238 AAKLKIJTEIAAIGEIKTETETTRFYVDYDDLMLSLIKE---AAKKMINTCNEYQKRHGK 294
                                                                                                                                                                                         1 MTEIVADKTVEVVKOVAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASV 60
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                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hawkins, Phillip R.
APPLICANT: Wilde, Craig G.
APPLICANT: Wilde, Craig G.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: HYALURONIAN RECEPTOR EXPRESSED IN HUMAN TITLE OF INVENTION: UMBILICAL VEIN ENDOTHELIAL CELLS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 7.4%; Score 111; DB 1; Length 477; Best Local Similarity 20.5%; Pred. No. 0.047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/402,217A
FILING DATE: 10-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF-0028US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/08402217A Patent No. 5587301 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Luther, Barbara J. REGISTRATION NUMBER: 33954 REFERENCE/DOCKET NUMBER: PF TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 10-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                477 amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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LIBRADY
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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MOLECULE TYPE:
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STATE:
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, ORGANISM: Candida albicans
US-09-248-796A-18798
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Best Local Similarity
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                                                                                                                                          | ::| ::| ::| :: | :: | :: | 309 NQLRQODEDFRKQLEEKGKRTAEKENVMTELT------MEINKWRLLYEEL 353
                                                                                                                       227 NTVKQANKDI------DAAKLKLTTEIAAIGEIKTETETTRFYVDYDDL 269
                                                                                                                                                                                                                    US-08-995-654-3
; Sequence 3, Application US/08995654
; Patent No. 602518;
GENERAL INFORMATION:
APPLICANT: Hawkins, Phillip R.
APPLICANT: Wilde, Craig
APPLICANT: Wilde, Craig
TITLE OF INVENTION: UMBILICAL VEIN ENDOTHELIAL CELS
TITLE OF INVENTION: UMBILICAL VEIN ENDOTHELIAL CELS
CORRESPONDENCES: 3
CORRESPONDENCES: 3
CORRESPONDENCE ADDRESS:
STREET: 3174 POLTER Dr.
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62;
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20.5%; Pred. No. 0.047;
iive 63; Mismatches 108; Indels
                                                        178 YAGAAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: Windows SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/995,654
FILING DATE: December 22, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF-0028-2 DIV
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APPLICATION NUMBER: 08/700,178
FILING DATE: August 20, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/402,217
FILING DATE: March 10, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFRENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEPAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 477 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
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Best Local Similarity 20.5;
Matches 60; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                         266 LTAESTNQ----
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CLASSIFICATION:
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CITY: Palo
STATE: CA
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Sequence 18799, Application US/09248796A

Sequence 18799, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN:
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: NUMBER: US/09/248,796A

CURRENT APPLICATION NUMBER: US 60/074,725

PRIOR PEPLICATION NUMBER: US 60/074,725

PRIOR PELING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 18798

LENGTH: 924
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Patent No. 6562958
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BADWANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BADWANNII FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT APPLICATION NUMBER: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5793
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                                                                                                                                                                                                                                 178 YAGAAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNK-----LKSVQNFF----TTLS
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18.2%; Pred. No. 0.14;
rative 59; Mismatches 98;
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APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196-132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-13
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 20145
LENGTH: 829
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                                                                                                                                                                                                                                                                                                                   225 QYRFYEYIYSQETKSWINESAENFSNGISLVMEIVANAKESNYTDLIWFPEDFISPELII 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQKDILIKVLDDGITKLNEAQKSLLVS 137
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                          64 DVDYNKKQDRIQDVKLVLASNFDNFDYFNQRDGEHEKSNILLNSLTKYPDLKAFHNNLKF 123
                                                                                          SAQXDILIKVLDDGITKLN-EAQKSLLVSSQSFNNASGKLLALDSQLTNDFSEKSSY--- 165
                                                                                                                                   124 LYLLDAYSHIESDSTSHNNGSSDKSLDSSNASFNN-OGKL-----DLFKYFTELSHYIRQ 177
                                                                                                                                                                                  - POSOV - - DKIRKEAYAGAAAGVVAGPFGLIISYSIAAGVVEGKLIPELK - - - - NKLKS 217
                                                                                                                                                                                                                                178 CFÓDNCCDFKVRTN-----LNDKFGI---YILTQG-INGKEVPLAKIYLEENKSDS 224
                                                                                                                                                                                                                                                                              218 VQNFFTTL--SNTVKQANKDID--AAKLKLTTEIAAIGEIKTETETTRFYVDY----- 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238 CSIFGRPNPISVKVGMIDSTPLNQIDQKLHVLLKSESSELLRLSNLMLIENYMIDISFEN 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     298 VMTLKLKFDTDILTLEDSYDSIHGKITCSLIGGSEQQNKSNDNANKWIGYDDYTKGSLTT 357
------GDIKTLLMDSQDK--YFEATQTVYEWCGVATQLLAAYILLFDEYNEKKA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 DGALDL---YNKYLDQVIPWQTFDETIKELSRFKQEYSQAASVLVGDIKTLLMDSQDKYF 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --LSLLKEAAKKMINT-----CNEYOKRHGKKTLFE 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 7.1%; Score 107.5; DB 4; Best Local Similarity 19.5%; Pred. No. 0.23; Matches 66; Conservative 57; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | : :: | :: EWKMMFHACSISFSIGLHIMNQFRETN-----
                                                                                                                                                                                                                                                                                                                                                                           267 DDLMLSLLKEAAKKMIN--TCNEYQKR 291
                                                                                                                                                                                                                                                                                                                                                                                                           DKVTCSSNSSSSPPIIDLFSNNNYNSR 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----KLKLTTEIAAI-----GEI----
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US-09-248-796A-20145
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                                                                                                                                                                                                                                          336 QAEYAEATAALINAAKAHLANVRATNAETQAK-FGATAAATRYAQAQAAVTAATNAQTAAQ 394
                                                                                                                                                                                                                                                                                                                                                                                                 ------KKASAQKDILI 117
                                                                                                                                                                                                                                                                                                                                                                                                                                             395 IKLNTATSIAGRLAKGAFGLIGGWAGVATLGVMGLAAAYSYFNNKAEEAKQKLAEQAKVA 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KVLDDGITKL--NEAQKSLLVSSQSFNNASGKLLALDSQLTNDF---SEKSSYFQSQVDK 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    514 ISQEARTGT-----ISYTEAI-----ERLNKIKLPTDLYENLKKQAAQY 552
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APPLICANT: Giot, Loic
APPLICANT: Giot, Loic
APPLICANT: Giot, Loic
APPLICANT: Giot, Loic
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15566-54
CURRENT APPLICATION NUMBER: U009/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR PILING DATE: 1999-04-01
PRIOR FILING DATE: 2000-02-01
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuraPatSeqFormatter Version 0.9
SEQ ID NO 807
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 VETLDSMIELFKDYKPGSITLENITRLCQTLGLESFTEELSNELSRL----STASKIIVI 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IRKEAYAGAAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNKLKSVQNFFTTLSNTVKQ-
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                                                                                                                                                                131;
                                                                                                                  Length 1454;
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7.2%; Score 108.5; DB 4; Length 566;
Best Local Similarity 23.9%; Pred. No. 0.11;
Matches 78; Conservative 43; Mismatches 131; Indels 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              613 AKQKDSVIDSIYKSGWLDKGYTVAQANAILELQKAKGMSAILSKDEI 659
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                                                                                                                                                                IndelB
                                                                                                                                                                                                          3 EIVADKTVEVVKNAIETADGALDLYNKYLDQVIPWQTFDETIKE--
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US-09-538-092-807
                                                                                                                DB 4;
                                                                                                                                                            54; Mismatches 137;
                                                                                                                                                                                                                                                                                                       51 KQEYSQAASVL-----VGDIKTLLMDSQDKYFEAT----
                                                                                                             7.3%; Score 109.5; Di
20.9%; Pred. No. 0.35;
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Patent No. 6753314
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                                           ORGANISM: Acinetobacter baumannii
                                                                                                                                                                Conservative
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LOCATION: (0)...(0)
                                                                                                                                        Similarity
                                                , ORGANISM: Acino
US-09-328-352-5793
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-09-538-092-807
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                                                                                                                Query Match
                                                                                                                                        Best Local
Matches 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1312;
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                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Gregory Dolganov
TITLE OF INVENTION: Transcripts Encoding Immunomodulatory
TITLE OF INVENTION: Polypeptides
NUMBER OF SEQUENCES: 151
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
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                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,126
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---YVDYDDLMLSLLKEAAKK
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7.0%; Score 105.5; Di
Best Local Similarity 18.8%; Pred. No. 0.72;
Matches 75; Conservative 58; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                          Sequence 148, Application US/08592126
Patent No. 5821091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38.615
REFERENCE/DOCKET NUMBER: 466
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (415) 324-0880
TELEPAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 148:
SEQUENCE CHARACTERISTICS:
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                247 IAAIGEIKTETETTRF-
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                             Sequence 5150, Application US/09107532A

Patent No. 6583275

GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION:
TITLE OF INVENTION:
BUTTER OF INVENTION:
CONTRIBED AND ANINO ACID SEQUENCES RELATING TO
ENTEROCCOCCUS PAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIISYSIAAGVVEGKLIPELKNKLKSVONFFTTLSNTVKQ--ANKDI----DAAKLKLTTE 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        495 YLHSYDLVKGLKPGGIF--LINTLWSDEQLETHLPLKLKRYLAENNIRFYTINAMRLAQE 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | | | : : | : : | | : : | | 326 VLDRSKEPGAGGEPLL----TPDQISA--- 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : : | : :: | : | 436 KSAIKIIGDHTDKYAQGYFYYDSKKSGGLTVSHLRFGDTPIRSAYLVEHADLVACHTP-A 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 ADKITVBVV---KNAIETADGALDLYNK------YLDQVIPWQTFDB-----TIK 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46 ELSRFKQEYSQAASVLVGDIKTLIMDSQ-----DKYFEATQTVYEWCGVATQLLAAYI 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99 LLFDEYNEKKASAQKDILIKVLDDGITKLNEAQKSL-LVSSQSFN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.1%; Score 106.5; DB 4;
23.1%; Pred. No. 0.52;
tive 58; Mismatches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:

APPLICATION DATA:
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/08151
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: ATINIBALIO, PARMER: 40,489
REFERENCE/DOCKET NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...1231
;
SEQUENCE DESCRIPTION: SEQ ID NO: 5150:
US-09-107-532A-5150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
COMPATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1231 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 5150:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                             7310
                                                                                                                                                                                                                                                                                                                                                                                  STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 23.1%
Matches 78; Conservative
                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
         US-09-107-532A-5150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146
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SQAASVLVGDIKTLLMDSQDKYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQKD 114
                                                                                                                                                                      218 VONFFITLSNTVKQANKDIDAAKLKLTTEIAAIGEIKTETETT------RFYVDY 266
                                                                                                                                                                                                          757 V------NRDIORLKNDIEEOETLLGTIMPEEESAKVCLTDVTIMERFQMEL 802
                                      641 DLDRLKEEIEKSSKORAMLAGATA--VYSOFITQLTDENQSCCPVCORVFQTEAELQEVI 698
                                                                                   ----GLI-ISYSIAAGVVEGKLIPELKNKLKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 171; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL: NO
PORTINAL SOURCE:
NDIVIDUAL ISOLATE: Rad50.pro-translation of SEQ ID NO:54
US-09-168-595-148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transcripts Encoding Immunomodulatory Polypeptides
                                                                                                                                                                                                                                                                                     267 DDLMLSLLKEAAK-----KMINTCNE--YQKRHGKKTL 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 VEVVICNALETADGALDLYNKYLDQVIPWQTFDETIK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96;
                                                                                                                                                                                                                                                                                                                      Sequence 148, Application US/09168595
; Sequence 148, Application US/09168595
; Patent No. 655566;
dEMEMAL INFORMATION:
APPLICANT: Gregory Dolganov
; TITLE OF INVENTION: Transcripts Encoding II:
TITLE OF INVENTION: Polypeptides
NUMBER OF SEQUENCES: 151
CORRESPONDENCE ADDRESS:
ADDRESSEE: Deblinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
CONTRY: USA
ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.0%; Score 105.5; DE Best Local Similarity 18.8%; Pred. No. 0.72; Matches 75; Conservative 58; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 39,615
REFERENCE/FOCKET NUMBER: 4600-0111
TELECOMMUNICATION:
TELEPHONE: (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/168,595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
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169 QVDKIRKE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
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                                                                                     191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VQNFFTTLSNTVKQANKDIDAAKLKLTTEIAAIGEIKTETETT------RFYVDY 266
                           55 SQAASVLVGDIKTLLIMDSQDKYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQKD 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDELTSLLG------YPPNKKQLEDWLHSKSK------BINQTR---- 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 ILIKVLDDGITKLNEAQKSLLVSSQSFNNASGKLLALDSQLTNDFSEK-----SSYFQS 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 105.5; DB 2; Length 1312;
; Pred. No. 0.72;
58; Mismatches 96; Indels 171; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 VEVVKNAIETADGALDLYNKYLDQVIPWQTFDETIK-------ELSRFKQEY
                                                                                                                                                                                                                                                                                                                           Human RAD50 Gene and Methods of Use Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANS. OF RAD50 CDNA (SEQ. 54), NT. 389 TO 4324
                                                                                                              | : ::||| | : :||| | 803 KDVERKIAQQAAKLQGIDLDRTVQQVNQEKQEKQHKLDTV 842
                                                                                   267 DDLMLSLLKEAAK-----KMINTCNE--YQKRHGKKTL 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
PILING DATE: 17-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                       APPLICANT: Gregory Dolganov
APPLICANT: Gregory Dolganov
TITLE OF INVENTION: Human RAD50 Gene and M
NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0111.30
                                                                                                                                                                                                                                 Sequence 51, Application US/08687080 Patent No. 5965427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
TELEPRA: (415) 324-0960
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 1312 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 7.0%;
Best Local Similarity 18.8%;
Matches 75; Conservative 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INDIVIDUAL ISOLATE: INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 350 Cambz
CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE
                                                                                                                                                                                                                 US-08-687-080-51
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OY 253 IKTETETTREYUDYDDLMLSLLKBAAKKMINTCNEYOKRHGKKTL 297 DD 528 LNKRLDTLRNYIKKELNRNLLAVSNEITDQLNKGQNTL 565	RESULT 26 US-09-134-001C-4497 Sequence 4497 Sequence 1497 Patent No. 6380370 Fatent No. 6380370 Fatent No. 6380370 FILE REPERENCE: BEIDERAIDS FOR DIAGNOSTICS AND THERAPEUTICS FILE REPERENCE: GTC-007 CURRENT FILING DATE: 1998-08-13 FRIOR APPLICATION NUMBER: US 60/064,964 FRIOR APPLICATION NUMBER: US 60/064,964 FRIOR PAPLICATION NUMBER: US 60/065,779 FRIOR PILING DATE: 1997-08-14 FRIOR FILING DATE: 1997-08-14 FRIOR FILING DATE: 1997-08-14 FRIOR FILING DATE: 1997-08-14	LENGTH: 962 FRT PR	304	щ
DD 560 SDELTSLIGYPPNKKQLEDWLHSKSKEINQTR 591 QY 115 ILIKVLDDGITKLNEAQKSLLVSSQSFNNASGKLLALDSQLTNDFSEKSSYFQS 168 DD 592	169 QVDKIRKEAYAGAAGVVAGPF 1641 DLDRLKEEIEKSSKQRAMLAGATAVYSQFITQLTDENG 191	RESULT 25 US-09-710-279-1050 i Sequence 1050, Application US/09710279 j Patent No. 6703492 j GENERAL INFORMATION: APPLICANT: KIMMERLY, WILLIAM JOHN TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND. PROTEINS TILE REPRENCE: PU3480US CURRENT EILING DATE: 2000-11-09 CURRENT FILING DATE: 1999-11-09 PRIOR APPLICATION NUMBER: 60/164,258 PRIOR FILING DATE: 1999-11-09 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 1050 TYPE: PRIOR	; ORGANISM: Artificial Sequence ; FEATURE: ; OTHER INFORMATION: Description of Artificial Sequence: synthetic ; OTHER INFORMATION: amino acid sequence US-09-710-279-1050	Db 239 GNVLDÄÖEKLNAVNSSIPÄLNERÄKLIÄALDSYMPNIERILINVAANDVPÄQFPRI 293 QY 114DILIKVLDDGITKLNEAQKSLLVSSQSFNNASGKLLALDSQ

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LTEALLSLSN 422
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QFRSLGKYK 248
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                                                                                                                                                                                                                           58 --ASVLVGDIKTLIMDSQDKYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQKDI 115
                                                                                                                                                                                                                                                                                                                                          LIKVLDDGITKLNEAQKSLLVSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDKIRK 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 225 LSNTVKQ----ANKDIDAAKLKLTTEIAAIGE------IKTETETTRFYVDYDDLM 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                             194 HAYTCTQS-LVDGPRGKDLRASRAABINVIPHTTGAAKAIGLVIPSLSGKLKGHAQRVPT 252
                                                                                                                                                                                                      9 TVEVVKNAIETADGALDLYNKYLDQVIPWQTFD-ETIKELSRF--KQEYSQA----- 57
                                                                                                                                                                        Gaps
                                                                                                                                                                        99;
                                                                                                                                      Length 349;
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Sequence 1. Application US/09091117

Patent No. 6171589

GENERAL INFORMATION:
APPLICANT: The University of Melbourne
TITLE OF INVENTION: Mycoplasma Recombinant Polypeptides and
TITLE OF SEQUENCES:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                  Similarity 18.9%; Pred. No. 0.15;
Similarity 18.9%; Pred. No. 0.15;
Similarity 18.9%; Pred. No. 0.15;
Similarity 18.9%; Pred. No. 0.15;
Similarity 18.9%; Pred. No. 0.15;
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|34 VLISAPAGEMKTIVYNVNDDTLTPDDTIISVASCTTNCLAP--
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B: GREENLEE, WINNER and SULLIVAN P.C. 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/091,117
FILING DATE: 12 JUNE 1998
FILING DATE: 12 JUNE 1998
FILING DATE: 13-DEC-1996
FILING DATE: 13-DEC-1996
FILING DATE: 13-DEC-1995
ATTORNEY AGENT INFORMATION:
NAME: WINNER: BILDE DEC-1995
ATTORNEY AGENT INFORMATION:
NAME: WINNER: BILDE DEC-1995
TELECOMMUNICATION INFORMATION:
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                                                                   ; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13939
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TELEFAX: +1 303 499 8089
INFORMATION FOR SEQ ID NO: 2:
 1999-01-29
                                                                                                                                                                      61; Conservative
PRIOR FILING DATE: 19
NUMBER OF SEQ ID NOS:
SEQ ID NO 13939
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STREET: 53
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STATE: Co
COUNTRY:
                                               LENGTH: 349
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GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICANTON NUMBER: US 60/064,964
CURRENT PILING DATE: 1997-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5080
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                                                                                                                                                                                                             Query Match 6.9%; Score 103.5; DB 3; Best Local Similarity 21.2%; Pred. No. 0.77; Matches 59; Conservative 45; Mismatches 115;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EQNEAIRQVEAHSSDAIA-----
SEQUENCE CHARACTERISTICS:
LENGTH: 1030 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                 , MOLECULE TYPE: protein US-09-091-117-2
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US-09-134-001C-5080
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US-09-134-001C-5178
US-09-134-001C-5178
US-09-134-001C-5178
US-09-134-001C-5178
Sequence 5178, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: LYMIN DOUGETE-Stamm et al APPLICANT: LYMIN DOUGETE-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: DEPDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: UNMER: US/09/134,001C
CURRENT FILING DATE: 1997-08-13
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
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                                                                                                                                                                                                                                                                                                                                                              280 LVTIDGEDARDFDDAVYAEKRPGGGYRVVVAIADVSHYVRLDSALNEEAERGTSVYFPH 339
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                                                                                                                                                                                                                                                                                                                               67 ILLMDSOD-KYFEATQTVYEWCG-----VATQLLAAYILLFDEYNEKKASAQKDI---- 115
                                                                                                                                                                                                                                                                   9 TVEVVKANAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQ--EYSQAASVLVGDIK 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                164 SYFQSQVDKIRKEAYAGAAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNKLKSVQNFFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         224 ILSNIVKQANKDIDAAKLKLTIEIAAIGEIKTETETTRFYVDYDDL-----MLSLLKEAA
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19.5%; Pred. No. 0.84;
tive 63; Mismatches 130; Indels 7
                                                                                                                                               6.8%; Score 103; DB 4; Length 815; ilarity 17.5%; Pred. No. 0.61; Conservative 54; Mismatches 130; Indels
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                                                                     TYPE: PRT ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     400 OYFEGATDAIPKDR-----
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NUMBER OF SEQ ID NOS: 8252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 65; Conserv
                                                                                                                                                                                      Similarity
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                                                                                                                     US-09-328-352-4284
                                                                                                                                                                                                           58;
                          SEQ ID NO 4284
                                                  LENGTH: 815
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Matches 5
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Sequences relating to acinetobacter TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
                                                                                                                                                                                                                                                                   Sequence 1358, Application US/09710279
; Sequence 1358, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
APPLICANT: KIMMERIN'S HAPPHICOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; CURRENT APPLICATION NUMBER: 00164,258
; RIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PATENTIN Ver. 2.1
; SEQ ID NO 1358
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                               NTVKQANKDIDAAKLKLITEIAAIGEIKTETETTRFYVDYDDLMLSLLKEAAKKMINTCN 286
                                                         ----EYSQAASVLVGDIKTLLMDSQDKYFEATQTVYEWCGVAT----QLLAAY-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       255 -TETETTRFYVDYDDLMLSLLKEAAKKMINTCNE 287
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833 TAQGNDDVTEAQNNGTNTIQQVP 855
                                                                                                                               287 EYQ-----KRHGKKTLFEVP 301
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ORGANISM: Artificial Sequence
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US-09-328-352-4284
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US-09-710-279-1358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 AGAAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNKLKSVQNFFTTLSNTV----KQA 232
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Sequence 302, Application US/09492709A

Batent No. 6720139

GENERAL INPORMATION:
APPLICANT: Zyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Carr, Ally
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Tawancto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: GENER IDENTIFIED AS REQUIRED FOR PROLIFERATION IN
TITLE OF INVENTION: ESCHERICHIA COLI
FILE REFERENCE: ELITRA.001A
CURRENT APPLICATION NUMBER: US/09/492,709A
CURRENT FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 485

SOFTWARE: FELSEED for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                         ch 6.8%; Score 102; DB 3; Length 10182;
1 Similarity 20.7%; Pred. No. 33;
65; Conservative 47; Mismatches 104; Indels 98; Gaps
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PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3159
LENGTH: 10182
TYPE: PRT
CREADISM: Staphylococcus epidermidis
US-09-134-001C-3159
                                            60/055,779
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LENGTH: 2383
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ORGANISM: E.
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Best Local S
Matches 65
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APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
APPLICANT: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: 107196.132
CURRENT APPLICATION NUMBER: US 60/248,796A
CURRENT APPLICATION NUMBER: US 60/074,725
PRIOR PILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 20613
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FILE REPERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
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288 KIKFD-----DLKKEQNY----IDKLKQELKMIQESKYLJITYFTRLQSLKKDKDELVSLH 338
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                                                                                                                                                                                                                                             : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | : | | : | : | | : | : | | : | : | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    200 AGVVEGKLIPE-LKNKLKSVQN--FFTTLSNTVKQANKDIDAAKLKLTTEIAAIGEIKTE 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         198 IAAGVVEGKLIPELKNKLKSVQNFFTTLSNTVKQANKDIDAAKLKLTTEIAAIGEIK--- 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38 QTFDETIKELSRFKQEYSQAASVLVGDIKTLLMDSQDKYFEATQ-----TVYEWCGVATQ 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.8%; Score 102; DB 4; Length 722; 20.0%; Pred. No. 0.63; tive 51; Mismatches 99; Indels
                                            148 LLALDSQLTNDFSEKSSYFQSQVDKIRKEAYAGAAAGVVAGPF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                398 VIEEEIKRLYSEYNDLITK--KEELTKEMNNKNK 429
                                                                                                                                                                                                                                                                                                                                                     -TETETTREYVDYDDIMLSLLKEAAKKMINTCNE 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20613, Application US/09248796A Patent No. 6747137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3159, Application US/09134001C Patent No. 6380370 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KENKKLQLDYEDVLL 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             257 TETTRFYVDYDDLML 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Candida albicans
US-09-248-796A-20613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51; Conservative
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ORGANISM:
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578 NKAIQDPRLF--AEEKAVA-----DTRDQADGSRASVDSGSSEEQGGSSRALVSTLVP 628
                                                                                                                                                        132 KSLLVSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDKIRKEAYAGAAAGVVAG--P 189
                                                                                                                                    190 FGLIISY-SIAAGVVEGKLIPELKNKLK-SVONFFTTLSNTVKQ-----ANKDIDAAKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE LISTING
SEQUENCE LISTING
SEQUENCE CHARACTERISTICS:
EDUGTH: 746 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
DESCRIPTION: BEQ ID NO: 4
                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/09312157
Sequence 10. 6303341
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ANDREW C. HIATT, JULIAN
K.-C. MA, THOMAS LEHNER
TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
PROTEINS IN PLANTS AND THEIR USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 746;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86 WCGVAT-----QLLAAYILLFDEYNEKKASAQKDILI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
6.7%; Score 100.5; DE
Best Local Similarity 22.6%; Pred. No. 0.92;
Matches 45; Conservative 41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/312,157
FILING DATE: 14-May-1999
CLASSIFICATION: CURKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MBDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOS 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Gaise, Jeffrey W.
REGISTRATION NUMBER: 34,613
REFERENCE/DOCRET NUMBER: 212/127
TELECOMUNICATION INFORMATION:
TELEPHONE: (619) 552-8400
TELEPRAX: (619) 552-0159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/434,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSEB: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                      242 KLTTEIAAIGEIKTETETT 260
                                                                                                                                                                                                                                                        686 TOETSLGGKEEFVATTEST 704
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 19
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                                                                                                                                                                                            135 LV---SSOSFWNASGKLLALDSQLTNDFSEKSSYFQSQVDKIRKEAYAGAAAGVVAGPFG 191
                                                                                                                                                                        LIISYSIAAGVVEGKLIPELKNKLKSVQNFFTTLSNTVKQANK------DIDAAKL 241
                      ---SAQKDILIKVLDDGITKLNEAQKSL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human Polyimmunoglbulin Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: ANDREW C. HIATT, JULIAN
APPLICANT: K.-C. MA, THOMAS LEEINER
APPLICANT: K.-C. MA, THOMAS LEEINER
APPLICANT: K.-C. MA, THOMAS LEEINER
APPLICANT: K.-C. MA, THOMAS LEEINER
APPLICANT: K.-C. MA, THOMAS LEEINER
APPLICANTION: PROTEINS IN PLANTS AND THEIR USES
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
                                                                                                                                    805 AVLSGŠATSFNNONTAKTDVNGLAT--FDLKŠSKQEDNTVEVILE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.7%; Score 100.5; DB 3;
22.6%; Pred. No. 0.92;
... Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application DATOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/367,395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41; Mismatches
                                                                                                                                                                                                                                                                                            913 KLSOTEVNSHDGİATATLİSLKNGDY 938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
                                                                                                                                                                                                                                                          KLT-TEIAAIGEIKTETETTRFYVDY 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,000A
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08434000A
Patent No. 6046037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 34,613
REGISTRATION NUMBER: 212/312/SELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 552-8400
TELEPAX: (619) 552-8400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                              ------AAYILLFDEYNEKKA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 12/30/94
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: SEQUENCE LISTING
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               746 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
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Best Local Similarity
Matches 45; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-434-000A-4
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525 WCGVKQGHFYGETAAVYVAV----BERKAAGSRDVSLAKADAAPDEKVLDSG---FREIE 577 ...---KVLDDGITKLNEAQ 131 43; 셤

86 WCGVAT----QLLAAYILLFDEYNEKKASAQKDILI------KVLDDGITKLNEAQ 131

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Sequence 52, Application US/09315793
Sequence 52, Application US/09315793
Sequence 52, Application US/09315793
GENERAL INFORMATION:
APPLICANT: ROBERTS, Christopher J.
TITLE OF INVENTION: BSSENTIAL GENES OF YEAST AS TARGETS FOR ANTIFUNGAL
TITLE OF INVENTION: DRUGS
TITLE OF INVENTION: DRUGS
FILE REPERENCE: 9301-048
CURRENT APPLICATION NUMBER: US/09/315,793
CURRENT PILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 52.
                                                               578 NKAIQDPRLF--ABEKAVA-----DTRDQADGSRASVDSGSSERQGGSSRALVSTLVP 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             664 INLKNEYNDRK---STLDALSNQKSGYRHELSELAS-KNDDINRBAHQLNEIRKKYTWRK 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   132 KSLLVSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDKIRKEAYAGAAAGVVAG--P 189
                                                                                                                                                                           190 FGLIISY-SIAAGVVEGKLIPELKNKLK-SVQNFFTTLSNTVKQ-----ANKDIDAAKL 241
                                                                                                                                                                                                                            81 QTVYEWCGVATQLLAAYILLFDEYNEKKASAQKDI--LIKVLDDGI------TKL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128 NEAQKSL-----LVSSQ-----SFNNASGKLLALDSQLTNDFSEKSSY---- 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --- IISYSIA 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 LDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASVLVGDIKT---LLMDSQDKYFEAT 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INPOGNATION:
APPLICANT: Giot, Loic
APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REPERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT PILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/127,352
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21.6%; Pred. No. 1.6;
Live 47; Mismatches
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Patent No. 6753314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) ORGANISM: Saccharomyces cerevisiae US-09-315-793-52
                                                                                                                                                                                                                                                                                                                                                 242 KLTTEIAAIGEIKTETETT 260
                                                                                                                                                                                                                                                                                                                                                                                                                                       686 TOETSLGGKEEFVATTEST 704
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Best Local Similarity 21.69
Matches 63, Conservative
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766 ASSMKSLKNCQKELISTQILQFBAQNMDVSMNDVIGFFNEREADLKSQYEDKKKFVKEMR 825
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128 NEAQKSL----LVSSQ-----SFNNASGKLLALDSQLTNDFSEKSSY---- 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/08328254
Patent No. 5710022
GENERAL INFORMATION:
APPLICANT: Zhu, Xueliang
APPLICANT: Lee, Wen-Hwa
TITLE OF INVENTION: A No. 5710022el Nuclear Mitotic Phosphoprotein
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           200 AGVVEGKLIPELKNKLKSVQNFFTTLSNTVKQANKDIDAAKLKLTTEIAAI 250
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                                                                                                                                                                                                                                                                                                                        Length 1093;
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; OTHER INFORMATION: Polypeptide Accession Number YOL034W
US-09-538-092-701
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                                                                                                                                                                                                                                                                                                                   Query Match
6.7%; Score 100.5; D
Best Local Similarity 21.6%; Pred. No. 1.6;
Matches 63; Conservative 47; Mismatches
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuraPatSegFormatter Version 0.9
SEQ ID NO 701
LENGTH: 1093
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/141,239
FILING DATE: 22-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGIGTRATION NUMBER: 31,815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: P-CJ 1191
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,254
FILING DATE: 24-OCT-1994
CLASSIFICATION: 435
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy
                                                                                                                                                                                              NAME/KEY: misc_feature LOCATION: (0)...(0)
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STATE: California
COUNTRY: USA
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US-08-328-254-6
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2678 TLEVILOSSYKNILENELELTKMDKMSFVEKVNKWTAKETELQREMHEMAQKTAELQBELSG 2737
2738 EKNRLAGELQLILEEIKSSKÖQLKELTLENSELKKSLDCMHKDQVEKEGKVREEJAEYQL 2797
                                                                                                                                                                                         2856 ---LKATTQILBELKKTKMDNLKYVNQLKKENER-----AQGKMKLLIK-SCKQLEEEK 2905
                                                                                                                                                                                                                                                            2906 BILQKELSQLQAAQEKQKT--GTVMDTKVD-----BLTTBIKELKETLEEKTKEADEYL 2957
                                                              -----QKDILIKVLDDGITKLNEAQKS-----LLVSSQSFNNAS 145
                                                                                                                                                 146 GKLIALDSQLTNDFSEKSSYFQSQVDKIRKEAYAGAAAGVVAGPFGLIISYSIAAGVVEG 205
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                                                                                           2798 RLHE-AEKKKQALLLDTNKQYEVEIQTYREKLISKEECLSSQKLEIDLLKSSKEELNNS-
                                                                                                                                                                                                                                      206 KLIPELKNKLKSVQNFFTTLSNTVKQANKDIDAAKLKLTTEIAAIGE-IKTETETTRFYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08353700;
Sequence 1, Application US/08353700;
Patent No. 559919
GENERAL INFORMATION:
APPLICANT: YEN, TIMOTHY J.
APPLICANT: PEN, TIMOTHY J.
TITLE OF INVENTION: NUCLEIC ACID ENCODING A
TITLE OF INVENTION: TRANSIENTLY-EXPRESSED KINETOCHORE PROTEIN,
TITLE OF INVENTION: AND METHODS OF USE
TITLE OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: DANN, DORFWAN, HERRELL AND SKILLMAN
STREET: 1601 MARKET STREET, SUITE 720
CITY: PHILADELPHIA
STRATE: PA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CLASSIFICATION NUMBER: US/08/353,700
FILING DATE: 09-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: REED, JANET E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   2958 DKYCSLLISHEKLEKAKEMLETQVAHLCSQQSKQDSR 2994
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22.0%; Pred. No. 8.3;
:ive 63; Mismatches 129;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3248 amino acids
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                           100 LFDEYNEKKASA-
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Matches 74; Conser
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ORGANISM: HU
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US-08-353-700-1
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; Sequence 1154, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Glot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same;
; TITLE REFERENCE: 15966-54
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT PILING DATE: 2000-03-29
; PRIOR FILING DATE: 1999-04-01
; PRIOR FILING DATE: 2000-02-01
; PRIOR FILING DATE: 2000-02-01
; RIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SEQ ID NO 1154
; LENGTH: 3210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  206 KLIPELKNKLKSVQNFFTTLSNTVKQANKDIDAAKLKLTTEIAAIGE-IKTETETTRFYV 264
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                                                                                                                                                                                           Similarity 22.0%; Pred. No. 5.6; An Indels 74; Conservative 63; Mismatches 129; Indels
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OTHER INFORMATION: Polypeptide Accession Number P49454
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                               9
                                              SEQUENCE CHARACTERISTICS:
LENGTH: 2482 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 22.0
Matches 74; Conservative
                             INFORMATION FOR SEQ ID NO:
                                                                                                                                 , MOLECULE TYPE: protein US-08-328-254-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature LOCATION: (0)...(0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
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US-09-538-092-1154
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                                                                                                                                                                                                           Local Sim
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2798 RLHE-AEKKHQALLLDTNKQYEVEIQTYREKLTSKEECLSSQKLEIDLLKSSKEELNNS- 2855
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                                                                                                                                                                                                                                                        8856 ---LKATTQILEELKKTKMDNLKYVNQLKKENER-----AQGKMKLLIK-SCKQLEEEK 2905
                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 032794-03134,000C CURRENT APPLICATION NUMBER: US/09/134,000C CURRENT FILING DATE: 1998-08-13 PRIOR PILLING DATE: 1998-08-15 NUMBER OF SEQ ID NOS: 6812 SOFTHWARE: PARONE ILING DATE: 1937-08-15 NUMBER OF SEQ ID NOS: 6812
2678 TLEVLQSSYKNLENELELTKMDKMSFVEKVNKMTAKETELQREMHEMAQKTAELQEELSG 2737
                                                                  100 LFDEYNEKKASA-----QKDILIKVLDDGITKLNEAQKS-----LLVSSQSFNNAS 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                226
                                                                                                                                                                                                            146 GKLLALDSQLTNDFSEKSSYFQSQVDKIRKEAYAGAAAGVVAGPFGLIISYSIAAGVVEG 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 LVGDIKTLLMDSQ-DKYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQKDILIKV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  247 LAGSIGTLMLAKKVSAAFTAWOKATEGLSIAQAILNSTWL------ANPFVAILAAV 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---KLTTEIAAIGEIKTETETTRF-YV-D 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----GNAADWVKNKWNGTKEFFSGLW 391
                                          ---QTVYEWCGVATQLLAAYIL 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MTEIVADKTVEVVKNAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAMEXKEY: MISC FEATURE
1 LOCATION: (600)..(600)
1 OTHER INFORMATION: Amino acid 600 is Xaa wherein Xaa = any amino acid.
US-09-134-000C-3870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.6%; Score 100; DB 4; Length 604;
22.0%; Pred. No. 0.75;
tive 57; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             2958 DKYCSLLISHEKLEKAKEMLETQVAHLCSQQSKQDSR 2994
                                                                                                                                                                                                                                                                                                                                                                                     D-YDDLMLSLLK-EAAKKMINT----CNEYQKRHGK 294
                                          57 AASVLVGDIKTLLMD---SQDKYFEAT----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3870, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 22.08
Matches 70; Conservative
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                                                                                                                                2798 RIHE-AEKKHQALLIDTUKQYEVEIQTYREKLISKECLSSQKLEIDLIKSSKEELNNS-2855
                                                                                                                                                                                                                     ---LKATTQILEELKKTKMDNLKYVNQLKKENER-----AQGKMKLLIK-SCKQLEEEK 2905
                                                2738 EKNRLAGELQLILEEIKSSKDQLKELTLENSELKKSLDCWHKDQVEKEGKVREEIAEYQL 2797
                                                                                                                                                                                                                                                                                                       16;
                                                                                                                                                                                            146 GKLLALDSQLTNDFSEKSSYFQSQVDKIRKEAYAGAAAGVVAGPFGLIISYSIAAGVVEG 205
                                                                                                        100 LFDEYNEKKASA-----QKDILIKVLDDGITKLNEAQKS-----LLVSSQSFNNAS 145
                                                                                                                                                                                                                                                                            206 KLIPELKNKLKSVQNFFTTLSNTVKQANKDIDAAKLKLTTEIAAIGE-IKTETETTRFYV 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Year, Timothy J.
APPLICANT: Ratiner, Jerome B.
TITLE OF INVENTION: Nucleic Acid Encoding a Transiently
TITLE OF INVENTION: Syressed Kinetochore Protein, and Methods of Use
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                      ----- QTVYEWCGVATQLLAAYIL
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22.0%; Pred. No. 8.3;
ive 63; Mismatches 129; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
BELING DATE: 09-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet B.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-404
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
"FANGTH: 3248 amino acida
"ANANTION ANANTION ANANTION:
"REGISTRATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
"FANGTH: 3248 amino acida
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ZUP: 19103-2307

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

"WUTTER: IBM PC compatible
"""""" PC-DOS/MS-DOS
                      AASVLVGDIKTLLMD---SQDKYFEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application PC/TUS9516216 GENERAL INFORMATION:
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Best Local Similarity 22.0
Matches 74; Conservative
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HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 VLDDGITKLNBAQKSLLVSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQV----DKIR 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1346 EEEEERKHNLEKQIATLHAQVADMKKKMEDSVGCLETAEEVKRKLQKDLEGLSQRHEEKV 1405
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| YVEAQLQELQVKFNEGERVRTELADXVTKL------QVELDNVTGILSQSDSKSSK 1298
                                                                                                                                                                                                                                                                           89
                                                                                                                                                                                                                                                                                                                               ASVIVGDIKTLLMDSQDKXFEAT----QTVYEWCG-VATQLLAAVILL----FDEYNEK 107
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                                                                                                                                                                                                                                                                                                                                                                                                                  108 KASAQ-KDILIKV-----LDDGITKLNEAQKSLLVSSQSFNNASGKLLALD---SQ
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                                                                                                                                                                                                                                                 3 EIVADKTVEVVKNAIETADGALDLYNKYLDQV-IPWQTFDETIK----ELSRFKQEYSQA
                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                155 LTNDFSEKSSYFQSQVDKIRKEAYAGAAAGVVAGPFGLIISYSIAAGVVEGK-----
                                                                                                                                                                                                              95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           248 AAIGEIKTETETTRFYVDYDDLMLSLLKEAAKKMINTCNEYQKR 291
                                                                                                                                                                     6.6%; Score 99.5; DB 4; Length 1:
llarity 20.6%; Pred. No. 4.9;
Conservative 59; Mismatches 119; Indels
                 TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
COTHER INFORMATION: Polypeptide Accession Number P35579
US-09-238-092-1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hyman, Paul APPLICANT: Hyman, Paul APPLICANT: Williams, Mark TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES FILE REPERSENCE: 8471-010-999 CURRENT APPLICATION NUMBER: US/09/914,259 CURRENT FILING DATE: 2000-11-21 NUMBER OF SEQ ID NOS: 180 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.6%; Score 99.5; DB 4;
20.0%; Pred. No. 14;
tive 51; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 11, Application US/09914259
; Patent No. 6495336
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US-09-914-259-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 65; Conserv
                                                                                                                                                                                Query Match
Best Local Similarity
Matches 71; Conserve
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APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: 0599-02-12
PRIOR PILING DATE: 1999-02-13
PRIOR FILING DATE: 1999-02-13
PRIOR FILING DATE: 1999-02-13
PRIOR FILING DATE: 1999-02-13
PRIOR FILING DATE: 1999-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 20284
LENGTH: 1078
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; Sequence 1077, Application US/09538092
; Patent No. 6753314
; GENERAL INPORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Giot, Loic
; APPLICANT: Giot, Loic
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same; TITLE OF INVENTION: WUMBER: US/09/538,092
; CURRENT APPLICATION NUMBER: 60/127,352
; CURRENT FILING DATE: 1999-04-011
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 2000-03-29
; PRIOR FILING DATE: 2000-03-04
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatsGeformatter Version 0.9
; SEQ ID NO 1077
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Best Local Similarity 20.5%; Pred. No. 2;
Matches 70; Conservative 57; Mismatches
                                                                                               3-09-248-796A-20284
Sequence 20284, Application US/09248796A
Patent No. 6747137
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452 YIGPYVTGIKNAFKMVVN 469
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                                                                          ----IIEELNTKIIEEEKKTLELKDK 363
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APPLICANT: Enemer, Guido P.
APPLICANT: Siderovai, David P.
APPLICANT: Samzami, Naoufal
APPLICANT: Sum, Santos A.
APPLICANT: Sum, Evyan E.L.
TITLE OF INVENTION: APOPTOSIS-INDUCING FACTOR FILE REFERENCE: 01017/36780
CURRENT APPLICATION NUMBER: US/09/447,497
CURRENT FILING DATE: 1999-11-23
EARLIER APPLICATION NUMBER: 60/109,595
EARLIER APPLICATION NUMBER: 60/109,595
BARLIER FILING DATE: 1998-11-23
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
                                                                          319 VYEMEQDKKVENSNKEEIQEKET-----
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Patent No. 6773911
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Patent No. 6773911
GENERAL INFORMATION:
APPLICANT: Penninger, Josef M.
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ORGANISM: Homo sapiens
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US-09-447-497-14
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LENGTH: 526
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125 TKINEAQKSLLVSSQSFNNA----SCKLLALDSQLTNDFSEKSS-----YFQS-QV 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --V 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73 QD---KYPEATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQ----KDILIKVLDD--GI 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37 WQTFDETIKELSRFKQ-----EYSQAAS-------VLVGDIKTLLMDS 72
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ORGANN Homo sapiens
ORGANN HOMO Sapiens
OTHER INFORMATION: human apoptosis-inducing factor (hAIF isoform #1
OTHER INFORMATION: ); hAIF-alt-exon-Gold; mature polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           330 ETDHIVAAVGLEPNVELAKTGGLEIDSDFGGFRVN 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            231 QANKDIDAAKLKLTTEIAAIGEIKTETETTRFYVD 265
APPLICANT: Kroemer, Guido P.
APPLICANT: Siderovsi, David P.
APPLICANT: Salerovsi, David P.
APPLICANT: Saneani, Nacutal
APPLICANT: Susin, Santces A.
TITLE OF INVENTION: APPRICAL:
FILE REFERENCE: 0101/36780
CURRENT APPLICATION UNMERR: US/09/447,497
CURRENT FILING DATE: 1999-11-23
EARLIER APPLICATION NUMBER: 60/109,595
EARLIER FILING DATE: 1998-11-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Recently Josef M. APPLICANT: Riderova; Josef M. APPLICANT: Siderova; Josef M. APPLICANT: Siderova; David P. APPLICANT: Zamazami, Nacoufal APPLICANT: Susin, Santos A. APPLICANT: Snow, Bryan E. L. TITLE OF INVENTION: APPRICAND: APPLICANTON: APPLICANTON NAMBER: US/09/447,497 CURRENT FILING DATE: 1999-11-23 EARLIER APPLICATION NUMBER: 60/109,595 BARLIER FILING DATE: 1999-11-23 NUMBER OF SEQ ID NOS: 25 SEQ ID NO 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.6%; Score 99; DB 21.8%; Pred. No. 0.82 tive 46; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12, Application US/09447497
Patent No. 6773911
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
LENGTH: 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens
US-09-447-497-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 60; Conserv
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us-09-993-292b-28.rai

Search completed: January 5, 2005, 10:59:05 Job time: 20.9474 secs

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January 5, 2005, 10:52:17 ; Search time 17.4424 Seconds (without alignments) 1671.423 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                      OM protein - protein search, using sw model
                                                                                                                                                               Run on:
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US-09-993-292B-28 1508 1 MTEIVADKTVEVVKNAIETA......TCNEYQKRHGKKTLFEVPEV 303 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 50 summaries

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ro.	Description	hemolysin E - Esch	E E	probable pore form	in H	hypothetical prote				transmembrane prot	hypothetical prote	Ψ	membrane associate	ORF MSV156 hypothe	nonmuscle myosin I	myosin heavy chain	myosin II heavy ch	probable myosin he	probable alpha-car		rhoptry protein -	hemolysin A - Esch	hypothetical prote		hypothetical prote	급	hyaluronan recepto	myosin-like protei	٠.	myosin heavy chain	
SUMMARIES	Ω	C64864	E90838	E85696	AE0673	875986	B59102	T05634	S18199	AH1369	B70232	AG1739	A97222	T28317	A59282	A36014	S61477	F84730	B84800	T14867	T28676	S10056	T22716	A35254	S48385	G97827	JC4298	8	267087	82	
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•	& Query Match	100.0	0.66	99.0	92.8			•			7.8		•	7.6	7.6	7.6	7.6	7.6	7.6	7.6	7.6	7.5	7.5	7.5	7.5	7.4	7.4	7.4	7.4	7.4	
	Score	1508	1493	1493	1400	133.5	126	122	120	117.5	117.5	116.5	115.5	115	115	115	115	114.5	114	114	114	113.5	113	113	112.5	112	112	112	111.5	111.5	
	Result No.	:	7	٣	4	ഹ	9	7	80	6	. 10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	

protein T22A3.8 (i	hypothetical prote	laminin alpha chai	protein R06B10.2 [hemolysin A - Esch	hypothetical prote	gas-vesicle protei	bPS2 protein homol	ATPase involved in	364K Golgi complex	minor capsid prote	hypothetical prote	hypothetical prote	conserved hypothet	type I site-specif	conserved hypothet	protein T23J18.9 [endopeptidase La (nuclear/mitotic ap	hypothetical prote	hypothetical prote
F87908	T23064	T43291	H88391	LEECA	T12818	T44967	A90394	G97236	JC5837	T13216	A64465	S54091	H69378	T44802	A90551	A86248	E97778	T30336	T18281	T13329
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2823	2823	3102	934	1023	478	540	587	1163	3187	1608	1005	266	886	1025	2819	636	779	2253	1474	1517
7.4	7.4	7.4	7.4	7.4	7.3	7.3	7.3	7.3	7.3	7.3	7.2	7.2	7.2	7.2	7.2	7.2	7.2	7.2	7.1	7.1
111.5	111.5	111.5	111	111	110.5	110.5	110	110	110	109.5	109	108.5	108.5	108.5	108.5	108	108	108	107	107
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	20

ALIGNMENTS

RESULT 1 C64864 hemolysin N,Alternat C;Species C;Date: 12 C;Accessic R;Blattnee: 2 A;Tience: 2 A;Tience: 2 A;Tience: 2 A;Accessic A;Accessic A;Accessic A;Accessic A;Accessic A;Accessic A;Accessic A;Accessic A;Accessic A;Accessic A;Accessic A;Accessic A;Accessic A;Accessic A;Accessic	RESULT 1 C64864
Cybenetics: Cyfunction: Cyfunction: AyDescripti AyNote: por Cyfoywords: Cyfoywords: F;181-197/D	A;Gene: hlyB; hpr A;Gene: hlyB; hpr C;Function: A;Description: hemolytic activity A;Description: hemolytic activity C;Superfamily: Escherichia coli hemolysin E C;Superfamily: Escherichia coli, hemolysis; transmembrane protein C;Keywords: cytolysis; cytotoxin; hemolysis; transmembrane protein F;181-197/Domain: transmembrane #status predicted <tmm> F;123/Active site: Asp #status predicted</tmm>
Quer Best Matc	Query Match Best Local Similarity 100.0%; Pred. No. 2.4e-87; Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
\$ Q	1 MTEIVADKTVEVVKNAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASV 60
op ox	61 LVGDIKTLIANDSQDKYFBATQTVYEWCGVATQLIAAYILLFDBYNEKKASAQKDILIKVL 120
Oy Op	121 DDGITKLNEAQKSLLVSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDKIRKEAYAG 180
8 %	181 AAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNKLKSVONFFTTLSNTVKQANKDIDAAK 240

ö

Gaps

6

9 62 240

242

300

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A;Molecule type: DNA
A;Residues: 1-305 <STO>
A;Cross-references: UNIPROT:O9REB3; GB:AE005174; NID:g12514879; PIDN:AAG56033.1; GSPDB:G]
A;Experimental source: strain O157:H7, substrain EDL933
A;Genetics:
A;Genetics:
A;Genetics: C;Superfamily: Escherichia coli hemolysin E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            haemolysin HlyE [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain C). C;Species: Salmonella enterica subsp. enterica scrovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: AE0673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Riberhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Asture 413, 848-852, 201,
Asture 413, 848-852, 201,
Asture 8 Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serova, A; Reference number: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LVGDIKTLIADSQDKYFBATQTVYEWCGVATQLIAAYILLFDEYNEKKASAQKDILIKVL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 DDGITKLNEAQKSLLVSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDKIRKEAYAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Residues: 1-305 <PAR>
A,Cross-references: GB:AL513382; PIDN:CAD01758.1; PID:g16502606; GSPDB:GN00176
                                                                                                                                                                                                                                                                                                                                                                                   61 LVGDIKTLLMDSQDKYFBATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQKDILIKVL 120
                                                                                                                                                                                                                                                                                                                                                                                                                 63 LVGNIKTLLADSQDKYFEATQTVYSWCGVATQLLAAYILLFDEYNEKKASAQKDILIKVL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DDGITKLNEAQKSLLVSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDKIRKEAYAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243 LKLTTEIAAIGEIKTETETTRFYVDYDDLMLSLLKEAANKMINTCNEYQKRHGKKTLFEV 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LKLTTEIAAIGEIKTETTRFYVDYDDLMLSLLKEAAKKMINTCNEYQKRHGKKTLFEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 AAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNKLKSVQNFFTTLSNTVKQANKDIDAAK
                                                                                                                                                                                                                                                                                                                                    3 MTEIVADKTVEVVKNAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 305;
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                                                                                                                                                                                                Score 1493; DB 2;
Pred. No. 2.1e-86;
                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Superfamily: Escherichia coli hemolysin E
                                                                                                                                                                                                Query Match
Best Local Similarity 99.0%;
Matches 300; Conservative
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Matches 276; Conservative
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                                                                                                                                                                                                                                                                                                                  C;Species: Escherichia coli
C;Species: Bacherichia coli
C;Species: Bacherichia coli
C;Date: 18-Uul-2001
Bequence_revision 18-Uul-2001 #text_change 09-Uul-2004
C;Date: 18-Uul-2001
Bequence_revision 18-Uul-2001 #text_change 09-Uul-2004
C;Accession: E90838
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and gency A;Reference number: A99629; MUD:21156231; PMID:11258796
A;Accession: E90838
A;Accession: E90838
A;Actus: preliminary
A;Molecule type: DNA
A;Residues: 1-305 c-MAY
A;Residues: 1-305 c-MAY
A;Access-references: UNIRROT:09REB3; GB:BA000007; PIDN:BAB35100.1; PID:gl3361141; GSPDB:C
C;Genetics: ECs1677
C;Superfamily: Escherichia coli hemolysin E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 3
E85696
E95696
Eprobable pore forming hemolysin hlyE [imported] - Escherichia coli (strain O157:H7, subserbacies: Escherichia coli
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: E85696
E;Perb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
E;Perb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
E;Perb-2001 #sequence Diavis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: E85696
A;Status: preliminary
                                                                                                                                                                                                                                                                                            hemolysin E [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DDGITKLINEAQKSLLVSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDKIRKEAYAG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNKLKSVQSFFTTLSNTVKQANKDIDAAK 242
                                  LKLTTEIAAIGEIKTETETTRFYVDYDDLMLSLLKEAAKKMINTCNBYQKRHGKKTLFEV 300
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Pred. No. 2.1e-86;
2; Mismatches 1;
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-652 <0XL>
A;Cross-references: UNIPROT:Q9X360; GB:AF065404; NID:g4894216; PIDN:AAD32394.1; PID:g489
A;Experimental source: strain Sterne
A;Note: similar to hypothetical protein; PFB0765w (980 as); Plasmodium falciparum (AB001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.F
Database, February 1999
                          harboria
                    A;Title: Sequence and organization of pXO1, the large Bacillus anthracis plasmid A;Reference number: A59091; MUID:99445483; PMID:10515943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53 EYSQAASVLVGDIKTL--LMDSQDKYFEATQTVYEWC-GVATQLLAAYILLFDEYNEKKA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | : : | | : | : | : | | EWEEEKSKILIDEIYSLQTKILDSVTRISEDLQKKLQMCNGALTQ------EFTRRKHL 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 ILIKVLDDGITKLNEAQK-----SLLVSSQSFNNASGKLLALDSQLTNDFSE 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       162 KSSYFQSQVDKIRKEAYAGAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNKLKSVQNF 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      222 FITLSNIVKQANKDIDAAKLKLITELAAIGEIKTETETTRFYVDYDDLMLSLLKEAAKKM 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----SELVQLNKKI 472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein F20D10.190 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TLLMDSQDKYFEATQ-----TVYEWCGVATQLLAAYILLFDEYNE--KKASAQKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         282 NKLKESÓSRLLELNKKDSNRLELNSEIKKLNDRKAELLSLIMELIKOGSEFDKKIKNEKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 DKTVEVVKNAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASVLVGDIK
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                                                                                                                                                                                                                                                                                                                                                                                                        Length 652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           57; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-1496 <BEV>
A;Cross-references: UNIPROT:Q9SZK7; EMBL:AL035538
A;Experimental source: cultivar Columbia; BAC clone F20D10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72; Mismatches 124;
                                                                                                                                                                                                                                                                                                                                                                                                     8.4%; Score 126; DB 2; 20.5%; Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Map position: 4
A;Introns: 1042/2; 1212/2; 1232/1; 1263/3; 1349/3
A;Note: F20D10.190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     282 INTCNEYQKRH------GKKTLFEVPEV 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---- DELGKRHKHRQELEASOKKALDEAKEI 499
Bacteriol. 181, 6509-6515, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C.Accession: T05634 ". Kutzner, Subwan, M.; Wedlar, H.; Kutzner, submitted to the Protein Sequence A;Reference number: 215420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 18.99
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Best Local Similarity
--hos 68; Conserva
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                                                                                                                                                                                                                                                                                      C;Genetics:
A;Gene: pXO1-90
A;Genome: plasmid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Residues: 1-584 <KAN>
A, Cross-references: UNIPROT.Q55486; EMBL.D64006; GB.AB001339; NID.g1001291; PIDN.BAA1083
A, Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C, Superfamily: arginine-tRNA ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety-PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S75986
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C;A
                                                                                AAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNKLKSVQNFFTTLSNTVKQANKDIDAAK 240
                                                                                                              LKLTTEIAAIGEIKTETETTRFYVDYDDLMLSLLKEAAKKMINTCNEYQKRHGKKTLFEV 300
                                                                                                                                                                                                                       243 LKLATEIAAIGEIKTETETTRFYVDYDDLMLSLLKGAAKKMINTCNEYQQRHGKKTLFEV 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | : : ||:| | : | | : | 342 DAGQANHFAQFPQVAEKAGILTDPTQVV---HVPFGLVKGEDGKKLKTRAGDTIRLKDLL 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DDGVKKLNEAQKSLLTSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDRIRKEAYAG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---LLMDSQDKYFEATQTVYEWCGVATQ-----LLAAYILLFDEYNEKKASAQKDI 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIK-----VLDDGITKLNEAQKSLLV--SSQSFNNASGKLLALDSQLTNDFSEKSSYF- 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -QSQVDKIRKEAYAGAAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNKLKSVQNFFTTL 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNTVKOANKDIDAAKLKLT------TEIA---AIGEIK---TETETTRFYVDYDD 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------KDL 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 EVVKNAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASVL-VGDIKT-- 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S75986
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hypochetical protein BBG10 - Lyme disease spirochete plasmid G/lp28-2 (Species: Borrelia burgdorferi (Lyme disease spirochete) (Datte: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Ju1-2004 (Species: Borrelia burgdorferi (Lyme disease spirochete) (Species: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Ju1-2004 (Species: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Ju1-2004 (Species: 13-Feb-1998 #text_change 09-Ju1-2004 (Species: 13-Feb-1998 #text_change 09-Ju1-2004 (Species: 13-Feb-1998 #text_change 09-Ju1-2004 (Species: 13-Feb-1998 #text_change 09-Ju1-2004 (Species: 13-Feb-1998 #text_change 09-Ju1-2004 (Species: 13-Feb-1998 #text_change 09-Ju1-2004 (Species: 13-Feb-1998 #text_change 09-Ju1-2004 (Species: 13-Feb-1998 #text_change 09-Ju1-2004 (Species: 13-Feb-1998 #text_change 09-Ju1-2004 (Species: 13-Feb-1998 #text_change 09-Ju1-2004 (Species: 13-Feb-1998 #text_change 09-Ju1-2004 (Species: 13-Feb-1998 #text_change 09-Ju1-2004 (Species: 13-Feb-1998 #text_change 09-Ju1-2004 (Species: 13-Feb-1998 #text_change 09-Ju1-2004 (Species: 13-Feb-1998 #text_change 09-Ju1-2004 (Species: 13-Feb-1998 #text_change 09-Ju1-2004 (Species: 13-Feb-1998 #text_change 09-Ju1-2004 (Species: 13-Feb-1998 #text_change 09-Ju1-2004 (Species: 13-Feb-1998 #text_change 09-Ju1-2004 (Species: 13-Feb-1998 #text_change 09-Ju1-2004 (Species: 13-Feb-1998 #text_change 09-Ju1-2004 (Species: 13-Feb-1998 #text_change 09-Ju1-2004 (Species: 13-Feb-1998 #text_change 09-Ju1-2004 (Species: 13-Feb-1998 #text_change 09-Ju1-2004 (Species: 13-Feb-1998 #text_change 09-Ju1-2004 (Species: 13-Feb-1998 #text_change 09-Ju1-2004 (Species: 13-Feb-1998 #text_change 09-Ju1-2004 (Species: 13-Feb-1998 #text_change 09-Ju1-2004 (Species: 13-Feb-1998 #text_change 09-Ju1-2004 (Species: 13-Feb-1998 #text_change 09-Ju1-2004 (Species: 13-Feb-1998 #text_change 09-Ju1-2004 (Species: 13-Feb-1998 #text_change 09-Ju1-2004 (Species: 13-Feb-1998 #text_change 09-Ju1-2004 (Species: 13-Feb-1998 #text_change 09-Ju1-2004 (Species: 13-Feb-1998 #text_chan
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A;Gross-references: UNIPROT:050733; GB:AE000786; NID:g2690008; PIDN:AAC66075.1; PID:g2690
A;Experimental source: strain B31
Riglaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker.
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mai, A;Authors: Kreft, J.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Scatus: prellminary
A;Molecule type: DNA
A;Residues: 1-927 <GIA>
A;Kross-references: UNIPROT:QSY4S2; GB:NC_003210; FIDN:CAD00438.1; PID:gl6411848; GSPDB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 EATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQKDILIKVLDDGITKLNEAQKSLLVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            333 IDŠLVDGŠNKLSAGLKELDGNLTDKOGKLAQLKOGMNDLQQGIDQLNQSVNGEDAA----
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20.2%; Pred. No. 12;
iive 63; Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 7.8%; Score 117.5; DB 2; Local Similarity 21.1%; Pred. No. 9.7; leg 73; Conservative 33; Mismatches 141;
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Matches 78; Conserv
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Best Local Si
Matches 73;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151
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ELQEATIQGSGNSALSKLKNKFRNLEN 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transmembrane protein [imported] - Listeria monocytogenes (strain EGD-e) C;Species: Listeria monocytogenes C;Species: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004 C;Accession: AH1369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MTEIVADKTVEVVKNAIETADGALDLYNK - YLDQVIPWQT - FDETIKELSRFKQEYSQA
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8.0%; Score 120; DB 2; Length 10;
Best Local Similarity 19.0%; Pred. No. 7.8;
Matches 62; Conservative 73; Mismatches 132; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        423 QYEEISIMFLVLSRTVSEAQSRLANAKDKQIKDEKREG 460
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DD 389	RESULT 12 A97222 membrane associated methyl-chemotaxis protein, HAMP domain containing [imported] - Clost C; Species: Clostridium acetobutylicum C; Species: Clostridium acetobutylicum C; Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004 C; Accession: A97222 R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Bacteriol. 183, 4823-4838, 2001 A;Title: Ganome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo A;Reference number: A96900; MUD:21359325; PMID:21359325 A;Status: preliminary A;Nocession: A97222 A;Status: preliminary A;Residues: 1-664 <kur> A;Residues: 1-664 <kur> A;Coss-references: UNIPROT:Q97FV9; GB:AE001437; PIDN:AAK80564.1; PID:g15025642; GSPDB:G C;Genetics: A;Gene: CAC2617</kur></kur>	Query Match	Qy 246 EIAAIGEIKTETETTRFYUDYDDLMLSLLKEAAKKMINTCNEYQ 289
Db 552 VGVEKSVNEFNNSNYDFVNEYQNLLKEKESRERIIKTLPHTDQVSALQKLNDEINEKNK 611 Qy 50 -FKQEYSQAASVLVGDIKTLLMDSQDKYFBATQTVYFWCGVA 90 1: 1	QY 91 TQLIAAYILLFDEYNEKKASAQKDILIKVLDDGITKLNEAQK	RESULT 11 AG1713 Listeria innocua (strain Clip11262) C;Species: Listeria innocua C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004 C;Accession: AG1739 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004 C;Accession: AG1739 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke C;Dominguez-Bernal, G.; Duchaud, B.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H D; Jonnes, L.M.; Karst, U. Science 294, 849-852, 2001 A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M A;Title: Comparative genomics of Listeria species A;Actaus: Ag1739 A;Actaus: Ag1739 A;Actaus: Preliminary A;Nolecule type: DNA A;Residues: 1-927 <gla> A;Actaus: L-927 <gla> A;Actaus: L-927 <gla> A;Actaus: L-927 <gla> A;Actaus: L-927 <gla> A;Actaus: L-927 <gla> A;Actaus: L-927 <gla> A;Actaus: L-927 <gla> A;Actaus: L-927 <gla> A;Actaus: L-927 <gla> A;Actaus: L-927 <gla> A;Actaus: L-927 <gla> A;Actaus: L-927 <gla> A;Actaus: L-927 <gla> A;Actaus: L-927 <gla> A;Actaus: L-927 <gla> A;Actaus: L-927 <gla> A;Actaus: L-927 <gla> A;Actaus: L-927 <gla> A;Actaus: L-927 <gla> A;Actaus: L-927 <gla> A;Actaus: L-927 <gla> A;Actaus: L-927 <gla> A;Actaus: L-927 <gla> A;Actaus: L-927 <gla> A;Actaus: L-927 <gla> A;Actaus: L-927 <gla> A;Actaus: L-927 <gla> A;Actaus: L-927 <gla> A;Actaus: L-927 <gla> A;Actaus: L-927 <gla> A;Actaus: L-927 <gla> A;Actaus: L-927 <gla> A;Actaus: L-927 <gla> A;Actaus: L-927 <gla> A;Actaus: L-927 <gla> A;Actaus: L-927 <gla> A;Actaus: L-927 <gla> A;Actaus: L-927 <gla> A;Actaus: L-927 <gla> A;Actaus: L-927 <gla> A;Actaus: L-927 <gla> A;Actaus: L-927 <gla> A;Actaus: L-927 <gla> A;Actaus: L-927 <gla> A;Actaus: L-927 <gla> A;Actaus: L-927 <gla> A;Actaus: L-927 <gla> A;Actaus: L-927 <gla> A;Actaus: L-927 <gla> A;Actaus: L-927 <gla> A;Actaus: L-927 <gla> A;Acta</gla></gla></gla></gla></gla></gla></gla></gla></gla></gla></gla></gla></gla></gla></gla></gla></gla></gla></gla></gla></gla></gla></gla></gla></gla></gla></gla></gla></gla></gla></gla></gla></gla></gla></gla></gla></gla></gla></gla></gla></gla></gla></gla></gla></gla></gla></gla></gla></gla></gla></gla></gla>	Query Match 7.7%; Score 116.5; DB 2; Length 927; Best Local Similarity 21.1%; Pred. No. 11; 11 Matches 71; Conservative 34; Mismatches 124; Indels 107; Gaps 11; Qy 3 EIVADKTVEVVKNAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAA 58 1 :

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Mycosin heavy chain, nonmuscle - fruit fly (Drosophila melanogaster)
Nycontains: myosin ArPase (BC 3.6.4.1)
C;Species: Drosophila melanogaster
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
R;Retchum, A.S.; Stewart, C.T.; Stewart, M.; Kiehart, D.P.
R;Retchum, A.S.; Stewart, C.T.; Stewart, M.; Kiehart, D.P.
A;Title: Complete sequence of the Drosophila nonmuscle myosin heavy-chain transcript: Con A;Title: Complete MoulD:90349506; PMID:2117279
A;Accession: A36014;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1263 KTVLEKAKGTLEAENADLATELRSVNSSRQENDRRRKQAESQIAELQV---KLAEIERAR 1319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1320 SELGEKCTKLQOBAENITNQLEBAELKASAAVKSASNMESQLTEAQQLLEBETRQKLGLS 1379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1380 SKLRQIESEKBALQEQLEEDDEAKRNYERKLAEVTTOMQEIKKKAEBDADLAKELEEGKK 1439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126 KLN-----EAQ-KSLLVSSQSFNNASGKL-----LALDSQLTNDF8-EKSSYFQSQ 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----DQVIPWQTFDETIKELSRFK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QEYSQAASVLVGDIKTLLMDSQDKYFEATOTVYEWCGVATQLLAAYILLFDEYNEK----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C, Superfamily: wyosin heavy Chain; wyosin motor domain homology C, Superfamily: myosin heavy Chain; worsin motor domain homology C, Superfamily: myosin heavy chain, form I #status predicted <MAI> P;1-2017/Product: myosin heavy chain, form II #status predicted <MAI> P;45-2017/Product: myosin motor domain homology <MMOT> P;25-232/Region: myosin motor domain homology <MMOT> P;25-232/Region: actin binding #status predicted F;788-2017/Pomain: actin binding #status predicted F;888-2017/Domain: coiled coil #status predicted <COI> F;888-2017/Domain: S2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F:1329-2017/Region: light meromyosin
F:1329-2017/Region: light meromyosin
F:176/Modified site: N6.N6.Lrimethyllysine (Lys) #status predicted
F:231/Binding site: ATP (Lys) #status predicted
F:745,755/Active site: Cys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          170 VDKIRKBAYAGAAAGVVAGPFGLIISYSIA------AGVVEGKL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.6%; Score 115; DB 1; Length 2017; ilarity 21.3%; Pred. No. 37; Conservative 48; Mismatches 107; Indels 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Status: nucleic acid sequence not shown A,Molecule type: mRNA A,Residues: 1-2017 <KET> A,Cross-references: UNIPROT: 099323; GB:M35012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 KNAIETADGALDLYNKYL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: FlyBase:zip
A;Cross-references: FlyBase:FBgn0005634
                                               L--DHORQIVSNLEKKÖKK 1445
LLKEAAKKMINTCNEYOKR 291
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nes 80; Conserv
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A; Recidues: 1-1964 <BHA>
A; Cross-references: UNIPROT: 093522; GB: AF055895; NID: 93660671; PIDN: AAC83556.1; PID: 9366
A; Cross-references: UNIPROT: cell line XTC
A; Experimental source: cell line XTC
C; Superfamily: myosin heavy chain; myosin motor domain homology
F; 84-764/Domain: myosin motor domain homology <MMO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RQK-----LSFSTKLKQMEDEKNGLLEQLEEBERAKKNLCKQISTLQSQMTD 1368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               228 TVKQANKDID-----AAKLKLTTBIAAIGBIKTET-------BTTRFY---- 263
                                                                                                                                                                                                                                                                                                     GDIKTLIMDSQ-----DKYFEATQTVYENCGVATQLLAAYILLFDEYNEKKASAQKDILI 117
                                                                                                                                                                                                                                                                                                                                                               243 EELIKKLNDKEINFNIDEKQKLLDQINSKINTLNENIKGVMNLYTETKNKISNLQNEILN 302
                                                                                                                                                                                                                                                                                                                                                                                                                                      KVLDDGITKLNEAQKSLLVSSQSFNNASGKLLALDSQLTN------DFSEKSSYFQ 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----INELKSKIKLFDNDIQKLNN 378
                                                                                                                                                                                                                                           92 INNKEIEFKNIDNVQXEINKKODELNKLL-----DESKKEFIKKQEELNKTIDKKQ 242
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                                                                                                                                                                             5 VADKTVEV--VKNAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASVLV
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                                               ; Score 115; DB 2; Length 1127;
; Pred. No. 18;
51; Mismatches 124; Indels 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 7.6%; Score 115; DB 2; Length 1964; Best Local Similarity 18.8%; Pred. No. 36; Matches 60; Conservative 64; Mismatches 113; Indels 82
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                                                                Query Match
Best Local S:
Matches 70
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RiLin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; i. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: B84800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : |: || |:| | : | : | : SGDLAEVNLKINLELANHGSEANELQTKLSALEAEKEQTANELEASKTTIEDLTKQLTSE 1063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         471 BOILKAKETSTEAEPSSEVLNEMİEKLKSEIDDEYTEAAIAV----GLEERLTA----MR 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SVLVGDIKTLLMDSQDKYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQKDILIK 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E-----KSLQSSSESELLAETNNQLK---IKIQELEGLI------GSGSVEKETALK 925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 VLDDGITKLNEAQKSLLVSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDKIRKEAY 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            179 AGAAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNKLKSVQNFFTTLSNT-----VKQA 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           233 NKDIDAAKLKLTTEIAAIGEIKTETETTRFYVDYDDLMLSLLKEAAKKMINTCNEYQKRH 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102 DEYNEKKASAQKDILIKVIDDGITKLNEAQKSLLVSSQSFNNASGKLLAL-----DS 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EEFS--KASSEEHLMHPVLIEKIEKIKEEFNTRLTDAPNYESLKSKLNMLRDFSRAKAAS 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42 BTIKELSRFKQEYSQAASVLVGDIKTLLMDSQDKYFEATQTVYEWCGVATQLLAAYILLF 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QLTNDFSEKSSYFQSQVDK-----IRKEAYAGAAAGVVAGPFGLIISYSIAAGVVE 204
                                                                                                                                                                      A;Cross-references: GB:AE002093; NID:g6598483; PIDN:AAC69932.2; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable alpha-carboxyltransferase [imported] - Arabidopsis thaliana
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MTEIVAD -- KTVEVVKNAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                               69;
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                                                                                                                                                                                                                                                                                                                                                Length 1269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.6%; Score 114; DB 2; Length 796; 24.9%; Pred. No. 13; tive 44; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               Indels
A; Reference number: A84420; MUID: 20083487; PMID: 10617197
                                                                                                                                                                                                                                                                                                                                         Query Match 7.6%; Score 114.5; DB 2; Best Local Similarity 18.0%; Pred. No. 22; Matches 56; Conservative 63; Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Best Local Similarity
Matches 68; Conserv
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                                                               A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1269 <S'
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                               Accession: F84730
                                                                                                                                                                                                                           A;Gene: At2g32240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Gene: At2g38040
A,Map position: 2
                                                                                                                                                                                                                                                                         A, Map position:
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                            myosin II heavy chain, non-muscle - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 19-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: 861477; 865349
R;Mansfield, S.G.; Al-Shirawi, D.Y.; Ketchum, A.S.; Newbern, E.C.; Kiehart, D.P.
A;Tile: Molecular organization and alternative splicing in zipper, the gene that encode A;Reference number: 861477; MuID:96144835; PMID:8568878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable myosin heavy chain [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (C.Species: Arabidopsis thaliana (mouse-ear cress) (C.Species: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 (C.Accession: F84730 (C.Accession: F84730 (C.A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) (A.C. S.) 
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A;Introns: 10/3; 90/3; 162/3; 215/1; 255/3; 263/3; 303/3; 334/3; 1248/1; 1349/3; 1526/3;
A;Introns: 10/3; 90/3; 162/3; 215/1; 255/3; 263/3; 303/3; 334/3; 1248/1; 1349/3; 1526/3;
C;Superfamily: myosin heavy chain; myosin motor domain moroleotide binding; P-loop
F;135-855/Domain: myosin motor domain homology <MMOT>
F;225-232/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                               D.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1420 SKLRQIESEKEALQEQLEEDDEAKRNYERKLAEVTTQMQEIKKKAEEDADLAKELEEGKK 1479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1537 FDKILAEBKA------ISEQIAQERDTAEREAREKETKVLSVSRELDEAFDK 1582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QEYSQAASVLVGDIKTLLMDSQDKYFEATQTVYEWCGVATQLLAAYILLFDEYNEK---- 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----KASAQKDI-LIKVLDDGIT 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KLN-----EAQ-KSLLVSSQSFNNASGKL-----LALDSQLTNDFS-EKSSYFQSQ 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPELKNKLKSVQNFFTTLSNTVKQANK---DIDAAKLKLTTBIAAIGBIKTETTRFYV 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----DQVIPWQTFDETIKELSRFK 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-1908,'NL',1911-2057 <MAW>
A;Cross-references: EMBL:U35816; NID:g1141789; PIDN:AAB09049.1; PID:g1572481
C;Genetics:
                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-2057 < WAN>
A;Cross-references: UNIPROT:Q94987; EMBL:U35816
R;Mansfield, S.G.; Al-Shirawi, D.Y.; Ketchum, A.S.; Newbern, B.C.; Kiehart, aubmitted to the EMBL Data Library, September 1995
A;Reference number: S65349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.6%; Score 115; DB 2; Length 2057;
21.3%; Pred. No. 38;
tive 48; Mismatches 107; Indels 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    170 VDKIRKEAYAGAAAGVVAGPFGLIISYSIA----AGVVEGKL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --DDLQLT---EDAK 1646
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Best Local Similarity 21.31
Matches 80; Conservative
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C;Accession: S10056
R;Hess, J.; Wels, W.; Vogel, M.; Goebel, W.
Britle: Nucleotide sequence of a plasmid-encoded hemolysin determinant and its comparist A;Reference number: S07209
A;Accession: S10056
Mol. Biochem. Parasitol. 42, 241-246, 1990
A;Title: Identification of the gene for a Plasmodium yoelii rhoptry protein. Multiple A;Title: Identification of the gene for a Plasmodium yoelii rhoptry protein. Multiple A;Reference number: A45521, MUID:91101660; PMID:2270106
A;Accession: A45521
A;Molecule type: DNA
A;Residues: 2260-2401 <KEE>
A;Cross-references: GB:M34281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14;
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2;Species: Bscherichia coli
2;pate: 19-Mar_1997 #sequence_revision 25-Apr-1997 #text_change 04-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 TEIVADKTVEVVK------NAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----IISYSIAAGVVEG------KLIPELKNKLKSVQNFFTTL---SNTVK
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564,690/Binding site: palmitate (Lys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                              Match 7.6%; Score 114; DB 2; Length 2401; Local Similarity 19.4%; Pred. No. 54; Local Similarity 19.7; Mismatches 141; Indels 134; Les 80; Conservative 57; Mismatches 141; Indels 134;
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21.4%; Pred. No. 20;
1ve 59; Mismatches 121;
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C;Superfamily: hemolysin A; hemolysin A homology
C;Keywords: lipoprotein
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Best Local Similarity 21.4
Matches 70; Conservative
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A; Residues: 1-1024 < HES>
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Best Local S:
Matches 80
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A;Cross-references: UNIPROT:Q26216; EMBL:U36927; NID:g1041784; PID:g1041785; PIDN:AAB412
R;Keen, J.; Holder, A.; Playfair, J.; Lockyer, M.; Lewis, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Species: Dictyoatelium discoideum C; Species: Dictyoatelium discoideum C; Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004 (Jaces 1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004 (Jaces 1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004 (Jaces 1999 #sequence_revision 20-Sep-1999 #text_change 142, 735-750, 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 Jaces 1998 J
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C;Species: Plasmodium yoelii
C;Species: Dasmodium yoelii
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T28676; A45521
R;Sinha, K.A.; Keen, J.K.; Ogun, S.A.; Holder, A.A.
Mol. Biochem. Parasitol. 76, 329-332, 1996
A;Title: Comparison of two members of a multigene family coding for high-molecular 1A;Reference number: Z20507; MUID:97077455; PMID:8920022
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                                    GKLIPELKN----KLKSVQNFFTTLSNTVKQANKDIDAAKLKLTTEIAA-IGEIKTETETT 260
                                                                                                                                                                                                     25 DLYNKYLDQVIPW-----QTFDETIKELSRFKQEYSQAASVLVGDIKTLLMDSQDKYFBA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            interaptin - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14867
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1738;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                      S------MVELLKVETAKASKTPGVTEAYÖK 725
                                                                                                                                                                                                                                                                                                                  RFYVDYDDLMLSLLK-EAAK--KMINTCNEYQK 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
7.6%; Score 114; DB Best Local Similarity 21.1%; Pred. No. 36; Matches 55; Conservative 35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 L-----LVSSQSFNNASGKLLALDSQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FITLSNTVKQANKDIDAAKLK 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --ELNQLIEKNESDHKEQQLK 996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KLIQLQODYDQLKQQNRSNDEKD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: abpD
A;Introns: 173/2; 1680/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         162
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                                                                                            581
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Db 209 LNTLGSVLSNTKHLNGVGN-KLQNLPNLDNIGAGLDTVSGILSAISASFILGNADAD 264	C:Species: Pasteurella haemolytica C;Date: 10-Aug-1990 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004 C;Accession: S37145; A38254; S34237; S34235
Qy 105 NEKKASAQKDILIKVLDDGITKLNEAQKSLLVSSQSFNNASGKLLALDSQLTNDFSE 161	R; Lainson, A.F.; Aitchison, K.; Donachie, W. submitted to the EMBL Data Library, September 1993 A; Description: DNA sequence of the leukotoxin A gene from P. haemolytica T10 serotype.
OY 162 KSSYFQSQVDKIRKEAYAGAAAGVVAGFGLIISYSIAAGVVEGKLIPELKNKLKS 217	A; Relefence number: S3/145 A; Accession: S37145 A; Molecule type: DNA A: Residues: 1-955 < LAI>
218 VONFFITLSNIVKQANKDIDAAKLKITEIAAIGEIKTETETTRFYUDYD 267	A;Cross-references: UNIPROT:P55117; EMBL:Z26247; NID:g400424; PIDN:CAA81206.1; PID:g4004 R;Hishlander, S.K.; Engler, M.J.; Weinstock, G.M. T. Hacheriol 172, 2343-2340.
369TISTVLASVSSGISAAATTSLVGAPVSALVGAVTGIISGILEASK 414	A; Title: Secretion and expression of the Pasteurella haemolytica leukotoxin. A; Reference number: A35254; MUID:90236888; PMID:2185213
Oy 268 DIMISLIAKEAAKKOIINTCHEYOKRHGK 294 DD 415QAMPEHVASKOADVIABWEKGHGK 438	A.Accesion: A35254 A.Status: preliminary A.Molecule type: DNA
. 22	A;Residues: 950-955 <hig> A;Cross-references: GB:M24197; GB:M34943; GB:M34944 R;Lainson, A.F.; Aitchison, K.D.; Donachie, W.</hig>
	submitted to the EMBL Data Library, June 1993 A, Description: DNA sequence of the carboxy terminal end of leukotoxin A from the T3 sero A, Reference number: S34235
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C;Accession: T22716	A; Accession: S34237 A; Molecule type: DNA
, Data Library, August 1996 19604	A;KOBIQUOB: 745-755 CLALA: A;CTOSE-TEGETOGOES: EMBL:Z22884; NID:G311828; PIDN:CAA80498.1; PID:G311829 A;Experimental source: Berotype T3
y; translated from GB/EMBL/DDBJ	A;Accession: S34235 A;Molecule type: DNA
L> NITBPOT - 020822 - EMRI - 278198 - DIDN - CARDI573 1 - GSDDR - CNOOD23 - CRSD - FG	A;Residues: 723-955 <la3> A;Cross-references: EMBL:222897; NID:g311824; PIDN:CAA80501.1; PID:g311825 A:Evnevimental monyres earch yne T10</la3>
- 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1	A; Departmental Bource: Belonging 110 A; Punction: A; Description: attacks cell membranes and causes cell lysis
SP:P55C5.8 tion: 5	C; Superfēmily: hemolysin A; hemolysin A homology C; Keywords: calcium binding; cytolysis; exotoxin; hemolysis; lipoprotein; tandem repeat;
; 44/2; 147/3; 251/3; 561/3	F;240-786/Domain: hemolysin A homology <hlya> F;718-809/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIYF]-X)</hlya>
Query Match 7.5%; Score 113; DB 2; Length 622; Best Local Similarity 20.6%; Pred. No. 11; Matches 67; Conservative 54; Mismatches 100; Indels 104; Gaps 15;	F;718-726/Region: repeat F;727-735/Region: repeat F;736-744/Region: repeat
Qy 41 DETIKELSRPKQEYSQAASVLVGDIKTLLMDSQDKYPEATQTVYEMCGVAT 91	F;745-753 Region: repeat F;754-762/Region: repeat F;754-771/Region: repeat
231 DALISEM-RASAISAEVIIEMGGARSIVUDERARQVVQBWAQIEVELAQCQIFN 304 92 OHABAYII.EDRYNRKKASAOKDII.IKVI.DBGTTKINR-AOKSHIVSSOSFNNA 144	F;772-700/Region: repeat F;781-789/Region: repeat F:792-800/Recion: repeat
305 ERWALPEKATADITRDAIDRISDIIRRKSSENADITVLOSIKAYLEFLKONGT 356	F;801-809/Region: repeat F;801-809/Region: repeat F;556/Binding site: palmitate (Lys) (covalent) #status predicted
Qy 145 SGKLLALDSQLTNDFSEKSSYFQSQyDKIRKE 176 :	Query Match 7.5%; Score 113; DB 1; Length 955; Best Local Similarity 18.6%; Pred. No. 19; Matches 69; Conservative 67; Mismatches 136; Indels 98; Gaps 12;
	Qy 6 ADKTVEVVKANAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASVLVG 63
CY 220 NFPTLESNTVKQANKDIDAAKLKLTTEIAALGEIKTETETTRFYVDYDDLMLSLLKBAAK 279	OY 64DIKTLIMDSQDKYFBATQTVYEWCGVATQLLAAYILLFDEYNEK 107
280 KMINTCNEYQKRHGKKTLFEVP 30	108
DD 511 PLLETVNEWRQWDVRNSLKDXKTIP 535	209 LONVKGLGALGDKLKNIGGLDVKSKLLSGATAALVLADKDASIAKNVGAG
RESULT 23 A35254	Qy 153SQLTNDFSEK-SSYFQSQVDKIRKEAYAGAAAGVVA-GPFGLIISYSTAAGVVE 204 Dy 266 FELANOVVGHTKAVSSYLLAORAAGLSSTGPVAALIASTVAVALSFLS 315
leukotoxin A - Pasteurella haemolytica (serotype T10) N,Alternate names: lktA protein	205 GKLIPELKNKLKSVQNFFTTLSNTVKQANKDIDAAKLKLTTEIAAI 25

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Note: authors translated the codon AGT for residue 377 as Thr and CTA for residue 507; Hardwick, C.; Hoare, K.; Owens, R.; Hohn, H.P.; Hook, M.; Moore, D.; Cripps, V.; Auster. Cell Biol. 117, 1343-1350, 1992; Title: Molecular cloning of a novel hyaluronan receptor that mediates tumor cell motil; Reference number: A41923; MUID:92299690; PMID:1376732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Introns: 20/3; 54/2; 79/2; 137/3; 187/3; 259/2; 382/2; 431/2; 482/2; 515/3; 574/3; 625, superfamily: hyaluronan receptor ; Keywords: glycoprotein; receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;256-382/Región: 21 residue repeats
F:516-574/Región: hyaluronan binding #status predicted
F:5516-574/Region: hyaluronan binding #status predicted
F:516,283,304,325,346,367,398,438,619/Binding site: carbohydrate (Asn) (covalent) #statu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A.Note: this sequence has been corrected in reference A42925
C.Comment: This protein regulates cell motility and transformation, and focal adhesion d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Deter: 16-Nov-1995 #sequence revision 08-Feb-1996 #text_change 09-Jul-2004
C;Accession: 074298; A42225; A41923; S21586
R;Entwistle, J.; Zhang, S.; Yang, B.; Wong, C.; Li, Q.; Hall, C.L.; A, J.; Mowat, M.; Gr Agene 163, 233-238, 1995
A;Title: Characterization of the murine gene encoding the hyaluronan receptor RHAMM. A;Reference number: JC4298; MUID:96011639; PMID:7590272
A;Accession: JC4298
                                      11;
                                                                                                                                                                                                 1 MTEIVADKTVEVVKNAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASV 60
                                                                                                                                                                      203
                                                                                                                                                                                                                                                     204 EGKLIPELKNKLKSVQNFFTTLSNTVKQANKDIDAAKLKLTTEIAAIGEIKTETETTRFY 263
                                                                                 151
                                                                                                                         28
                                                                              94 LAAYILLFDEYNEKKASAQKDILIKVLDDGITKLNE--AQKSLLVSSQSFNNASGKLLAL
                                                                                                            4 LILIITVPFTFNVAQASL-PNIVASVNDEPIT-LNEFRARKKMIM---ALNNVESLTPAQ
                                                                                                                                                                  152 DSQLTN----DFSEKSSYFQSQVDK-IRKEAYAGAAAGVV---AGPFGLIISYSIAAGVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62;
                                          46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.4%; Score 112; DB 2; Length 631; 20.5%; Pred. No. 13; ve 63; Mismatches 108; Indels
Length 295;
                                                                                                                                                                                                                                                                                                                                          264 VDYDDLMLSL----LKEAAKKMINTCNEYQKR-----HGKKTLFE 299
                                                                                                                                                                                                                                                                                                                                                                     157 SDQKDVEISMQVFTSKDGGNKAFTQMMNLKNRLKKCADVKKSLYD 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 155-376,'S',378-504,'E',506-507,'L',508-630 <HA2>
A;Cross-references: GB:X64550
                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .Hardwick, C.
. Cell Biol. 118, 753, 1992
.Reference number: A42925; WUID:92348516; PMID:1639856
.Contents: erratum
                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molecule type: mRNA
Residues: 155-376,'S',378-504,'E',506-631 <HAR>
Cross-references: GB:X64550
                      24.9%; Pred. No. 5;
tive 40; Mismatches
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  7.4%; Score 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hyaluronan receptor - mouse
C;Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ilarity 20.5%;
Conservative 6
    Query Match
Best Local Similarity 24.9
Matches 56; Conservative
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Best Local Similarity
Matches 60; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ,Molecule type: mRNA ;Residues: 1-631 <ENT>
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Status: preliminary
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-295 <KUR>
A;Cross-references: UNIPROT:Q92GU9; GB:AE006914; PIDN:AAL03561.1; PID:g15620140; GSPDB:G
C;Genetics:
A;Gene: RC1023
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C'Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C'Accession: 697827
R'Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, Science 293, 2039-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----NILKENNAILQKSLKNVTEKNREIYKQLNDRQEEISRLQRDLIQTKEQVSINS 1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGVVEGKLIPELKNKLKSVQNFFTTLSNTV----KQANKDIDAAKLK---LTTEIAAIG 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --LIKVLDDGITKLNEAQKSLLVSSQSFNNAS 145
      316 FAGIADKFDRAKSLENYAERPKKLGYEGDSLLAEYQHGTGTIDASVTAINTALAAIAGGV 375
                                                                                              376 SAAAAGSVVASPIALLVSGITGVISTILQYSK-----QAMFEHVANKIHNKIVEWE 426
                                                                     --GEIKTETETTRFYVDYDDLMLSLLKEAAKKMINTCNEYQ 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39 TFDETIKELSR----FKQEYSQAASVLVGDIKTLLMDSQDKYFBATQTVYEWCGVATQLL 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 1679;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1227 NKILVYESEMEQCKORYQDLSQQQKDAQKKDIEKLTNE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.5%; Score 112.5;
20.6%; Pred. No. 42;
tive 44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAYILLFDEYNEKKASAQKDI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Gene: SGD:MLP2; MIPS:YIL149c
A, Cross-references: SGD:S0001411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51; Conservative
                                                                                                                                                                                        1316 AIKDKLE 1322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               252 EIKTETE 258
                                                                                                                                                               290 KRHGKKTLFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Map position: 9L
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Matches 5
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Db 851 LKTDYESVITSVDSKQTDIEKLQYKVKSLEKEIEEDKIRLHTYNVMDET 899 Qy 193 IISYSIAAGVVEGKL-IPELKNYKKSVQNFFTTLSNTVKQANKDIDAAKLKLTTEIAAIG 251 Db 900 INDDSLRKELEKSKINITAAYSQIKEYKDYFTTLSSNTVKQANKDIDAAKLKLTTEIAAIG 251 Qy 252 EIKTETETTRFYVDYDDIMISLLKEAAKKNINTCNEYQKBHGKK 295 Db 960 DEKTSLEDKISLLKEQMFNLNNELDLQKKGMEK 992 RESULT 28 \$67087 hypothetical protein YOR195w - yeast (Saccharomyces cerevisiae) N;Alternate names: hypothetical protein 04806 C;Species: Saccharomyces cerevisiae C;Species: Saccharomyces cerevisiae C;Accession: S47087	K;Hughes, B.; Pohl, T.M. submitted to the Protein Sequence Database, July 1996 A;Reference number: \$66685 A;Reference number: \$66685 A;Reference number: \$66685 A;Recession: \$67087 A;Molecule type: DNA A;Residues: 1-821 cHUG> A;Cross-references: UNIPROT:Q08581; EMBL:Z75103; NID:g1420464; PID:e252389; PID:g. A;Cross-references: UNIPROT:S88C C;Genetics: A;Gene: \$GD:SLK19; MIPS:YOR195w A;Cross-references: \$GD:S0005721 A;Map Position: 15R	Query Match 7.4%; Score 111.5; DB 2; Length 821; Best Local Similarity 21.8%; Pred. No. 20; Matches 72; Conservative 52; Mismatches 112; Indels 95; Gaps 14; Qy 10 VEVVKNAIETADGALDLYNKYLDQVIPWQTPDETIKELSRFKQEYSQAASVL61 Db 373 VEKFKKRIKELNTEIKVLNSNQKILQEKFDASITEVNHIKGEHENTVNTLQQNEKILN 430	Cy 62VGDIKTLLMDSQDKYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQKDIL 116	CANKDI DAAKLKITTEIAAIGEKETVET	Qy 270 MLSLLKEAAKKMINTCNBYQKRHGKKTLFBV 300 :: : : : Db 619 TITELENKVHKLENEC-ELEKQKFEKTSLEL 648	RESULT 29 T18296 myosin heavy chain - Entamoeba histolytica C;Species: Entamoeba histolytica C;Species: Entamoeba histolytica C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C;Accession: T18296 R;Guillen, N. submitted to the EMBL Data Library, February 1997 A;Reference number: Z18865 A;Reference number: Z18865 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA
Db 253 LDNLLREKEVELEKHIAAHAQAILIAQEKYNDTAQSLRDVTAQLESVQEKYNDTAQS 309 Qy 61 LVGDIKTLLMDSQDKYFEATQTVYEWGQVATQLLAAYILLFDEYNEKKASAQKDILIKVL 120	RESULT 27 338173 myosin-like protein MLP1 - yeast (Saccharomyces cerevisiae) N.Alternate names: protein YKR095w; protein YKR415 C;Species: Saccharomyces cerevisiae C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004 C;Accession: S38173; S40647; S31207 R;Baladron, V.; Ballesta, J.P.G.; Bou, G.; del Rey, F.; Esteban, P.F.; Garcia-Cantalejo, submitted to the Protein Sequence Database, March 1994 A;Reference number: S38158 A;Accession: S38173 A;Molecule type: DNA	A; Cross-references: UNIPROT:002455; EMBL:228320; NID:g486586; PID:g486587; MIPS:YKR095w A; Experimental source: strain S288C A; Experimental source: strain S288C R; Bou, G.; Bsteban, P.F.; Baladron, V.; Gonzalez, G.A.; Cantalejo, J.G.; Remacha, M.; Ji Yeast 9, 1349-1354, 1993 A; Title: The complete sequence of a 15 820 bp segment of Saccharomyces cerevisiae chromo A; Reference number: S40644; MUD:94205265; PMID:8154186 A; Molecule type: DNA	A; Residues: 1-1875 <bous \$288c="" \$31207;="" \$33207;="" 1993="" 237,="" 359-369,="" 93247549;="" 9450550;="" 9450554="" 9483450="" 9483450<="" a="" a;="" accession:="" b.y.;="" botstein,="" caa51948.1;="" chen,="" cross-references:="" d.="" embl:="" experimental="" extrain="" gen.="" gene="" genet.="" heptad="" koelling,="" mol.="" muid:="" myosin-like="" new="" nguyen,="" nid:="" number:="" pid:="" pidn:="" pmid:="" r.;="" r;="" reference="" repeat="" source:="" strain="" structure.="" t.;="" td="" title:="" with="" x73541;="" yeast=""><td>Afroiscule Lype: DNA A, 302-1875 «KOE» A;Residues: 1-300, 'A, 302-1875 «KOE» A;Cross-references: EMBL:L01992; NID:g171958; PIDN:AAA34783.1; PID:g171959 C;Genetics: A;Genetics: SGD:MLP1 A;Gene: SGD:MLP1 A;Cross-references: SGD:S0001803; MIPS:YKR095w A;Map position: 11R</td><td>Query Match 7.4%; Score 112; DB 2; Length 1875; Best Local Similarity 19.7%; Pred. No. 52; Matches 68; Conservative 66; Mismatches 122; Indels 90; Gaps</td><td>SRILABERFKILSNTLDLTKAENDQLRKRFDYLQNTILKQDSKTHBTLNBYVSCKSKLSI 7 ELSRFKQBYSQAASVLVGDIKTLLMDSQDKYFBATQT 8 </td></bous>	Afroiscule Lype: DNA A, 302-1875 «KOE» A;Residues: 1-300, 'A, 302-1875 «KOE» A;Cross-references: EMBL:L01992; NID:g171958; PIDN:AAA34783.1; PID:g171959 C;Genetics: A;Genetics: SGD:MLP1 A;Gene: SGD:MLP1 A;Cross-references: SGD:S0001803; MIPS:YKR095w A;Map position: 11R	Query Match 7.4%; Score 112; DB 2; Length 1875; Best Local Similarity 19.7%; Pred. No. 52; Matches 68; Conservative 66; Mismatches 122; Indels 90; Gaps	SRILABERFKILSNTLDLTKAENDQLRKRFDYLQNTILKQDSKTHBTLNBYVSCKSKLSI 7 ELSRFKQBYSQAASVLVGDIKTLLMDSQDKYFBATQT 8

PID:91420465

Db 1940 EDQIAYSRNSIEKARSEELMNMFEDKEKINMTLAELPDLVEQCQNITLLVSQLIDEY 1996 Oy 105 NEKKASAQXDILIKVLDDGITKLNEAQKSLLVSSQSFNNAS 145	RESULT 31 723064 172064 172064 172064 172064 172064 172064 172064 172066 172064 172066 172066 172066 172066 172066 172067 17207 17	C, Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin T, 4%; Score 111.5; DB 2; Length 2823; Best Local Similarity 21.3%; Pred. No. 95; Matches 73; Conservative 56; Mismatches 100; Indels 113; Gaps 1 25 DLYNKYLDQVIPWQT-FDETIKELSRFKQEYSQAASVLVGDIKTLLMDS 72 Qy 25 DLYNKYLDQVIPWQT-FDETIKELSRFKQEYSQAASKLVVG
A; Residues: 1-2139 <gui> A; Cross-references: UNIPROT: Q07569; EMBL: L03534; NID: 91850912; PID: 91850913; PIDN: AAB480 C; Genetics: A: Genetics: A: Genetics: A: Genetics: C; Superfamily: myosin heavy chain; myosin motor domain homology </gui>		

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1,Title: Fatty acylation of two internal lysine residues required for the toxic activity 1,Reference number: A55387; MUID:95099325; PMID:7801126
1,Contents: annotation: lysine palmitcylation
1,Note: lysine modification is performed by the hlyC gene product
1,Haartlein, M.; Schiessi, S.; Wagner, W.; Rdest, U.; Kreft, J.; Goebel, W.
1, Cell Biol. 22, 87-97, 1983
1,Title: Transport of hemolysin by Escherichia coli.
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C; Superfamily: hemolysin A; hemolysin A homology
C; Keywords: calcium binding; cytolysis; exotoxin; hemolysis; lipoprotein; tandem repeat;
F; 246-791/Domain: hemolysin A homology <HLYA>
F; 723-851/Region: 9-residue repeats (G-X-K-GIN)-D-X-[LVIYF]-X)
F; 563,689/Binding site: palmitate (Lys) (covalent) #status experimental
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,Residues: 1-1023 <FEL>
,Cross-references: UNIPROT:P09983; GB:M10133; GB:M12863; NID:g146377; PIDN:AAA23975.1;
,Experimental source: strain J96, O4 serotype
,Stanley, P.; Packman, L.C.; Koronakis, V.; Hughes, C.
                                                                                                                                                                                                      137
                                                                                                                                                                                                                                                        64 DIKTLLMDSQDKYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQKDILIKVLDDG 123
                                                                                                                                                                                                                                                                                                                                                                                       164 VYAQNQHLRNIHISYPSLNLVYKAVAEFFPYKNSLDGSLLPQVQENINKLNTLAEKIKPE 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                            236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DAAKLKLTTEIAAIGEIKTETETTRFYVDYDDLMLSLLKEAAKKMINTCNEYQKRHGKKT 296
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Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 09-Jul-2004;
Accession: A24433; 141280
                                                                                                                                                                                   5 VADKTVEVVKNAIETADGALDLYNKYLDQV-IPWQTFDETIKELSRFKQEYSQAASVLVG
                                                                                                                                                                                                                                                                                                                                                          124 ITKLNEAQKSLLVSSQSFN---NASGKLL----ALDSQLTNDFSEKSSYFQSQVDKIRKE
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                                                                                                    Gaps
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. Bacteriol. 163, 94-105, 1985
;Title: Nucleotide sequence of an Escherichia coli chromosomal hemolysin.;Reference number: A24433; MUID:85234404; PMID:3891743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1,'T',3,'V',5,'T',7-44 <RES>
A;Cross-references: GB:M29173; NID:g146337; PIDN:AAA23957.1; PID:g146338
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                                                  Length 934;
                                                                                                       Indels
                                                                                                                                                                                                                                                                                                        ----TLEEYN-
                                                  7.4%; Score 111; DB 2; L 21.6%; Pred. No. 25; tive 43; Mismatches 131;
                                                                                                                                                                                                                                                                                                        DDANIKLSDMAPHLPKFK---DW-----
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21.3%;
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                       Query Match
Best Local Similarity
Local 69; Conserve
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  A; Map position: 3
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A;Note: see websites genome.wustl.edu/gsc/C_elegand www sanger.ac.uk/Projects/C_ele A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Genetics:
A;Map position: 1
A;Note: lama1/2
C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSNVDNSNAVKIVEELKKEKKD-----LTDRLGHLN-----ELK-TSIVKRLGVIKN 2140
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                                                                                                                                                                                                                                                C; Accession: T43291
R; Zhu, X.; Kao, G.; Joh, K.; Hall, D.H.; Wadsworth, V.K.; Hutter, H.; Vogel, submitted to the EMBL Data Library, June 1998
A; Description: Expression, function and evolution of laminin alpha chains. A; Reference number: 222397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Caenorhabditis elegans
C;Date: 11-Jan 2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
7.4%; Score 111.5; DB 2; Length 3102;
Best Local Similarity 21.3%; Pred. No. 1.1e+02;
Matches 73; Conservative 56; Mismatches 100; Indels 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: UNIPROT: 045614; EMBL: AF074902; PIDN: AAC26793.1
                          | : : | | | | : | | BASS---WDDXHDRMHSILKNGAKTAHERSANVKKESEGIKT. 2179
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ETETTRPYVDYDDLMLSLLKEAAKKM-INTCNEYQKRHGKKT
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-3102 <ZHU>
                                                                                                                                                                      - Caenorhabditis elegans
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A;Molecule type: DNA
A;Residues: 1-934 <STO>
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A, Gene: R06B10.2
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A;Experimental source: strain DSM 3638
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C;Species: Halorubrum vacuolatum
C;Species: Halorubrum vacuolatum
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T44967
R;Mayr, A.; Pfelfer, F.
Arch. Microbiol. 168, 24-32, 1997
A;Title: The characterization of the gvpACNOFGH gene cluster involved in gas A;Reference number: 222885; MUID:97361906; PMID:9211710
A;Reference number: 722885; MUID:97361906; PMID:9211710
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A;Molecule type: DNA
A;Residues: 1-540 <MAY>
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A; Accession: T12018
A; Status: translated from GB/EMBL/DDBJ
A; Status: translated from GB/EMBL/DDBJ
A; Status: translated from GB/EMBL/DDBJ
A; Status: translated from GB/EMBL/DDBJ
A; Residues: 1-478 cLAZ>
A; Cross-references: UNIPROT: O64067; EMBL: AF020713; NID: G3025478; PID: G302532; PIDN: AACI
A; Residues: 1-478 cLAZ>
A; Cross-references: UNIPROT: O64067; EMBL: AF020713; NID: G3025478; PID: G302532; PIDN: AACI
B; Broul S: Broullet, S.; Bruschi, C.V.; Caldwall, B.; Capuano, V.; Carter, N.M.; ChC
A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, B.
Nature: 390, 249-256, 1997
A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler, A; Authors: Lauber, D.; Fritz, C.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler, Koetter, P.; Koningstefah, G.; Krodh, S.; Kumano, M.; Kurita, X.; Lapidus, A.; Lardinois, A; Luthors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, A; Authors: Lauber, G.; Rocha, B.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Sortetalle, Y. Muthors: Schleich, S.; Schroeter, R.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Seronlon, A; Authors: Schleich, S.; Schroeter, R.; Yamaneco, R.; Yamaneco, W.; Yamaneco, W.; Yamaneco, W.; Yamaneco, W.; Yamaneco, W.; Yamaneco, W.; Yamaneco, W.; Yamaneco, W.; Yamaneco, W.; Yamaneco, W.; Yamaneco, M.; Yamaneco, W.; Yamaneco, W.; Ajtile: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A; Reference number: A69580; MUID: 98044033; PMID: 9384377
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R;Lazarevic, V; Duestroeft, A.; Soldo, B.; Hilbert, H.; Mauel, C.; Karamata, D. submitted to the EMBL Data Library, August 1997
A;Description: The complete nucleotide sequence of the Bacillus subtilis SPbetac2 propha
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Experimental source: strain 168
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A;Status: nucleic acid sequence not shown; translation not shown
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C,Species: Bacillus subtilis phage SPBc2
C,Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change
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tive 41; Mismatches
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Wed Jan

Db 166 NMLERLFNLQEYGDELSFKLARKIRKEREKENVLVGELKGYENINEDVLKERRELLKENN 225	Qy 259TTRFYUDYDDIMISILKEBARKMINTCNEVQKR 291 :	Query Match	187 AGPFGLIISYSIAAGVVBGKLIPBLKNKLKSVQNFFTTLSNTVKQA 232
DPS2 protein homolog (bps2) [imported] - Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Species: Sulfolobus solfataricus c;Date: 24-May-2001 #text_change 09-Jul-2004 C;Accession: A90394 C;Accession: A90394 C;Accession: A90394 C;Accession: A90394 C;Accession: A90394 A.C.; Kozera, C.J.; Medina, N.; Allard, G.; Awayez, M.J.; Charyon, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thl-Ngoc, H.P.; Redder, submitted to GenBank, April 2001 A;Description: Sulfolobus solfataricus complete genome. A;Reference number: A90394 A;Accession: A90394 A;Status: preliminary A;Molecule type: DNA A;Status: preliminary A;Molecule type: DNA A;Crosereferences: UNIPROT:Q97WH8; GB:AE006641; NID:g13815540; PIDN:AAK42408.1; GSPDB C;Genetics: A;Gene: bps2	Query Match Best Local Similarity 20.6%; Pred. No. 16; Bast Local Similarity 20.6%; Pred. No. 16; Matches 59; Conservative 56; Mismatches 106; Indels 66; Gaps 12; QY 23 ALDLYNKYLDQVIPWQTFDETIKELSERKQEVSQAASVLVGDİKTLIAMDSQDKYFEAT 80 51 AEDLLANVFADSGYVAAELDNKYYRIKARINGLGEEKNLIMDDDRALLLTYFSPB 106 QY 81 QTVYEWGGVATQLLAAYILLFDEYNEKKASAQKDILIKVLDDGITKLINEAQKSL 134	RESULT 38 G97236 ATREAGUS 186 G97236 ATREAGUS 197236 ATREAGUS 197236 ATREAGUS 197236 ATREAGUS 197236 ATREAGUS 1972301 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004 C;Accession: G97236 G;Accession: G97236 A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium A;Reference number: A96900; MUID:21359325; PMID:21359325 A;Accession: G97236 A;Accession: G97236 A;Accession: G97236 A;Accession: G97236 A;Accession: G97236 A;Accession: G97236 A;Accession: G97236 A;Accession: G97236 A;Accession: G97236 A;Accession: G97236 A;Generical type: DNA A;Residues: 1-1163 <kur> A;Cross-references: UNIPROT:Q97FK1; GB:AE001437; PIDN:AAK80682.1; PID:g15025772; GSPI A;Accession: G97236 A;Acces</kur>	Query Match 7.3%; Score 110; DB 2; Length 1163; Best Local Similarity 17.9%; Pred. No. 38; Matches 73; Conservative 69; Mismatches 114; Indels 152; Gaps, 14; Qy 1 MTELVADKTVEVVKNAIETADGALDLYNKYLDQVIPWQTFDETIK

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,Molecule type: DNA
,Residues: 1-566 <BAD>
,Cross-references: UNIPROT:Q12321; EMBL:Z49219; NID:g805025; PID:g805050; MIPS:YPR070w
,Experimental source: strain AB972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 DVDYNKKQDRIQDVKLVLASNFDNFDYFNQRDGEHEKSNILLNSLTKYPDLKAFHNNLKF 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            110 SAQKDILIKVLDDGITKLN-EAQKSLLVSSQSFNNASGKLLALDSQLTNDFSEKSSY--- 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                               792
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                                                                                                                                                                                                                                                                                   ----LIEIENRRSLKFDKYKEYLGL 710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEL----KNKLKSVQNFFTTLSNTVKQANKDIDAAKLKLTTEIAAIGEIKTETETRFYV 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62
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                                                                                                                                                       26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein YPR070w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YP9499.25
C;Species: Saccharomyces cerevisiae
C;Species: 08-Jul-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 DKTVEVVKNAIETADGALDLYNKYLDQVIPWQTFDE----TIKELSRF----KQEYSQ
                                                                                                                                                                                                                                          57 AASVL-----VGDIKTLIMDSQDKYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKAS
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                                                                                                         Gaps
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A;Cross-references: EMBL:U51033; NID:g1230676; PID:g1230678; MIPS:YPR070w
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                                                                                                           98;
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                                                                Length 1005;
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                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                              111 AQKDILIKVLDDGITKINEAQKSLLVSSQSFNNASGKLLALD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, March 1996
A.Description: The sequence of S. cerevisiae cosmid 9513.
A.Reference number: S69057
A.Accession: S69058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 108.5; DB 2;
; Pred. No. 19;
43; Mismatches 131;
                                                                                                           93;
                                                                  DB 2;
                                                                                         pred. No. 37;
55; Mismatches
                                                                                       37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'Badcock, K.; Churcher, C.M.
ubmitted to the EMBL Data Library, May 1995, Reference number: $54059
                                                                  7.2%; Score 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               758 ILEVNKEINDIEERISYINQKLDE-----
                                                                                                                                                                                                                                                                       662 ELNKLREDEREINRLKDKLNELKNKEKE
A,Map position: REV1273394-1270377
C,Superfamily: hypothetical protein MJ1322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 IETADGALDLYNKY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23.9%;
                                                                                    19.1%;
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                                                                                       Best_Local Similarity 19.19
Matches 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Accession: $54091; $69058
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Best Local Similarity
Tag Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Map position: 16R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Gene: SGD: MED1
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                                                                                                                                                                                                                                                                                                                                                                                                                          153
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C; Specias: Methanococcus jannaschii
C; Specias: Methanococcus jannaschii
C; Specias: Methanococcus jannaschii
C; Date: 13-Sep-196 #sequence_revision 13-Sep-1996 #text_change 09-Ju1-2004
C; Accession: A64465
R; Mile, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, i. Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A; Juthors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.A; Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A; Reference number: A64300; MUID: 96337999; PMID: 8688087
A; Accession: A64465
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-1005 cBUL>
A; Cross-references: UNIPROT: Q58718; GB: U77117; NID: 91591958; PIDN: AAB99331.1;
C; Genetics:
                                                                                                                                  C;Species: Lactobacillus phage phi-gle
C;Species: Lactobacillus phage phi-gle
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 13-Aug-1999
C;Accession: T13216
R;Kodaira, K.I.; Oki, M.; Kakikawa, M.; Watanabe, N.; Hirakawa, M.; Yamada, K.; Taketo, A;Kodaira, K.I.; Oki, M.; Kakikawa, M.; Watanabe, N.; Hirakawa, M.; Yamada, K.; Taketo, A;Title: Geneme structure of the Lactobacillus temperate phage phi gle: the whole genome A;Reference number: Z17631; MUID:97225795; PMID:9073065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 L----IKVLD----DGITKINEAQKSLLVSSQSFNNAS-----GKLLALDSQLTND 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                521 IETAAVSKWVDLFGGSGVTSAGGKAVTQTVAKEAGGTAATAGSSKVLGRLFAKGGATSTA 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----YFQSQVDKIRKE------AYA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     581 ELEAASGLGGGKAMMAARGLTKAVPYMSIAASIPELFGTTOKTLGKHLGGFAGSAGGPAA 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----GVVAGPFGLIISYSIAAGVVEG--KLIPELKNKLKSV----- 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -ONFFITLSNIVKQANKDIDAAKLKLTTEIAAIGEIKTETTT---- 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MTEIVADKTVEVVKNAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASV 60
                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-1608 <KOD>
A;Cross-references: EMBL:X98106; NID:e917136; PID:e247162; PIDN:CAA66745.1
C;Genetics:
A;Note: Rorf1608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1608;
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                                                                                                                capsid protein 1608 - Lactobacillus phage phi-gle
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                                                                                                                                                                                                                                                                                            A;Accession: T13216
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.3%; Score 109.5; 18.6%; Pred. No. 62;
      2049 KSOIKOKDEDLLRRLEQAEEKHRKE 2073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76; Conservative
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                                                                                                                                                                                                                                                                                                                                        A; Molecule type:
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Matches 7
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R;Solow, B.T.; Somkuti, G.A.
submitted to the EMBL Data Library, August 1999
A;Description: Comparison of low molecular weight heat stress proteins encoded on plasmic
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R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm.
A;Reference number: A99512; MUID:21267165; PMID:11353084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:Q98QP8; GB:AL445566; PID:g14089727; PIDN:CAC13486.1; GSPDB:G
A;Experimental source: strain UAB CTIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          conserved hypothetical protein MYPU_3130 [imported] - Mycoplasma pulmonis (strain UAB CT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              852 PEEDFEKLLQEIAFSSQLNATHKD-------VVDSFYINQLLKAIQLNEAGA 896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             897 VE-KFEKEIQQKDPQIQKMYHTLKDQLVNTTEEIDVAQLKETSIQNEI----QRQLQKEA 951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DELVEIMKE------YEKQFD-ASPYQ--DEKLYNQNINKRLARKEKQYQSDGQW 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -------ILLFDEYNE-KKASAQKDILIKVLDDGITKLNEAQKSL 134
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C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 DKTVEVVKNAIETADGALDLYNKYLDQVIPWQTFDETI-----KELSRFKQEYSQAAS-
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                                                                                                                                                                                               A, Accession: T44802
A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Molecule type: DNA
A, Residues: 1-102.5 Soll->
A, Cross-references: UNIPROT: QSRNW2; EMBL: AF177167; PIDN: AAF04356.1
A, Experimental source: strain ST135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.2%; Score 108.5; DB 2;
20.1%; Pred. No. 40;
tive 52; Mismatches 109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 20.1%
Matches 80; Conservative
                                                                                                                                                   A; Reference number: Z22847
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A;Genetic code: SGC3
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124 LYLLDAYSHIESDSTSHNMGSSDKSLDSSNASFNN-QGKL----DLFKYFTELSHYIRQ 177
                                                                                                                                                                                                                                            178 CFQDNCCDFKVRTN-----LNDKFGI---YILTQG-INGKEVPLAKIYLEENKSDS 224
                                                                                                                                                                                                                                                                                                                                         VONFFTTL--SNTVKQANKDID--AAKLKLTTEIAAIGEIKTETETTRFYVDY----- 266
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                                                                                                                                  type I site-specific deoxyribonuclease (EC 3.1.21.3) chain hsdR [imported] N;Alternate names: type IC restriction subunit C;Species: Streptococcus thermophilus C;Date: 21-Jan.2000 #sequence_revision 21-Jan.2000 #sequence_revision 21-Jan.2000 #sequence_revision 21-Jan.2000 #sequence_revision 21-Jan.2000 #sequence_revision 21-Jan.2000 #sequence_revision 21-Jan.2000 #sequence_revision 21-Jan.2000 #sequence_revision 21-Jan.2000 #sequence_revision 21-Jan.2000 #sequence_revision 21-Jan.2000 #sequence_revision 21-Jan.2000 #sequence_revision 21-Jan.2000 #sequence_revision 21-Jan.2000 #sequence_revision 21-Jan.2000 #sequence_revision 21-Jan.2000 #sequence_revision 21-Jan.2000 #sequence_revision 21-Jan.2000 #sequence_revision 21-Jan.2000 #sequence_revision 21-Jan.2000 #sequence_revision 21-Jan.2000 #sequence_revision 21-Jan.2000 #sequence_revision 21-Jan.2000 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Db 556 NEFSKAKQEFDDMEQKIL	RESULT 47 B97778 endopeptidase La (EC 3.4.21.53) - Rickettsia conorii (strain Malish 7) C;Specises Rickettsia conorii C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004 C;Accession: B97778 R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Science 293, 2093-2098, 2001	A,Title: Mechanisms of Evolution in Rickettsia concrii and Rickettsia prowazekil. A,Reference number: A97700; MUID:21442074; PMID:11557893 A,Accession: E97778 A,Accession: E97778 A,Residues: preliminary A,Residues: 1-779 <	C;Superfamily: Air-depandent bon processes C;Keywords: hydrolase; serine proteinase Query Match Best Local Similarity 20.1%; Pred. No. 30; Matches 62; Conservative 61; Mismatches 102; Indels 84; Gaps 14;	QY 2 TEIVADKTVEVVKNAIETADGALDLYNKYLDQVIPWQTPDETIKELSRFKQEYSQAASVL 61	A	Ali, Db 119 EISNSTNFIDIINILASHLITSLEAKQHLLESTSFKRITTVISMLNSFUSFURL 218 Db 159 EISNSTNFIDIINILASHLITSLEAKQHLLEETSFKRITTVISMLNSNIVNSFTEQALQ 218 Oy 164 SYPQSQVDKIRKEAYAGAAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNKLKSVQNFFT 223 Db 219 KRVRKQIEKTQRDYYLHEQMKAIQKELDEDKSELADIENKIK 260	Qy 224 TLSNTVKQANKDIDAAKLKLTTEIAAIGBIKTETETTRPYUDYDDLMLSLL 274	RESULT 48 T10336 nuclear/mitotic apparatus protein - African clawed frog C.Species: Xenopus laevis (African clawed frog) C.Species: 22-0ct-1999 #sequence_revision 22-0ct-1999 #text_change 09-Jul-2004 C.Accession: T30336	Kiperdes, A.; Kampar, A.; Vecino, O.D.; Croctains, D	A;Residues: 1-2253 <mek> A;Cross-references: UNIPROT:P70012; EMBL:Y07624; NID:g1514670; PIDN:CAA68905.1; PID:g151 C;Genetics: A:Gene: NuMA</mek>
7 DKTVEVVKNAIETADGALDLYNKYLDQVIPWQTFDETIKELS	LLALDSQLTNDFSEKSSYFQSQV : : : ILVFVLQNBDTLEFFKSLVGKLIPELKNKLK : : NKNLVTQYFKKIAPKIASDSMLK	217 2023 255 2081	OY 298 FE 299 Db 2138 FE 2139 REGILT 46	A86248 procein 123J18.9 [imported] - Arabidopsis thaliana C.Species: Arabidopsis thaliana (mouse-ear cress) C.Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004	C; Accession: Ab6248 Y.Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. ansen, N.F.; Hughes, B.; Huizar, L.	Nature 408, 816-820, 2000 A, Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A, Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A, Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A, Reference number: A86141; MUID:21016719; PMID:11130712	A.Accession: A86248 A.Status: preliminary A.Molecule type: DNA A.Access references: UNIPROT:Q9LPZ2, GB:AE005172, NID:g6554201, PIDN:AAF16647.1, GSPDB:GA C.Genetics: A.Gene: T23J18.9 A.Map position: 1	Query Match 7.2%; Score 108; DB 2; Length 636; Best Local Similarity 20.6%; Pred. No. 24; Matches 59; Conservative 39; Mismatches 88; Indels 100; Gaps 11; Qy 6 ADKTVEVVKNAIETADGALDLYNKYLDQVIP	AASVLVGDIKTLIMDSQDKYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQKDIL	Db 500DVPVSQLNSLKDSFSELEKHGFNVTTPLSRIDKLLALKDRQLYIMEELKGFDKEMT 555 Qy 157 NDFSEKSSYFQSQVDKIRKEAYAGAAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNKLK 216

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hypothetical protein 40 - Streptococcus phage phi-01205
C;Species: Streptococcus phage phi-01205
C;Species: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accesion: T13129
R;Stanley, B.; Fitzgerald, G.F.; Le Marrec, C.; Fayard, B.; van Sinderen, D. Microbiology 143, 3417-3429, 1997
M;Title: Sequence analyais and characterization of phi 01205, a temperate bacteriophage : A;Reference number: Z17654; MUID:98048466; PMID:9387220
A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
Kasaiduse: 1-1517 <STA>
A;Cross-references: UNIPROT:034071; EMBL:U88974; NID:G2444080; PID:G2444119; PIDN:AAC7955
A;Experimental source: host Streptococcus thermophilus strain CNRZ1205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 GT------LAKWVSQAASAIAKFVSSIPKSVLNGITSGILAIAAGFVTAKVGISA 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             246 ETVSNKLQPVFEKLSAKAIKGIEGIIDAFSKIDDSKI--QSFANNLSKGIDKTVKDISQT 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89 VATQLLAAYILLFDEYNEKKA--SAQKD--ILIKVLDDGITKL---NEAQKSLLVSSQSF 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 NNASGKLLALDSQLTNDFSEKSSYFQSQVDKIRKEAYAGAAAGVVAGPFGLI---ISYSI 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          304 VQSFWEGFSNTSAIKGLTNAFRYVASQISLAFKGIDFKNLFKGLGGVFGDIAYGISRTLT 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 KQEY-----SQAASVLVG-DIKTLLMDSQDKYFEATQTVYEWCG 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              473 VGGALKGL---DFINSLNPFKKFGKDAAEGTEQAAKSASRSKSTITQLFSGISNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                199 AAGVVEGKLIPELKNKLKSVQNFFTTLSNTVKQANKDIDAAKLKLTTEIAAIGEI
1054 ILKRDSLISKLNERAKVYEKYISTSVEFLTSINTNNRNSKNNNENT 1099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 7.1%; Score 107; DB 2; Length 15:
Best Local Similarity 20.0%; Pred. No. 82;
Matches 59; Conservative 53; Mismatches 123; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 EIVADKTVEVVK----NAIETADGALDLYNKYLDQVIPWQTF---
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Job time : 21.4424 secs
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Cippecies: DictyOstelium discoideum
Cippecies: DictyOstelium discoideum
Cippecies: DictyOstelium discoideum
Cipate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
Cipate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
Cipate: 115-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
Cipate: 115-0ct-1999 #sequence_revision 110-2019
Cipate: 116-2019-1999 #sequence_revision 1117-1125, 1998
A;Title: DictyOstelium discoideum nuclear plasmid Ddp5 is a chimera related to the Ddp1
A;Reference number: 214684; MUID:98198836; PMID:9539429
A;Reference number: 214684; MUID:98198836; PMID:9539429
A;Actus: preliminary; translated from GB/EMBL/DDBJ
A;Actus: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-1474 cRIE>
A;Residues: 1-1474 cRIE>
A;Coss-references: UNIPROT:Q23870; EMBL:U00796; NID:g2702254; PID:g2702256; PIDN:AAC186
C;Genetics:
A;Introns: 33/2
                                                                                                                                                              1308 KEQAEQYQKEIEMKNKEVNSLQAB-----IKİLSSKVTTNEEVSVDFEQRLLKETSKS 1360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 994 LINSLKISNEHKSQLNDLNTKNYSLEKEIESLRSRIIQLETTPTVSNQITQPAFEYSYKHE 1053
                                                                                                                                                                                                                                            65 I-----KTLLMDSQDKYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKASA----Q 112
                                                                                                                                                                                                                                                                                                                                                      KDILIKVLDDGITKLNEAQKSLL-----VSSQSFNNASGKLLALDS-----QLTNDF 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEKSSYFOSOVDKIRKEAYAGAAAGVVAGPFGLIISYSIAAGV----VEGKLIPELKNK 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LKSVQNFFTTLSNTVKQANKDIDAAKLKLTTEIAAIGEIKTETETTRFYVDYDDLMLSLL 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLMDSQDKYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQ--KDILIKVLDDGIT 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KLNEAQKSLLVSSQSFNNASGKL-LALDSQ---LTNDFSEKSSYF-----QSQVDKI- 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNTVKQANK-----BIDAAKLKLTTEIAAIGEIKTETETT------RFYVDYD-- 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               777 ESOKGSNDIBIQOLKLNOSKYISTI --- NDRDSTİKSLOALINELNSSIFKLNOQSSİKD
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                                                                                                                                  6 ADKTVEVVKNAIETADGALDLYNKYLDQVIPWQTFD-ETIKELSRFKQEYSQAASVLVGD
                                                                                   Gaps
                                                                                   72;
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                           7.2%; Score 108; DB 2; Length 2253; 19.9%; Pred. No. 1.2e+02; tive 60; Mismatches 146; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----KEAAKKMINTCNEYQKRHGKKTLFE 299
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                                                    Similarity 19.98 Sep. Conservative
                                                                                                                                                                                                                                                                                                                                                   113
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                              Query Match
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

January 5, 2005, 10:42:38; Search time 63.7089 Seconds (without alignments) 1717.381 Million cell updates/sec

Title:

US-09-993-292B-2 1515 1 MTSIFAEQTVEVVKSAIETA.....NEYQQRHGKKTLFEVPDVAS 305 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2002273 seqs, 358729299 residues Searched:

2002273 of hits satisfying chosen parameters: Total number

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 50 summaries

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geneseqp2000s:*
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geneseqp2003bs:* geneseqp1980s:* geneseqp1990s:* geneseqp2004s:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	uo.	Salmonell	Salmonell	Haemolysi	Novel hum	Bacterial	Pathogen	Photorhab	Drosophil	E. faeciu	Candida a	Protein e	Protein e	Protein e	E. faeciu	Hyalurona	Intracell	Intracell	Intracell	Human gol	Protein d	Human gol	Human gol	Human gol	Protein e	Putative
	G	Abg73265	Abq73266	Aar67645	Abg25221	Ad£07451	Abj19025	Abm68103	Abb71280	Adc95690	Abp73774	Abu42996	Abu28937	Abu18419	Adc95523	Aar43563	Abu53070	Abu53071	Abu53077	Abr61599	Abu07445	Abr61600	Abr61601	Abr61602	Abu25599	Aab96493
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SUMMARIES	ΙD	ABG73265	ABG73266	AAR67645	ABG25221	ADF07451	ABJ19025	ABM68103	ABB71280	ADC95690	ABP73774	ABU42996	ABU28937	ABU18419	ADC95523	AAR43563	ABU53070	ABU53071	ABU53077	ABR61599	ABU07445	ABR61600	ABR61601	ABR61602	ABU25599	AAB96493
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de	Query Match	100.0	100.0	91.7	71.2	8.0	7.8	7.8	7.6	7.5	7.4	7.4	7.4	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.2	7.2
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Abu53079 Intracell	Abb59245 Drosophil		Abg72693 Fruitfly	Adg98862 Fruit fly	Abu43311 Protein e	Abp40235 Staphyloc	G	Abr53560 Protein s	Adk64380 Disease t	Abp39975 Staphyloc	Abb49720 Listeria	Aaw22775 Human RAD	Aaw71295 Human hom	Abb63519 Drosophil	Adh62807 Lactobaci	9	Abb64018 Drosophil	Ada32997 Acinetoba	Adb08930 Alloiococ	Aag82283 S. epider	0	Abb77985 Amino aci	Adj68860 Human hea	Adj66509 RAD50 hom
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92	1048	1066	1066	1066	3692	3696	129	187	187	1211	92	1312	131	2346	4734	7201	9	81	86	88	283	131	131	131
7.2	7.2	7.2	7.2	7.2	7.2	7.2	7.1	7.1	7.1	7.1	7.0	7.0	7.0	7.0	7.0	7.0	7.0	7.0	7.0	7.0	7.0	7.0	7.0	7.0
109	108.5	108.5	108.5	108.5	108.5	108.5	107.5	107.5	107.5	107	106.5	106.5	106.5	106.5	106.5	106.5	106	106	106	106	106	105.5	105.5	105.5
26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	20

ALIGNMENTS

Salmonella typhi cytolysin A (ClyA) protein. ABG73265 standard; protein; 305 AA (first entry) 17-APR-2003 ABG73265; RESULT 1

Protein expression vector; expression cassette; export protein; transformed host cell; bacterial cell; immune response; HlyE family; cytolygin. A; ClyA; recombinant protein; bioreactor; bacterial growth; live vector immunogenic composition; animal feed; animal vaccination; food industry; nutritional supplement; biomediation; waste disposal; waste treatment; host bacterium.

Salmonella typhi

US2002146430-A1.

10-OCT-2002.

23-NOV-2001; 2001US-00993292.

22-NOV-2000; 2000US-0252516P.

(GALE/) GALEN J E.

Galen JE;

WPI; 2003-228013/22. N-PSDB; ABX15174.

Novel system for expressing protein of interest, has expression vectowith cassette having export protein coding sequence fused to protein coding sequence, host cell transformed with vector, and culturing

environment

Claim 5; Page 18; 33pp; English.

The present invention relates to a system for expressing a protein of interest. The system comprises an expression vector having an expression

cassette expresses the tor the transformed nost cell, where the expression cassette expresses the export protein-protein of interest fusion protein cassette expression vector. Which is exported out of the host cell. The system is useful for expressing agene in a bacterial cell, by providing an expression vector to a population of untransformed bacterial cells, and expressing the expression protein is produced and exported into the culture medium. The protein of interest is preferably an antigen and this method is useful for the interest is preferably an antigen and this method is useful for celiciting an immune response from a host against the fusion protein. CC (ClyA). The system is useful for the production of recombinant proteins (ClyA). The system is useful for the production of recombinant proteins (ClyA). The system is useful for the system is also useful for providing an animal antigenic material against which an immune response may be mounted. The obtained recombinant bacterium (e.g. Salmonalla) can be used as a live vector immunogenic composition capable of facilitating the generation of an immune response in an animal. The system is also useful for preparing immunogenic compositions for vaccinating animals, and for use in the food, nutritional supplement, animal feed, and for use in the food, nutritional supplement, animal feed, to host bacterium can also be expression vector, and then the combinant host cells can be transformed with the expression vector, and then the population of bacterial host cells can be maintained in culture and used to produce protein swithout having to harvest and lyse the host cells. The present represents salmonella typhi ClyA protein coding sequence genetically fused to a DNA sequence encoding the protein of interest, a host cell transformed with the expression vector, and a culturing environment for the transformed host cell, where the expression cassette, where the expression cassette comprises an export protein

Sequence 305 AA;

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                                                                                                                                                                       LVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRIL 120
                                                                                                                                                                                                          DDGVKKLNEAOKSLLTSSOSFNNASGKLLALDSOLTNDFSEKSYFOSOVDRIRKEAYAG 180
                                                                                                                                                                                                                            DGGVKKLNEAQKSILITSSQSFNNASGKILALDSQLTNDFSEKSSYFQSQVDRIRKEAYAG 180
                                                                                                                                                                                                                                                                             AAAGIVAGPFGLIISYSIAAGVIEGKLIPELNNRLKTVQNFFTSLSATVKQANKDIDAAK 240
                                                                                                                                                                                                                                                                                                                                               LKLATEIAAIGEIKTETETTRFYVDYDDLMLSLLKGAAKKMINTCNEYQQRHGKKTLFEV 300
                                                                                                    1 MTSIFAEQTVEVVKSAIETADGALDLYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASV 60
                                                                                                                                                                                                                                                                                                                                                                   LVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRIL
                                                                    1 MTSIFAEQTVEVVKSAIETADGALDLYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASV
                                   Gaps
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100.0%; Score 1515; DB 6; Length 305; 100.0%; Pred. No. 9.5e-116; ive 0; Mismatches 0; Indels 0.
                al Similarity 100.
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Protein expression vector; expression cassette; export protein; transformed host cell; bacterial cell; immune response; HlyE family;
                                                                                                                          Salmonella typhi ClyA-Bacillus subtilis sacB fusion protein.
                              ABG73266 standard; protein; 749 AA.
                                                                                              (first entry)
                                                                                              17-APR-2003
                                                            ABG73266;
RESULT 2
               ABG73266
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live vector immunogenic composition; animal feed; animal vaccination; food industry; nutritional supplement; biomediation; waste disposal; waste treatment; host bacterium; sacB; mutant; mutein;

Salmonella typhi. Bacillus subtilis.

Synthetic. Chimeric.

US2002146430-A1.

10-OCT-2002

23-NOV-2001; 2001US-00993292

22-NOV-2000; 2000US-0252516P.

(GALE/) GALEN J

Galen JE;

WPI; 2003-228013/22. N-PSDB; ABX15191 Novel system for expressing protein of interest, has expression vector with cassette having export protein coding sequence fused to protein coding sequence, host cell transformed with vector, and culturing

Example 3; Page 25-28; 33pp; English.

Conting present Inventor Federa to a system for expressing a protein of interest. The system comprises an expression vector having an expression cassette comprises an export protein coding sequence genetically fused to a DNA sequence encoding the protein of interest, a host cell transformed with the expression vector, and a culturing environment for the transformed host cell, where the expression cassette expresses the export protein-protein of interest fusion protein cassette expresses the exported cell. The system is useful for expression a gene in a bacterial cell. By providing an expression vector cassette, such that the export protein-protein of interest their protein is produced and exported into the culture medium. The export protein in grade and exported into the culture medium. The export protein in grade and exported into the culture medium. The export protein may be a member of the HIMP family such as cytolysin A (ClyA). The system is useful for the production of recombinant proteins for the production of recombinant proteins can be used as a name of bacteria. The system is also useful for the production of recombinant proteins may be mounted. The obtainant bacterial against which an immune response composition capable of facilitating an alimal antigent excembinant bacterium of an immune response in an animal. The system is also useful for use in the food, nutritional supplement, animal feed, blomediation, waste disposal, and waste treatment industries. The system is very advantageous for protein expressed. A population of recombinant host cells can be transformed with the expression vector, and then the copulation of bacterial mediation, as proteins without having to harvest and lyse the host cells. The present sequence represents Salmonella typhi ClyA, as a fusion contract to export heterologous antigens out of S. typhi present invention relates to a system for expressing a protein of

Sequence 749 AA;

Gaps ö Length 749; Indels 100.0%; Score 1515; DB 6; ilarity 100.0%; Pred. No. 3e-115; Conservative 0; Mismatches 0; Query Match Best Local Similarity Matches 305; Conserva

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AAAGIVAGPEGLIISYSIAAGVIEGKGLIPELNNRLKTVQNFFTSLSATVKQANKDIDAAK 240
                                                                   DDGVKKLNEAQKSLLTSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDRIRKEAYAG 180
                                                                                                                                                                                                                           LKLATEIAAIGEIKTETETTRFYVDYDDLMLSLLKGAAKKMINTCNEYQQRHGKKTLFEV 300
                                                                                                                      MTSI FAEQTVEVVKSA I ETADGALDLYNKYLDQVI PWKTFDETI KELSRFKQEYSQEASV
                                                  LVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; chromosome mapping; gene mapping; gene therapy; forensic supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human diagnostic protein #25212.
                                                                                                                                                                                                                                                                                                                                                              ABG25221 standard; protein; 1035 AA.
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23-AUG-2000; 2000US-00649167.
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                                                                                                                     DGGVKKINEAQKSLITSSQSFNNASGKLIALDSQLTNDFSEKSSYFQSQVDRIRKEAYAG 180
                                                                                                                                                          240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      used as an immunogen in a vaccine composition against tuberculosis (Wycobacterium tuberculosis). (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PP field.) (Updated on 25-MAR-2003 to correct PA field.)
                                                  120
                                                                                                     DDGVKKLNEAQKSLLTSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDRIRKEAYAG 180
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                                                                                                                                                                       LVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid encoding haemolytic regulator of E coli - and vectors, proteins etc used to transform Mycobacterium cells to antituberculosis vaccines providing improved immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence represents the E. coli haemolysis regulator which
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91.0%; Pred. No. 1.7e-105;
iive 15; Mismatches 12;
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P-PSDB; AAQ75857.
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06-JUL-1995
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food
New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                 Claim 20; SEQ ID NO 55580; 103pp; English
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Gaps

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Indels

Conservative

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FGLIISYSIAAGVVECKLIPELKNKLKSVQNFFTTLSNTVKQANKDIDAAKLKLTTEIAA 180
supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences in the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                               130 AQKSLLTSSQSFNNASGKILALDSQLTNDFSEKSSYFQSQVDRIRKEAYAGAAAGIVAGP 189
                                                                                                                                                                                                                                                                                                                                   70 MDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDRYNEKKASAQKDILIRILDDGVKKUNE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New Proteus mirabilis polypeptides and polynucleotides, useful as reagents for diagnosis of bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proteus mirabilis infection; bacterial infection; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IGEIKTETETTREYVDYDDLMLSLLKGAAKKMINTCNEYQQRHGKKTLFE 299
                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                 71.2%; Score 1079; DB 4; Length 1035; 92.2%; Pred. No. 2.4e-79;
                                                                                                                                                                                                                                                                                    7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 7736; 870pp; English
                                                                                                                                                                                                                                                                                    11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADF07451 standard; protein; 1036 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THERAPEUTICS CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-APR-2000; 2000US-00543681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0128706P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacterial polypeptide #3564.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                   Query Match 71.2 Best Local Similarity 92.2 Matches 212; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-895291/82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ADF03279
                                                                                                                                                                                                                        Sequence 1035 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunostimulant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GENO-) GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US6605709-B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Breton GL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADF07451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  190
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                                                                                                                                                                                                                                                                                                                                                                                                                  61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----EISATVK---QANKDIDAAKLKLAT------EIAAIGEIKTETETTRFYV 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  516
                                                                                                                                                                                                                                                                                                                                                                            220
                                                                                                                                                                                                                                                                                                                                                                                                             54 YSQEASVL------VGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAXILL-FDEY 104
                                                                                                                                                                                                                                                                                                                                                                                                                                     149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            337 AIADOFKRANKIEEYSORFKKFGYEGDSLLAAFRKETGAIDASLTTINTALGTISÄGISÄ 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              224
The invention relates to new Proteus mirabilis polypeptides and polynucleotides. The invention also relates to antibodies against the polypeptides, amethod for producing the polypeptides, amethod of penerating vaccines for immunising an individual against P. mirabilis, a method for evaluating a compound for the ability to bind a P. mirabilis polypeptide and a method for screening test compounds for anti-bacterial activity. The polypeptides and polynucleotides are useful as molecular targets for diagnosing, preventing and treating pathological conditions resulting from bacterial infection, as reagents for diagnosis of bacterial diseases, as components of antibacterial vaccines, as targets for antibacterial drugs or as bio-control agents for plants. This sequence represents a proteus mirabilis polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                             53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV; hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen; auto-immunity; vaccine; staphylococcal infection; antibody; cancer; autoimmune disease; HIV; hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pathogen specific antigen related staphylococcal protein SEQ ID No 274.
                                                                                                                                                                                                                                                                                                                                                                       184 GIVAGPFGLIISYSIAA--GVIEG-----KLIPELNNRLKTV------QNFFTS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     457 YDARHSAFLEDNFKLLSQYNKEYSVERSVLITQQHWDELIGELASVTKNGAKTLSGKSYI
                                                                                                                                                                                                                                                                                                                                           2 TSIFAEQTVEVVK-----SAIBTADGALDLYNKYLDQVIPWKTFDETIKELSRFKQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALDSQL--TNDFSEKSSYFQ-----SQVDRIRKEA-------YAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --- AOKSLLTSSOSFNNASGKLL
                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                           Indels 115;
                                                                                                                                                                                                                                                                      Length 1036;
                                                                                                                                                                                                                                                                        8.0%; Score 121.5; DB 7;
20.7%; Pred. No. 0.67;
Live 66; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DYDDLMLSLLKGAAKKMINTCNEYOOR 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DYYE-----EGKRLEKKPNEFÖKQ 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105 NEKKASAQKDILIRILDDGVKKLNE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABJ19025 standard; protein; 2681 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JAN-2002; 2002WO-EP000546.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-JAN-2001; 2001AT-00000130.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-MAR-2003 (first entry)
                                                                                                                                                                                                                                                                                           Local Similarity 20.7
les 80; Conservative
                                                                                                                                                                                                                                         Sequence 1036 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus
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Matches
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producing hyperimmune serum-reactive antigens from a pathogen, tumour, allergen, a tissue or host prone to auto-immunity, where the antigens are used in a vaccine, comprises providing antibody preparation from a plasma pool of a type of animal, or individual sera with antibodies against the specific pathogen, tumour, allergen, tissue or host prone to auto-immunity. The hyperimmune serum-reactive antigens comprising any of the care sequences of 53-2261 amino acids fully defined in the specification, or their hyperimmune fragments are useful for the manufacture of a parameterical preparation, particularly a vaccine against staphylococcal infections or colonisation against S. aureus or S. epidermidis. The preparation of antibodies is useful for the manufacture of a medicament for treating or preventing staphylococcal infections or colonisation against S. aureus or S. epidermidis at the antibody preparation may also be used for diagnostic and imaging purposes other conditions that can be treated include cancer, autoimmune diseases or infections caused by viral (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This sequence represents a staphylococcal protein relating to the method for identifying and producing pathogen specific antigens of the invention
                                                                                                                                                                                                           Identifying, isolating and producing hyperimmune serum-reactive antigens from a pathogen, for preparing vaccine or medicament for treating or preventing e.g. staphylococcal infections, comprises providing antibody
                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel method for identifying, isolating and
                                                                               Hafner M;
                                                         Zauner W;
                                                 Von Ahsen U, Klade C, Henics T,
O, Etz H, Dryla A, Weichhart T,
(CIST-) CISTEM BIOTECHNOLOGIES GMBH.
                                                                                                                                                                                                                                                                                                                                                Example 7; Page 200; 252pp; English.
                                                 Meinke A, Nagy E, Vor.
Minh DB, Vytvytska O,
Tempelmaier B;
                                                                                                                                                             WPI; 2003-075410/07.
                                                                                                                                                                                                                                                                                              preparation.
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Gaps 91; 7.8%; Score 118.5; DB 6; Length 2681; 21.3%; Pred. No. 4; lve 50; Mismatches 125; Indels 91; Query Match
Best Local Similarity 21.3%; Sequence 2681 AA;

1162 TA-----VIEQIIADGKVDESEK 1193 89 VVTQLLSAYILLFDEYNEKKASAQKDILIRILDDGVKKLNEAQKSLLTSSQSFNNASGKL 148 LALDSQLTNDFSEKSSYPQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLI 208 209 PELNNRLKTVQNFFTSLSATVKQANKDI-----DAAKLKLATEIAAIGEIKTETETTRF 262 88 FKQEY------SQEASVLVGDIKVL-----LMDSQDKYFEATQTVYEWC--G 1254 QRDGAVITYYYSGVPTLSNDPAKSW--TTNDLKDLHIK 1289 2 TSIFAEQTVEVVKSAIETADGALDLYNKYLDQVIPWKTFDET-263 YVD-----YDDLMLSLLKGAAKKMINTCNEYQQRHGK 294 20 149 셤 g g g 셤 ద ઠે ઠે δ 8 ઠ à

Sequence 582 AA;

ABM68103 standard; protein; 582 ABM68103; ABM68103 ID ABM6 XX AC ABM6 XX DT 20-N

(first entry)

20-NOV-2003

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Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;
                                   detection; food; gene expression; plant; animal; microorganism; toxin; antibiotic; biopesticide; virulence factor; disease model; plague;
                                                                                                                                                                                                                                               Genomic sequence of Photorhabdus luminescens and encoded polypeptides, useful e.g. as therapeutic antimicrobials and agricultural pesticides.
                                                                                                                                                                                                 Danchin A;
                                                                                                                                                                                              Kunst F,
        Photorhabdus luminescens protein sequence #1200.
                                                                                                                                                                                                 Frangeul L,
                                                                                                                                                                                                                                                                           Claim 2; SEQ ID NO 1200; 1205pp; French.
                                                                                                                                                                                                 Taourit S, Glaser P,
                                                                                                                                                                      (INSP ) INST PASTEUR.
(CNRS ) CNRS CENT NAT RECH SCI.
                                                                                                                                07-FEB-2002; 2002WO-IB003040.
                                                                                                                                                   07-FEB-2001; 2001FR-00001659.
                                                                          Photorhabdus luminescens
                                                                                                                                                                                                                             WPI; 2003-148459/14.
                                                        whooping cough.
                                                                                            WO200294867-A2
                                                                                                                                                                                                          Buchrieser C;
                                                                                                                                                                     INSP ) INST
                                                                                                              28-NOV-2002
                                                                                                                                                                                                 Duchaud
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The invention relates to the isolation of genes and their encoded proteins from Photorhabdus luminescens. The isolated sequences are sources of probes and primers for detecting the genome of P. luminescens and related species; to study polymorphisms; for gene analysis and for detection/amplification of the genes. Antibodies (Ab) raised against the polymorphides encoded by the genes are used for detection/identification of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that carry a gene-containing vector are used to select compounds that carry a gene-containing vector are used to select compounds that carry a gene-containing vector are used to select compounds that carry a gene-containing vector inhibit expression of the genes in plants, animals or microorganisms other than P. luminescens and are able to alter response or sensitivity to toxins and antibiotics produced by P. cecombinant production of the proteins, particularly toxins and antibacterials useful as insecticides, bactericides and fungicides. The therapeutically (to treat microbial infection by bacteria or fungi that are sensitive to P. luminescens-ended toxins or antibiotics) and as biopesticides. Other uses of the genes and the proteins are as virulence are containing targets of human diseases for which P. Luminescens is a model (particularly plaque and whooping cough). This sequence represents one of the isolated P. luminescens

133 LETPPPAYYFLPFYIDQIKSWSSPWNSFENLGQYSNWKGPLIKYFTGYLKPEHFDIEENI 192 76 YFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKA-----SAQKDIL------ 116 253 LYDAQATI ---TSNIYDLESQYALAITSANELEADYKFAVESIPTDYLECPLCGTLHDNS 309 ----IRILDDGVKKLNEAQKSLLTSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDR 172 193 YEYSEIKKESAHKIEKFQSAVEVIVDNTVDSPITLDNNDFIKIONEIKNELYDLIDYOTR 252 75 Indels 109; Length 582; 17 IETADGALDLYNKYLDQV----IPWKTF-------7.8%; Score 117.5; DB 6; 19.2%; Pred. No. 0.68; iive 56; Mismatches 142; 45 KELSRFKQEYSQEASVLVGDIKVL-----Local Similarity 19.2% les 73; Conservative 117 Query Match Best Loca Matches

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69 LMDSQDKYFEA-----TQTVYEW-----CGVVTQLLSAYILLFDEYNEKKASAQ 112
                                                                                                                                                                                                                                                                                                   RESULT 9
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           -----NSIASKIVELKSSL-NSLNEDAQFITNEIER 357
                                      IRKEAYAGAAA---GIVAGPFGLIISYSIAAGV----IEGKLIPELNNRLKTVQNFFTS 224
                                                                INNKYITDDDAVKKGLIAQVIDTLSTENVSKNIQIKIDNEDLNISKANSSIKELKKDQKK 417
                                                                                            LSATVKQANKDIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDLMLSLLKGAAKKMI-N 283
                                                                                                                   LLST-KEKEELNSSFMSKLLANIBALGSTGINLSKVKSPTDYKQLLGGGAAEAARGLLAY 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABBS707). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                            Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 40632; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 588;
                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster polypeptide SEQ ID NO 40632.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.6%; Score 114.5; I 21.1%; Pred. No. 1.2; tive 38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Myers EW
                                                                                                                                                                                                                                                     ABB71280 standard; protein; 588 AA
                                                                                                                                                        284 TCNEYQQRHGKKTLFEVPDV 303
                                                                                                                                                                               QLSVLQQIHGAKTCVVPPFV 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAR-2001; 2001WO-US009231.
                 310 LPNRALLLSEKDSLLNEA-
                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-656860/75.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                               pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         interactions.
                                                                                                                                                                                                                                                                                                             26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-SEP-2001
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Best Local S:
Matches 67,
                                                                                                                                                                                                                                                                                  ABB71280;
                                                                                                   225
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                                             173
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The invention relates to an isolated nucleic acid derived from
Enterococcus faecium encoding an Enterococcus faecium polypeptide having
Enterococcus faecium encoding an Enterococcus faecium polypeptide having
Composition of 10 fully defined sequences given in the (or comprising 40
sequential nucleotides chosen from any of the nucleic acids, its
complement or sequences hybridising to it. Also included are a
recombinant vector comprising the nucleic acid operably linked to
transcription regulatory element, a cell comprising the vector and
transcription regulatory element, a cell comprising the vector and
transcription and eroperable sequences encoding 3654 disclosed proteins.
Chosen from 3654 disclosed sequences encoding 3654 disclosed proteins.
The nucleic acids is useful for diagnosing pathological conditions
resulting from E. faecium bacterial infection (e.g. urinary tract
infection, bacteraemia, endocarditis, wounds and abdominal-pelvic
infection, and for screening drugs such as agonists and antagonists. The
uncleic acid is useful for recombinant production of Candida albicans -
                                                                                                                                                               -----SQINSLIELKNVPEVRNLTKTSIRKLSFL 482
                                                                                                                                                                                                                               483 DNQLALFNQTQENRYYSVEAVIKAWTPTNLKEINDLTHALSISQKRTDLAIAISGSAEYN 542
334 -LDNQAEYLDAIEVTBELLRNQTQELLLWEVELLRGVVTSFQN-----LDIFANRSIEAV 387
                                           113 KDILIRILDDG-----VKKLNEAQKSLLTSSQSFNNASGKLLALDSQLTNDFSEKSSY 165
                                                                     -----TVQNPFTSLSATV-----KQANK-----DIDAAKLKLATEIAAIGEIK 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid derived from Enterococcus faecium encoding Enterococcus faecium polypeptide useful for detection, prevention and treatment of a pathological condition resulting from a bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vaccine; urinary tract infection; bacteraemia; endocarditia; wound; abdominal-pelvic infection.
                                                                                                                         166 POSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNNRLK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; SEQ ID NO 5317; 243pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E. faecium protein sequence SEQ ID 5317.
                                                                                                                                                                                                                                                                                                                                                                                                                                  ADC95690 standard; protein; 515 AA
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                                                                                                                                                                                                                                                                                            TETETTRF--YVDYDDL 269
                                                                                                                                                                                                                                                                                                                   ||| ||| |||
TETYPTRFISYKGIEDI 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-00107532
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98US-0085598P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                       444 LEDSFDNLNK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-799836/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Joucette-Stamm LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ADC92036.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US6583275-B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADC95690;
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13;

Indels 115;

97;

Similarity 21.1% 57; Conservative

67;

68

11 EVVKSAIETADGALDLYNKYLDQV--IPWKTFDETIKELSRFKQEYSQEASVLVGDIKVL

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RESULT 11
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derived peptides or antisense polypeptides. Pharmaceutical compositions and vaccines containing the nucleic acid are useful for preventing or treating Enterococcus faecium infections. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Constructing strains for identifying gene products as effective targets for therapeutic intervention, by inactivating in the strain one allele of a gene and placing other allele of the gene under conditional expression.
                                                                                                                                                                                                                                                                                          | | : : | | : : | | | | CRYEEYIRSQGEVRDG----VTTVNAAAVVPEEVIGEVFDLKRS--NYNLAQYATVKTV 282
                                                                                                                                                                                                                                                                          ---EAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNNRLKTVQNFFTSLSATVKQA 232
                                                                                                                                                                                                                                                                                                                                                 SN--GQGKYPVÅTNQQAVLATKAELAEIGDIDAEMFTS---VDYKVETRAGKIALSNEVV 337
                                                                                                                                                                                             DITYSNDVYENISKGVVDSMSFGFVLGLDSFDKK----EDGTIERSIDKIKALNEI--S
                                                                                                                                                                                                                                           ::| | : : | | : : : | 1.0 VVTVPAYDSSNVQVNKRSYESFMSNNQAKQTNNSLESTSKAQKESNNMEKTLIDNEKTEL
                                                                                                                                                       FVEVITP----EALKEVDLSNVFLLYGHDYSKPLASVKAGTLK-LNVDDTGLHFEAELT
                                                                                                                                                                              -----VYEWC--GVVTQLLSAYILLFDEYNEKKASAQKDILIRILDDGVKKLNEAQKS
                                                                                                                                                                                                                             LLT-----SSOSFNNASGKLLALDSQL--TNDFSEKSSYFQSQVDRIRK------
                                                                                                                                30 YLDQVIPWKTFDETIKELS-----RFKQEYSQE-ASVLVGDIKVLLMDSQDKYFEATQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pungus, yeast, tetracyclin, promoter, GRACE strain, biosynthesis, signal transduction, DNA replication, cell division, growth, proliferation, Candida albicans, fungicide, antifungal.
                                                                                                         96;
                                                                                 DB 7; Length 515;
                                                                                                                                                                                                                                                                                                                                                                                      EDSAVNIVQEVKDQLAKLVENTDNKHIMDLLKTFTKKTAATLDDL 382
                                                                                                                                                                                                                                                                                                                                                                        DDLMLSLLKGA----AKKMINTCNEY----QQRHGKKTLFEVPDV 303
                                                                                7.5%; Score 114; DB 7; Length 515
23.5%; Pred. No. 1.1;
tive 61; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                          NKDIDAAKLKLAT------EIAAIGEIKTETETTRFYVDY-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Candida albicans essential protein SEQ ID NO 7611.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ohlsen
                      treating Enterococcus faecium infections one if the disclosed E. faecium proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABP73774 standard; protein; 1948 AA
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20-FEB-2001; 2001US-00792024.
22-AUG-2001; 2001US-0314050P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-DEC-2001; 2001WO-US049486.
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                                                                                                         81; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Roemer T, Jiang B,
                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Candida albicans
                                                          Sequence 515 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200253728-A2
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The invention relates to constructing (M1) a strain of diploid fungal cells in which both alleles of a gene are modified, comprising modifying cone allele by insertion or replacement by a cassette having an expensable selectable marker and modifying other allele by promoter. So that expression of the second allele is regulated by the promoter. So that expression of the second allele is regulated by the promoter. (M1) is useful for constructing a strain of diploid fungal cells in which both alleles modified are useful for identifying a gene that contributes to the survival or growth of a fungus, a gene that contributes to the resistance of a diploid fungus to an antifungal agent, an antifungal agent that inhibits the growth of a fungus and for identifying a therapeutic agent for treatment of a mammalian agent, an autifungal agent that inhibits the growth of a mammalian compound catabolism, biosynthetic, transporter, transcriptional, compound catabolism, biosynthetic, transporter, transcriptional, compound actabolism, signal transduction, DNA replication and cell division activity. The method is useful for identifying a compound having the ability to inhibit growth or proliferation of C. albicans cells and for treating infection by C. albicans repeated sequence is that of an essential Candida albicans protein used in the method of the invention. Note: The sequence data for this patent is not represented in the printed contribution by the present sequence information supplied to Derwent by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1444 KTLKSTREELNGSKTEILR-----LKALLRESEDELYQVKQENYKTSVHDYEQDLAQ 1495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1496 LKVKHETLLSRNKDINESLEIYKKRSDEYYKKLELAESAIAISKRHEEQATKEMKESRSQ 1555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L-----LSAYILLFDEYNEKKASAQKDILI--RILDDGVKKLNEAQKS 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antisense, prokaryotic essential gene, cell proliferation, drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38 KTFDETIKELSRFKQEYSQEASVLVGDIKVLLMDSQDKYFEATQ----TVYEWCGVVTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLTSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194 ISYSIAAGVIEGKLIPE-LNNRLKTVQN--FFTSLSATVKQANKDIDAAKLKLATEIAAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1948;
Claim 44; SEQ ID NO 7611; 167pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1556 LLVREE------LRTTQILIKDFRIKVENLBATIEE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein encoded by Prokaryotic essential gene #28523.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.4%; Score 112.5; D
Local Similarity 22.2%; Pred. No. 8.3;
tes 58; Conservative 40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ź
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251 GEIKTETETTRFYVDYDDLML 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         specification but is based
the European Patent Office
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Zyskind JW; Xu HH;

Ohlsen KL, Forsyth RA,

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The invention relates to an isolated nucleic acid comprising any one of the foll antiesnes sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: of the nucleic acid inhibits proliferation of a cell. Also included are: comprising a promoter operably linked to the nucleic acid (1) a vector comprising a pronoter operably linked to the nucleic acid (2) a host cell containing the vector; (3) an isolated conclain acid; (2) a host cell containing the vector; (3) an isolated conclain acid; (4) an antibody capable of specifically binding antisense nucleic acid; (4) an antibody capable of specifically binding contines nucleic acid; (4) an antibody capable of specifically binding contines nucleic; (5) producing the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular poliferation; (7) identifying a compound that inhibits cellular proliferation; (8) cequired for proliferation, or that inhibits cellular proliferation; (8) identifying a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound, a activity; (11) a culture comprising strains in which the servent or compound; a activity; (11) a culture comprise or compound that inhibits the strent or compound; a activity; (11) a culture comprise or compound that inhibits the strent or continers or of the strains is present in a culture or collection of an organism. The antisense nucleic acids are useful for contineration of an organism. The antisense nucleic acids required contined and actional actional activity; (10) and organism or screening for homologous nucleic acids required for cellular proliferation or for arranging and antisense nucleic acids required contined and actional actional actional actional actional actional actional actional actional actional actional actional actional actional actional actional actional actional actional actional actional actional actional actional actional actional actional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LVGDIKVLLMDSQDKXFEATQTVYEWC-------GVVTQLLSAYILLFDEYNE 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       223 MEQSDVIVTVSDIDHYTEDNQRLDERLINHLKSQQAEKEGQQAQINQLLQRY----- 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161 EKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNNRL----K 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 EQTVEVVK-----SAIETADGALDLYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASV 60
                                                                                                                                                                                                                                                                                                                                                                                     New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KKASAQKDILIRILDDGVKKLNEAQKSLLTSSQSFNNASGKLLALDSQLTND-----FS
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                                                                                                                                                                                                                                               Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 25; SEQ ID NO 70920; 1766pp; English.
                                                                                                                                                                                                                                               Malone C,
Carr GJ,
                                          21-WAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00946993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-0362699P.
21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 7.4%
Best Local Similarity 18.3%
Matches 61; Conservative
                                                                                                                                                                                                  (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                 Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                         WPI; 2003-029926/02.
N-PSDB; ACA46866.
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                                                                                                                                                                                                                                                         Wang Wall
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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid concoling a polypeptide whose expression is inhibited by the antisense conclair acid; (2) a host cell containing the vector; (3) an isolated contisense nucleic acid; (4) an antibody capable of specifically binding configeration or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway the gene product or that has an activity against a biological pathway or a gene product for cellular proliferation or the biological identifying a gene required for cellular proliferation or the biological corresponding and activity against a biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of a strains; or (13) identifying the target of a compound that inhibits the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                      360 EVQELESLLYVSDEQHDEKLEEIKNSYYTLMSEQSDVNNDIRFLEHTINENEAKKSRLDS 419
217 TVONFFTSISATVKQANKDIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDLMLSLLKG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antisense; prokaryotic essential gene; cell proliferation; drug design.
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Xu HH;
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein encoded by Prokaryotic essential gene #14464.
                                                                                                                                                                                                                                                     277 AAKKMINTCNEYQQ-----RHGKKTLFEV 300
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Yamamoto R,
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Carr GJ,
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324 EELDNLESQIDSIKNEKAQNE-
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06-SEP-2001; 2001US-0094893.
25-0CT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-0362851.
06-MAR-2002; 2002US-0362859P.
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Trawick JD,
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N-PSDB; ACA32807.
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Wall
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proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                            DIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRILDDG 123
                                                                                                                                                                                                                                                                 VKKLNE-AQKSLLTSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDRIRKEAYAGAA 182
                                                                                                                                                                                                                                                                                                           AGIVAGPFGLIISYS-----IAAGVIEGKLIPEL-NNRLKTVQNFFTSLSATVKQANK 234
                                                                                                                                                                                                                                                                                                                               -GMVINQFSSFYTPSEQGSSGIYADFLSESKLFQETQGNRIGELQKEIAELHMQVEQ--- 375
                                                                                                                                                                                                                                                                                                                                                     DIDAAKLKLA----TEIAAIGEIKTETETTRFYVDYDDLMLSLLKGAAKKMINTCNEYQQ 290
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                                                                                                                                                                                                                                     4 IFAEQTVEVVKSAIETADGALDLYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVLVG
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Xu HH;
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                                                                                                                                       DB 6; Length 1158;
                                                                                                                                     7.4%; Score 111.5; DB 6; Length ilarity 21.0%; Pred. No. 5.1; Conservative 58; Mismatches 121; Indels
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Forsyth RA,
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Yamamoto R,
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25-OCT-2001; 2001US-034223P.
PEBS-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
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RL-EESLSEISFVS 440
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Best Local Similarity (
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Trawick JD,
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                                                                                                                   Sequence 1158 AA;
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Wall D,
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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the mucleic acid inhibites proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense concleic acid; (2) a host cell containing the vector; (3) an isolated containing the vector; (3) an isolated polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required by the activity of proliferation or that has an activity against a biological pathway required for proliferation, or that that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation, or that inhibits cellular proliferation of an orangement of an activity; (10) profiling a gene required for cellular proliferation of an orangement of an activity; (11) a culture comprising strains in which the test compound that inhibits proliferation of a compound; a activity; (11) a culture comprising strains in which the test compound that inhibits a proliferation of a compound; a activity; (11) a culture comprising strains in which the test compound that inhibits the proliferation of an ordanism. The antisense nucleic acids are useful for the which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation in cells other than S. aureus, S. typhimurium, C. cequired for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence is encoded by one of the target prokaryotic format directly from NIPO at collection, but was obtained the collection of the collection of the printed specification.
                                                                                                                                             screening
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                                                                                                                                   New antisense nucleic acids, useful for identifying proteins or scre
for homologous nucleic acids required for cellular proliferation to
isolate candidate molecules for rational drug discovery programs.
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20.1%; Pred. No. 4.3;
Ve 43; Mismatches
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Best Local Similarity 20.15
Matches 49; Conservative
2003-029926/02
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The invention relates to an isolateu nucleic acts ustrives them.

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complement or sequences hybridising to it). Also included are a recombinant vector comprising the nucleic acid operably linked to recombinant vector comprising the nucleic acid operably linked to recombinant vector comprising the nucleic acid. The nucleic acids are single-stranded probe comprising the nucleic acid. The nucleic acids are chosen from 3654 disclosed sequences encoding 3654 disclosed proteins. The nucleic acids is useful for diagnosing pathological conditions. The nucleic acid is useful for diagnosing pathological conditions and for screening drugs such as agonists and antagonists. The infection, bactersemia, endocarditis, wounds and abdominal-pelvic infection, and for screening drugs such as agonists and antagonists. The nucleic acid is useful for recombinant production of Candida albicans and vaccines containing the nucleic acid are useful for preventing or treating Entercoccus faccium infections. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     149 LALDSQLTNDFSEKSSYFQSQ-----VDRIR-----KEAYAGAAAGIVA--GPFGLII 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : | : :: | : :: | : 439 IKIIGDHTDKYAQQYFYXDSKKSGGLTVSHLRFODTPIRSAYLVEHADLVACHTP-AYLH 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       269 AEEVIVSMGSVAQTIEQTIDYLNANGRKTGFLNIHLYRPFPVETFVQKLPHTVKTIAVLD 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 AEQTVEVVKSALETADGALDLYNK-----YLDQVIPWKTFDE-----TIKELS 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid derived from Enterococcus faecium encoding an Enterococcus faecium polypeptide useful for detection, prevention and treatment of a pathological condition resulting from a bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEYNEKKASAQKDILIRILDDGVKKLNEAQKSL-LISSQSFN------NASGKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RFKQEYSQEASVLVGDIKVLLMDSQ------DKYFEATQTVYEWCGVVTQLLSAYILLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vaccine; urinary tract infection; bacteraemia; endocarditis; wound; abdominal-pelvic infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 7.3%; Score 111; DB 7; Length 1231; Best Local Similarity 23.3%; Pred. No. 6.1; Matches 78; Conservative 58; Mismatches 125; Indels 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; SEQ ID NO 5150; 243pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          treating Enterococcus faecium infections.
                                                 faecium protein sequence SEQ ID 5150.
                                                                                                                                                                                                                                                                                                                                                                    (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                            97US-0051571P.
                                                                                                                                                                                                                                                                                                                                 98US-0085598P
                                                                                                                                                                                                                                                                       98US-00107532
                                                                                                                                                                                                                                                                                                                                                                                                           Bush D;
                (first entry)
                                                                                                                                                     Enterococcus faecium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1231 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ADC91869.
                                                                                                                                                                                                                                                                       30-JUN-1998;
                                                                                                                                                                                                                                                                                                                                 14-MAY-1998;
                                                                                                                                                                                            US6583275-B1
                                                                                                                                                                                                                                                                                                                02-JUL-1997;
                01-JAN-2004
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101

Gaps

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The sequence is that encoded by a cDNA clone encoding the hyaluronan receptor (HARC). The sequence was obtd. by screening a 3T3 library in creeptor (HARC). The sequence was obtd. by screening a 3T3 library in clambda gill with antibodies to HARC. A clone of 1.9 kb was obtained and land to rescreen the library to obtain the full length, 2.9 kb clone. HA is dead to rescreen the library to obtain the full length, 2.9 kb clone. HA consider the library normal cells and is only expressed in stitutions where cell motility is desired, e.g. in wound healing, in cresponse to growth factors and in chemoteaxis by white blood cells. HA may compose to growth factors and in chemoteaxis by white blood cells. HA may compose to growth factors and in chemoteaxis by white and chronic clocomotion, e.g. tumour invasion, birth defects, acute and chronic clocomotion, e.g. tumour invasion, birth defects, acute and chronic clocomotion, e.g. tumour invasion, birth defects, acute and chronic course, surgical incisions and adhesions, strokes, multiple sclerosis, burns, surgical incisions and adhesions, strokes, multiple sclerosis, involving nerve sprouting; also in CNJ and spinal cord regeneration, invitro fertilisation and embryo development. See also contraception, in vitro fertilisation and embryo development. See also on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                         Hyaluronan binding protein; HA; RHAMM; mediated motility; wound; healing; diagnosis; treatment; cell locomotion; tumour invasion; birth defects; inflammatory disorder; Alzheimer's disease; dementia; barkinson's disease; Huntington's disease; AIDS; diabetes; auto; immune diseases; corneal dysplasia; hypertrophy; surgery; burns; strokes; multiple sclerosis; depression; schizophrenia; CNJ; contraception; in vitro fertilisation; embryo development.
                      SYSIAAGVIEGKLIPELNNRLKTVQNFFTSLSATVKQ--ANKDI----DAAKLKLATEIAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding hyaluronan receptor - used to produce proteins and antibodies for alteration of cell locomotion.
                                                                               250 IGEIKTETETTRF----YVDYDDLMLSLLKGAAKK 280
                                                                                                      (MANI-) MANITOBA CANCER TREATMENT & RES FOUND.
                                                                                                                                                                                                                        AAR43563 standard; protein; 476 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 7; Fig 23; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93WO-CA000158.
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                                                                                                                                                                                                                                                                                                       (revised)
(revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1993-351722/44.
                                                                                                                                                                                                                                                                                                                                                                                        Hyaluronan receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 476 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAQ51212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-APR-1993;
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09-JAN-2003
05-APR-1994
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This invention describes novel polynucleotides and polypeptides isolated from human cDNA libraries which can be used for gene therapy or in vaccines. The polynucleotides of the invention and antibodies encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The products of the invention may also be used to identify modulators of expression and activity and to down regulate expression and activity. The antibodies of the invention may also be used as diagnostic agents for detecting the presence of polypeptides in samples. This sequence represents a homologue of a polypeptide described in the disclosure of the invention
                                                                                    LVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRIL 120
                                                                                                                                                                                             DDGVKKLNEAQKSLLTSS---QSFNNASGKLLALDSQLTN-DFSEKSSYFQSQVDRIRKE 176
                                                                                                                                                                                                                                                            177 AYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNNR-----LKTVQNFF----TSL 225
                                                                                                                                                                                                                                                                                 265 ILTAESTN-----QEYA------RWVQDLQNRSTLKEBEIKEITSFLEKITDL 307
                                                                                                                                                                                                                                                                                                                           226 SATVKQANKDI------DAAKLKLATBI-----AAIGBIKTETETTRFYVD-YD 267
                                                                                                                                                                                                                                                                                                                                                          308 KNQLRQODEDFRKQLEEKGKRTAEKENVMTELTMEINKWALLYELYEKTKPFQQQLDAFE 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids having the sequences of clones isolated from libraries of different human tissues, useful in recombinant DNA methodologies.
                                                                                                                                                                                                                1 MTSIFAEQTVEVVKSAIETADGALDLYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASV
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Intracellular trafficking-associated DKFZphtes3 1913 homologue #3.
                               67;
 Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; gene therapy; vaccine; disease treatment; detection.
                               73; Mismatches 125; Indels
DB 2;
                                                                                                                                                                                                                                                                                                                                                                                           DLMLSLLK--GAAKKMINTCNB-YQQRHGKKTL 297
                                                                                                                                                                                                                                                                                                                                                                                                            368 AEKOALLNEHGATOEOLNKIRDSYAOLLGHONL 400
Score 110.5;
Pred. No. 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example III; Page 667; 1095pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABU53070 standard; protein; 951
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               20.4%;
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                                 Conservative
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                Similarity
68; Conserv
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28-SEP-1999;
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                                                                                                                               61
                                                                                                                                                                                             121
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Query Match
Best Local
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                                                                                                                          | : :| | | : :| | | : : | | | EKKMEKVKOKAKEMOETLK--KKLLDQBAKLKKELENTALELSQKEKQFNAKMLEMAQAN 451
                                                                                                                                                                  SVLVGDIKVLLMDSQDKYFEATQTVY--EWCGVVT------QLLSAYILLFDEYN 105
                                                                                                                                                                                                                             106 EKKASAQKDILI------RILDDGVKK---LNEAQKSLLTSSQSFNNASGKLL 149
                                                                                                                                                                                                                                                                                                                                                   257
                                                                                                                                                                                                                                                                                                                                                                                 999
                                                                                                                                                                                                                                                                                        150 ALDSQL-----TNDFSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVI 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids having the sequences of clones isolated from libraries of different human tissues, useful in recombinant DNA methodologies.
                                                                                                     7 EQTVEVVKSAIETADGALDLYNKYLDQVIPW-KTFDETIKELSRFKQEY-----SQEA
                                                                                                                                                                                             452 SAGISDAVSRLETNOKEQIESLTEVHRRELNDVISIWEKKLNOQAEELOEIHEIQLOEKE
                                                                                                                                                                                                                                                204 EGKLIPELNNRLKTVQNFFTSLSATVKQANKDIDAAKL---KLATEIAAIGEI---KTET
                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                       90;
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                                       ; Score 110; DB 4; Length 951; ; Pred. No. 5.3; 60; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; gene therapy; vaccine; disease treatment; detection.
                                                                                                                                                                                                                                                                                                            -----ALLEAKTNELIN 678
                                                                                                                                                                                                                                                                                                                                                                                                               258 ETTRFYVDYDDLMLSLLKGAAKKMIN 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example III; Page 668; 1095pp; English.
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                                          7.3%;
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                                                                       67; Conservative
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                                                         Similarity
              Sequence 951 AA;
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28-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             667
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                                          Query Match
Best Local 9
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                                                          Best Loc
Matches
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This invention describes novel polynucleotides and polypeptides isolated from human cDNA libraries which can be used for gene therapy or in vaccines. The polynucleotides of the invention and antibodies encoded by them may be used in the prevention, diagnosis and treatment of diseases
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                                                                                                                                                                            SVLVGDIKVLLMDSQDKYFEATQTVY--EWCGVVT------QLLSAYILLFDEYN 105
                                                                                                                                                                                                                              149
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                                                                                                                                                                                                                                                                                                                                 257
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the invention may also be used as diagnostic agents for detecting the presence of polypeptides in samples. This sequence represents a homologue of a polypeptide described in the disclosure of the invention
                                                                                                                                                                                            661
                                                                                                                                              28
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                                                                                                                                                                                                                                             ALDSQL-----TNDFSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVI
                                                                                                                              7 EQIVEVVKSAIETADGALDLYNKYLDQVIPW-KTFDETIKELSRFKQEY-----SQEA
                                                                                                                                                                                                                                                                                                                               EGKLIPELNNRLKTVQNFFTSLSATVKQANKDIDAAKL---KLATEIAAIGEI----KTET
                                                                                                                                                                                                                                                                                                                                                 Nucleic acids having the sequences of clones isolated from libraries different human tissues, useful in recombinant DNA methodologies.
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                                                                                                       Gaps
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                                                                                                       90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene therapy; vaccine; disease treatment; detection.
                                                                            Length 953;
                                                                              Score 110; DB 4; Length 95; Pred. No. 5.3; 60; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                   | : | : : | | : : | | : : | | 62 KLKAHLEKLEVDLNKSLKENTFLQEQLVELKMLAEE-
                                                                                                                                                                                                                                                                                                                                                                                      ETTRFYVDYDDLMLSLLKGAAKKMIN 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example III; Page 673; 1095pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                           -----ALLEAKTNELIN
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                                                                          7.3%;
1 Similarity 20.6%;
67; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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28-SEP-1999;
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                                                         Sequence 953
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                                                                                                          Matches
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associated with inappropriate polypeptide expression. The products of the invention may also be used to identify modulators of expression and activity, and to down regulate expression and activity. The antibodies of the invention may also be used as diagnostic agents for detecting the presence of polypeptides in samples. This sequence represents a homologue of a polypeptide described in the disclosure of the invention
                                                                                                                                                                                                                                                      SVLVGDIKVLLMDSQDKYFEATQTVY--EWCGVVT------QLLSAYILLFDEYN 105
                                                                                                                                                                                                                                                                                                                                                                           203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 569
                                                                                                                                                                                                                         297 EKKMEKVKQKAKEMQETLK--KKLLDQBAKLKKELENTALELSQKEKQFNAKMLEMAQAN 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diagnosing or prognosticating a neurodegenerative disease comprises comparing a level or activity of a transcription or translation product of golgin-245 gene in a test sample with a reference value of a known disease or health status.
                                                                                                                                                                                                                                                                           106 EKKASAQKDILI-------RILDDGVKK---LNEAQKSLLTSSQSFNNASGKLL
                                                                                                                                                                                                                                                                                                                                                                          150 ALDSQL-----TNDFSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 BQTVEVVKSAIETADGALDLYNKYLDQVIPW-KTFDETIKELSRFKQEY-----SQEA
                                                                                                                                                                                                                                                                                                                                    204 EGKLIPELNNRLKTVQNFFTSLSATVKQANKDIDAAKL---KLATEIAAIGEI---KTET
                                                                                                                                                                     Gaps
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                                                                                                                                                                    90;
                                                                                                                                       Length 961;
                                                                                                                                      n 7.3%; Score 110; DB 4; Length 96 Similarity 20.6%; Pred. No. 5.3; 57; Conservative 60; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                | : | : : : : | | : :: | 475 KLKAHLEKLEVDLNKSLKENTFLQEQLVELKMLAEE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human golgin-245 splice variant 1 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 258 ETTREYVDYDDLMLSLLKGAAKKMIN 283
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-------ALLEAKTNELIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GMBH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-APR-2002; 2002EP-00008553.
16-APR-2002; 2002US-0372424P.
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                                                                                                                Sequence 961 AA;
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                                   The invention relates to diagnosing or prognosticating a neurodegenerative disease in a subject, or determining whether a subject is at increased risk of developing the disease. The method involves determining a level and/or an activity of a transcription or translation product of a gene coding for golgin-245 and/or a fragment, derivative or variant in a sample from the subject and comparing the level and/or the activity to a reference value. The composition and methods are useful in diagnosing, preventing and/or treating neurodegenerative disease, such as Alzheimer's disease, Parkinson's disease, Huntington's disease, such as Alzheimer's disease, Parkinson's disease, Huntington's disease or amyotrophic lateral sclerosis. The recombinant, non-human animal is useful for screening, testing and validating compounds, agents and modulators in the development of diagnostics and therapeutics to treat neurodegenerative diseases, in particular Alzheimer's disease. Specific antibodies are used for detecting the pathological state of a cell in a sample from a subject. The present sequence represents a human golgin-245 splice variant 1 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | : | : | : | : | : | SAGISDAVSRLETNQXEQIESLTEVHRRELNDVISIWEKKLNQQAEELQEIHEIQLQEKE 1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EKKMEKVKQKAKEMQETLK--KKLLDQEAKLKKELENTALELSQKEKQFNAKMLEMAQAN 1010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EKKASAQKDILI------RILDDGVKK---LNEAQKSLLTSSQSFNNASGKLL 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204 EGKLIPELINNRLKTVQNFPTSLSATVKQANKDIDAAKL---KLATEIAAIGEI---KTET 257
                                                                                                                                                                                                                                                                                                                                                          7 EQTVEVVKSAIETADGALDLYNKYLDQVIPW-KTFDETIKELSRFKQEY-----SQEA 58
                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1131 KLKAHLEKLEVDLNKSLKENTFLØEQLVELKMLAEE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prostate cancer; gene expression; differential regulation; molecular marker; drug target; cancer detection; cancer diagnosis; cancer staging; cancer staging; cancer somitoring.
                                                                                                                                                                                                                                                                                                                              90;
                                                                                                                                                                                                                                                                                                    DB 7; Length 2228;
                                                                                                                                                                                                                                                                                                   7.3%; Score 110; DB 7; Length 222:
20.6%; Pred. No. 16;
tive 60; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein differentially regulated in prostate cancer #48.
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-------ALLEAKTNELIN 1237
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              Claim 18; Fig 5; Opp; English
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                                                                                                                                                                                                                                                                                                                               67; Conservative
                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                         Sequence 2228 AA;
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The invention describes genes (I) which are differentially regulated in prostate cancer. (I) Is useful for diagnosing a prostate cancer in a sample comprising prostate tissue, which involves determining the number of target genes which are differentially regulated in the sample comprises to prostate cancer. (I) Is useful for assessing a therapeutic or preventive intervention in a subject having a prostate cancer, which involves determining the expression levels in a sample comprising prostate tissue of target genes which are differentially-regulated in prostate cancer. Of target genes which are differentially-regulated in prostate cancer cells with a test agent that modulate a biological activity of a polypeptide differentially-regulated in prostate cancer cells with a test agent that conditions effective for the test agent to modulate a biological activity of the polypeptide, and cetermining whether the test agent modulates the biological activity of the polypeptide, and determining whether the test agent modulates the biological activity. (I) is useful as molecular markers, as drug targets, and for detecting, or products are used in the diagnostic test to assay for presence of cancer. Or products are used in the diagnostic test to assay for presence of cancer. (I) is useful for an also be used for expressing the polypeptide and thus to be oblogated etc. (I) is useful for an also be used for expressing the polypeptide and thus to the polypeptide end advanced for expressing the polypeptide and thus of specific genes, and groups of genes, expressed in pathways for presence of the polypeptide and thus to the polypeptide and discovery. (I) can also be used for expressing the polypeptide and thus of specific genes, and groups of genes, expressed in pathways and the delineation of targets in these pharmary which are useful in disease pathways and cellenged in pathways and cellenged in the delineated and disease pathways and educated and educated and educated and disease pathways and educated and educated and educate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 299-306; 416pp; English.
                                                                                       (ORIG-) ORIGENE TECHNOLOGIES INC.
06-APR-2001; 2001US-0281732P
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Best Local Similarity 20....
Best Local Conservative
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us-09-993-292b-2.rag

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SVLVGDIKVLLMDSQDKYFEATQTVY--EWCGVVT------QLLSAYILLFDEYN 105
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                  EGKLIPELNNRLKTVQNFFTSLSATVKQANKDIDAAKL---KLATEIAAIGEI---KTET 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diagnosing or prognosticating a neurodegenerative disease comprises comparing a level or activity of a transcription or translation product of golgin-245 gene in a test sample with a reference value of a known disease or health status.
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                                                                                                                                                                                                                                                                                                        Human golgin-245 splice variant 2 polypeptide.
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                                                                          258 ETTRFYVDYDDLMLSLLKGAAKKMIN 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Von Der Kammer H, Pohlner J;
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16-APR-2002; 2002US-0372424P.
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N-PSDB; ACF58151.
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Best Loc Matches

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1167 DKRKVSELTSKLKTTDEFFQSLKSSHEKSNKSLEDFSKLEFKKLSEELAIQLDICCKKTE- 1225
.011 SAGISDAVSRLETNOKROIESLTEVHRRELNDVISIWEKKLNOQABELOEIHEIOLOEKR 1070
                                         150 ALDSQL-----TWDFSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVI 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diagnosing or prognosticating a neurodegenerative disease comprises comparing a level or activity of a transcription or translation product of golgin-245 gene in a test sample with a reference value of a known disease or health status.
                                                                                                                         204 EGKLIPELNNRLKTVQNFFTSLSATVKQANKDIDAAKL---KLATEIAAIGEI---KTET
                           -----RILDDGVKK---LNEAQKSLLTSSQSFNNASGKLL
                                                                                                                                                                                                                                                                                                                                                           Golgin-245; neurodegenerative disease; neuroprotective; nootropic; antiparkinsonian; variant.
                                                                                           Human golgin-245 splice variant 3 polypeptide.
                                                                                                                                                                                           TCA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "encoded by CCT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "encoded by ACT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "encoded by AGT'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note= "encoded by GGT"
                                                                                                                                                                            ETTRFYVDYDDLMLSLLKGAAKKMIN 283
                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (EVOT-) EVOTEC NEUROSCIENCES GMBH.
                                                                                                                                                                                                                                                                ABR61601 standard; protein; 2250
                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pohlner J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-APR-2003; 2003WO-EP003958,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-APR-2002; 2002EP-00008553.
16-APR-2002; 2002US-0372424P.
                                 EKKASAQKDILI-----
                                                                                                                                                                                                                                                                                                                 (first entry)
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N-PSDB; ACF58152.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference 2250
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                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                  The invention relates to diagnosing or prognosticating a neurodegenerative disease in a subject, or determining whether a subject is at increased risk of developing the disease. The method involves determining a level and/or an activity of a transcription or translation product of a gene coding for golgin-245 and/or a fragment, derivative or variant in a sample from the subject and comparing the level and/or the activity to a reference value. The composition and methods are useful in diagnosing, preventing and/or treating neurodegenerative diseases, such as Alzheimer's disease, Parkinson's disease, Huntington's disease or amyotrophic lateral sclerosis. The recombinant, non-human animal is useful for screening, testing and validating compounds, agents and modulators in the development of diagnostics and therapeutics to treat methodsenerative diseases, in particular Alzheimer's disease. Specific antibodies are used for detecting the pathological state of a cell in a sample from a subject. The present sequence represents a human golgin-245 splice variant 3 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                   | : | : | : | : | SAGISSDAVSRLETNQKEQIESLTEVHRRELNDVISIWEKKLNQQAEELQEIHEIQLQEKE 1092
                                                                                                                                                                                                                                                                                                                                                                                                     EKKMEKVKOKAKEMOETLK--KKLLDOEAKLKKELENTALELSOKEKOFNAKMLEMAQAN 1032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1153 KLKAHLEKLEVDLNKSLKENTFLQEQLVELKMLAEE----------------- 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SVLVGDIKVLLMDSQDKYFEATQTVY--EWCGVVT------QLLSAYILLFDEYN 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EKKASAQKDILI------RILDDGVKK---LNEAQKSLLTSSQSFNNASGKLL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALDSQL-----TNDFSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVI 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EGKLIPELMNRLKTVQNFFISLSATVKQANKDIDAAKL---KLATEIAAIGEI---KTET 257
                                                                                                                                                                                                                                                                                                                                                                          7 EQTVEVVKSAIETADGALDLYNKYLDQVIPW-KTFDETIKELSRFKQEY-----SQEA 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Golgin-245; neurodegenerative disease; neuroprotective; nootropic; antiparkinsonian; anticonvulsant; gene therapy; human; variant.
                                                                                                                                                                                                                                                                                                                                              90;
                                                                                                                                                                                                                                                                                                                7.3%; Score 110; DB 7; Length 2250; 20.6%; Pred. No. 16; tive 60; Mismatches 109; Indels 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human golgin-245 splice variant 4 polypeptide.
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--------ALLEAKTNELIN 1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 258 ETTRFYVDYDDLMLSLLKGAAKKMIN 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABR61602 standard; protein; 2252
             Claim 18; Fig 9; Opp; English.
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                                                                                                                                                                                                                                                                                                                               Best Local Similarity 20.6 Matches 67; Conservative
                                                                                                                                                                                                                                                                                       Sequence 2250 AA;
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                                                                                                                                                                                                                                                                                                                Query Match
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The invention relates to diagnosing or prognosticating a neurodegenerative disease in a subject, or determining whether a subject is at increased risk of developing the disease. The method involves determining a level and/or an activity of a transcription or translation product of a gene coding for golgin-245 and/or a fragment, derivative or convariant in a sample from the subject and comparing the level and/or the activity to a reference value. The composition and methods are useful in diagnosing, preventing and/or treating neurodegenerative disease, such a Alzheimer's disease, Parkinson's disease, Muntington's disease or amyotrophic lateral sclerosis. The recombinant, non-human animal is useful for screening, testing and validating compounds, agents and methodics in the development of diagnostics and therappeutics to treat neurodegenerative diseases, in particular Alzheimer's disease. Specific antibodies are used for detecting the pathological state of a cell in a sample from a subject. The present sequence represents a human golgin-245 and in a sample from a subject and a control or services.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 EKKASAQKDILI------RILDDGVKK---LNEAQKSLLTSSQSFNNASGKLL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SVLVGDIKVLLMDSQDKYFEATQTVY--EWCGVVT------QLLSAYILLFDEYN 105
                                                                                                                                                                                                                                                                                                        Diagnosing or prognosticating a neurodegenerative disease comprises comparing a level or activity of a transcription or translation product of golgin-245 gene in a test sample with a reference value of a known disease or health status.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    204 EGKLIPELNNRLKTVQNFFTSLSATVKQANKDIDAAKL---KLATEIAAIGEI---KTET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 EQTVEVVKSAIETADGALDLYNKYLDQVIPW-KTFDETIKELSRFKQEY-----SQEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.3%; Score 110; DB 7; Length 22 Best Local Similarity 20.6%; Pred. No. 16; Matches 67; Conservative 60; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein encoded by Prokaryotic essential gene #11126.
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------ALLEAKTNELIN 1259
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                                                                    (EVOT-) EVOTEC NEUROSCIENCES GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 18; Fig 11; Opp; English.
16-APR-2002; 2002US-0372424P.
                                                                                                                                  Der Kammer H, Pohlner J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  splice variant 4 polypeptide
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                                                                                                                                                                                                       WPI; 2003-845345/78.
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                                                                                                                                                                                                                                       N-PSDB; ACF58153
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us-09-993-292b-2.rag

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Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                       Claim 25; SEQ ID NO 53523; 1766pp; English.
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                                                        21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00946993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-0362269P.
                                              21-MAR-2002; 2002WO-US009107
                                                                                         (ELIT-) ELITRA PHARM INC.
              Clostridium difficile
                                                                                                                  WPI; 2003-029926/02.
N-PSDB; ACA29469.
                                                                                                                                                                                                                                                                                                                                            Sequence 742 AA;
                         WO200277183-A2
                                    03-OCT-2002
                                                                                                   Wang L,
Wall D,
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Ohlsen KL, Forsyth RA,

Haselbeck R, Yamamoto R,

Malone C, Carr GJ,

Zamudio C, Trawick JD,

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The present invention relates to the genomic sequence of Pyrococcus abyssi (see AAP66431 and AAH41223-7) and P. abyssi proceins. P. abyssi is a hyperthermophilic archaeon, which is isolated from deep-sea hydrothermal vents. The present sequence is one such P. abyssi protein. The proteins of the present invention have various potential industrial uses, since the proteins are stable at very high temperatures, some up to 110 degrees centigrade. Note: This patent is in the same patent family as WO200065062, which contains additional sequences as shown in AAB99132-AAB99143, AAH75903-AAH75920 and AAG66436
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                                                                                                                                                                                                                             394 GQQPSISA--LINNVLSLSNGIGRINLANILANPDSKISKPINNIFAN---SIKVANDIITV 448
                                                                                                                                                                                                                                                                                            237 -DAAKLK----LATEIAALGEIKTETETTRFYVDYDDLMLSLLKGAAKKMINTCNEY 288
                                                                                                                                                                                              180 GAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNNRL-KTVQNFFTSLSATVKQANKDI-- 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Putative sensory transduction histidine kinase and response regulator #3.
                                 132 KSLLTSSQSFNNASGKLLALDSQLTN------DFSEKSSYFQSQVDRIRKEAYA 179
                                                                                                                               New nucleotide sequences isolated from Pyrococcus abyssi encode proteins useful in industry.
                                                                                                                                                                                                                                                                                                                           449 LDKABEAKLPKVBEILTTSIKLSGNAQESISLIR-----ERLPLAKGMLDDLIDTLSKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hyperthermophilic archaeon; hyperthermophilic protein.
78 EATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRILD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dietrich J, I
W, Heilig R;
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(IFRE-) IFREMER INST FR RECH EXPL MER.
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Weissenbach J, Saurin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB96493 standard; protein; 739 AA.
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                                                    289 ELSPLIKSDLNLMVDL-
                                                                                                                                                                                                                                                                                                                                                                                                       289 QQRHGKKTL 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                        502 SNGEDMKKL 510
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Querellou J,
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ID AAB9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, or that has an activity against a biological pethway required for that has an activity against a biological pethway in which a proliferation-required gene or the biological pethway in which a proliferation-required gene or the biological pethway in which a proliferation-required gene or the biological pethway in which a proliferation-required gene or the biological pethway in which a proliferation-required gene or the proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity, (11) a culture comprise selection of an organism acts of the strains is present in a culture or collection of an organism. The antisense nucleic acids required for proliferation in cells of nompologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimizing captured for proliferation in cells other than S. aureus, S. typhimized of the target prokaryotic essential genes in sequence data for this charged processed or accenting for homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimized or P. aeruginose. The present sequence is encoded by one of the target prokaryotic essential genes not sequence acuence of a patent did not form part of the present sequence 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zyskind JW;
Xu HH;
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11;

63;

Length 742; Indels

7.2%; Score 109.5; DB 6; 21.4%; Pred. No. 4.2; ve 49; Mismatches 131;

Query Match Best Local Similarity 21.4% Matches 66; Conservative

g 8

12;

94;

Indels

Mismatches 106;

59;

Conservative

67;

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from human cDNA libraries which can be used for gene therapy or in vaccines. The polynucleotides of the invention and antibodies encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The products of the invention may also be used to identify modulators of expression and activity and to down regulate expression and activity. The antibodies of the invention may also be used as diagnostic agents for detecting the presence of polypeptides in samples. This sequence represents a homologue of a polypeptide described in the disclosure of the invention
590
                                                                                                                                                                                                                                    651 ANIATLLOETSERMTTVKE-----QIVRTOBEVDKALRALBNLAASAEETTASAEEVS 703
                                                                                                                                                          201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes novel polynucleotides and polypeptides isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids having the sequences of clones isolated from libraries of different human tissues, useful in recombinant DNA methodologies.
                                                             :: ::: | |: | ::: | ::: | OHMMSRIBETTWSKVAEMSRNIEBITNVITSIAEQTN----LLALNAAIBAARAGEAGRGF
                                                                                                                                                                           AVVAQEIRKLAEESKQAADNIKSIIDKITDEIKEAVBATKEGVSVIGESSETLRDTIGYL
                                            SVLVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDI---
                                                                                                                                                          -----QLTNDFSEKSSYFQSQVDRIR---KEAYAGAAAGI-VAGPFGLIISYSIAAG
                                                                                                                                                                                                                 202 VIEGKLIPELMNRLKTVQNFFTSLSATVKQANKDIDAAKLKLATEIAAIGEIKTETETTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Intracellular trafficking-associated DXFZphtes3_1913 homologue
                                                                                                    --LIRILDDGVKKLNEAQKSL-----LTSSQSFNNASGKLLALDS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; gene therapy; vaccine; disease treatment; detection.
                                                                                                                                                                                                                                                                                         SAIEQQTAAIEELRRAAQELKDMVGRMRQIVGK 736
                                                                                                                                                                                                                                                                         FYVDYDDLMLSLLKGAAKKMINTCNEYQQRHGK 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example III; Page 674-675; 1095pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GEHU-) GERMAN HUMAN GENOME PROJECT.
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                                                                                                                                                                                                                                                                                                                                                                         ABU53079 standard; protein; 929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000WO-IB001496.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 929 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200112659-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ното варіеля
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L8-AUG-1999;
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4; Length 929;

Score 109; DB Pred. No. 6.2;

7.2%;

Query Match Best Local Similarity

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABIJ6176-ABIJ3611), expressed DNA sequences (ABIJ6175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                   269
                                                                                                                                               EKKASAOKDILI------RILDDGVKK---LNEAOKSLLTSSOSFNNASGKLL 149
                                                                                                        SAGISDAVSRLETNOKEQIESLTEVHRRELNDVISIWEKKLNQQABELQEIHEIQLQEKE 114
                                                                                                                                                                                  115 OEVÁELKOKÍLLFGCEKEEMNKEITWLKEEGVKODTTLNELÓEGLKOKSAHVNSLAQDET 174
                                                                                                                                                                                                                       203
                                                                                                                                                                                                                                                                                                257
                           -----LKKKLLDQEAKLKKELENTALELSQKEKQFNAKMLEMAQAN 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid detection reagent for detecting 1000 or more
genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                    EQTVEVVKSAIETADGALDLYNKYLDQVIPW-KTFDETIKELSRFKQEY-----SQEA
                                                                                                                                                                                                                       150 ALDSQL-----TNDFSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVI
                                                                                                                                                                                                                                                                                                204 EGKLIPELNNRLKTVQNFFTSLSATVKQANKDIDAAKL---KLATEIAAIGEI---KTET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 4527; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                           175 KLKAHLEKLEVDLNKSLKENTFLÓEÓLVELKMLÁEE------
                                                                     SVLVGDIKVLLMDSQDKYFEATQTVY---EWCGVVT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster polypeptide SEQ ID NO 4527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Myers EW
                                                                                                                                                                                                                                                                                                                                                                                               :||:
-------ALLEAKTNELIN 281
                                                                                                                                                                                                                                                                                                                                                                          ETTRFYVDYDDLMLSLLKGAAKKMIN 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB59245 standard; protein; 1048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-2001; 2001WO-US009231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAR-2000; 2000US-0191637P
11-JUL-2000; 2000US-00614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster.
                                    1 EKVKOKAKEMOET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001-656860/75.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ABL03348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pharmaceutical.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Venter JC,
7
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Nislow CE,
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                                                                                                                                                                                                                                                                                                                                                                                                                  ABG72693;
                                                                                                                                                                                                                                       139
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                                                                                                              Query Match
Best Local &
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                                                                                                                                   Matches
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ID ABG7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a bimc homologue, designated KLP61. BimC is a kinesin related protein, which is essential for fungal viability. The specification describes a method of identifying modulators of bimC. The method comprises adding a test agent to a mixture comprising bimC protein that directly or indirectly produces ADP or phosphate, subjecting the mixture to an enzymatic reaction that uses the ADP or phosphate, and determining the enzymatic activity in presence and absence of test
                                                                                                                                                                   QSFNNASGK------LLALDSQLTN--DFSEKSSYFQSQVDRIRKEAYAGAA 182
                                                                                                                                                                                                            ----AGIVAGPFGL----IISYSIAAGVIEGKLIPELNNRL--KIVQNFFTSLSATVK 230
                                                                                                                                                                                                                               KTSIIATISPGHKDIEETLSTLEYAHRAKNIONK--PEVNOKLTKKTVLKEYTE---EID 380
                                                                                                                                        ENVSKAGNEKGIRVRETVNINQSLLTLGRVITALVDRAPHVPYRESKLTRLLQESLGGRT 325
                                                                                              a
Or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying a modulator, e.g. antifungal agent, of a target protein comprising bimC or its fragment by determining enzymatic activity of reaction, in the presence and absence of the compound, that uses ADP phosphate produced by bimC.
                                                                                                                           84 YEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRILDDGVK-----KLNEAQKSLLTSS
                                                                                 24 LDLYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVLVGDIKVLLMDSQDKYFEATQTV
                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            kinesin related protein; fungal viability; antifungal; KLP61;
                                            Length 1048;
                                                                                                                                                                                                                                                     QANKDIDAAKLKLATEIA--AIGEIKTETETTRFYVDYDDIMLSLLK 275
                                                                                                                                                                                                                                                                   Indels
   from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                            7.2%; Score 108.5; DB 4;
21.6%; Pred. No. 7.9;
                                                                 62; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                         Amino acid sequence of bimC homologue, KLP61.
                                                                                                                                                                                                                                                                                                                                AAG67418 standard; protein; 1066 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Berand C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 8; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-APR-2000; 2000US-00541782
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                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CYTO-) CYTOKINETICS INC
                                                Query Match
Best Local Similarity 21.6
Matches 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sakowicz R,
                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster.
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N-PSDB; AAH78012.
                                                                                                                                                                                                                                                                                                                                                                                                                           fungal infection
                           Sequence 1048 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US6284480-B1
                                                                                                                                                                                                                                                                                                                                                                          13-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                      AAG67418;
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----AGIVAGPFGL-----IISYSIAAGVIEGKLIPELNNRL--KTVQNFFTSLSATVK 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     326 KTSIIĀTISPĢHKDIEETLSTLEVARRĀKNIQNK--PĒVNQKLTKKTVLKEYTE---EID 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QSFNNASGK------LILALDSQLTN--DFSEKSSYFOSQVDRIRKEAYAGAA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            266 ENVSKAGNEKGIRVRETVNINQSLJTLGRVITALVDRAPHVPRRESKLTRLLQESLGGRT 325
compound. A change in the activity level between the presence and absent of the candidate agent indicates a modulator of the target protein function. The method is useful for identifying a modulator, e.g. antifungal agents, of bimc. The modulators can be used, for example, to inhibit the growth or spread of fungi, mould, fruit files, etc. . The modulators can be used for preventing and treating infections caused by Chytridiomycetes, Hyphochrytridiomycetes, Plasmodiophoromycetes, competes, and Basidiomycetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 YEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRILDDGVK-----KLNEAQKSLLTSS
                                                                                                                                                                                                                                                                                                                                                                                                                24 LDLYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVLVGDIKVLLMDSQDKYFEATQTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fruitfly; bimC; kinesin related protein; mitosis; antifungal;
Candida infection; fusaria infection; zygomycosis; cryptococcosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fruitfly KLP61, a homologue of BimC, a Kinesin related protein.
                                                                                                                                                                                                                                                                                                                                                                   53;
                                                                                                                                                                                                                                                                                                             Length 1066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              231 QANKUIDAAKLKLATEIA--AIGEIKTETETTRFYVDYDDLMLSLLK 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 7.2%; Score 108.5; DB 4; Length 1 Similarity 21.6%; Pred. No. 8.1; 62; Conservative 62; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG72693 standard; protein; 1066 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-NOV-2000; 2000US-00723820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sakowicz R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Candida infection; fus
histoplasmosis; KLP61.
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                                                                                                                                                                                                                                                                      Sequence 1066 AA;
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03-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABÚ43311;
                                                                                                                                                                                                                              Query Match
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Matches
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The invention relates to a kit for screening for modulators of bimC, comprises a biologically active bimC (a kinesin related protein essential for mitosis), its fragment or homologue, and instructions for testing bimC activity. The kit is used for screening for modulators of bimC. The kit is also useful for identifying therapeutic agents (antifungal agents against Candida infections, fusaria infections, sygomycosis, cryptococcosis and histoplasmosis) and agricultural compounds. The present sequence represents the fruitfly bimC homologue, KLP61
                                                                                                                                                                                   84 YEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRILDDGVK-----KLNEAQKSLLTSS 138
                                                                                                                                                                                                                                                             QSFNNASGK------LLALDSQLTN--DFSEKSSYFQSQVDRIRKEAYAGAA 182
                                                                                                                                                                                                                                                                           ----AGIVAGPFGL----IISYSIAAGVIEGKLIPELNNRL--KTVQNFFTSLSATVK 230
                                                                                                                                                                                                                                                                                                                       326 KTSIIATISPGHKDIEETLSTLEYAHRAKNIQNK--PEVNOKLTKKTVLKEYTE---EID 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identification of candidate agent as modulators of tar protein function by adding candidate agent to mixture of target protein, subjecting mixture to enzymatic reaction, and determining level of activity of
                                                                                                                                                                                                                                | | | | :: | :: | :: | :: | :: | KERRKTATTLMNA------QSSRSHTVFSIVVHIRENGIEGEDMLKIGKLNLVDLAGS
                                                                                                                                                                       24 LDLYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVLVGDIKVLLMDSQDKYFEATQTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adenosine diphosphate, ADP, phosphate, bimC, kinesin related protein, KRP, fruit fly, KLP61.
                                                                                                                         Length 1066;
                                                                                                                                                                                                                                                                                                                                                     QANKDIDAAKLKLATEIA--AIGEIKTETETTRFYVDYDDIMLSLLK 275
                                                                                                                                                                                                                                                                                                                                                                   7.2%; Score 108.5; DB 6; Length 21.6%; Pred. No. 8.1; tive 62; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 8; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                  ADG98862 standard; protein; 1066 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-OCT-2002; 2002US-00270085.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-APR-2000; 2000US-00541782.
28-NOV-2000; 2000US-00723820.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fruit fly KLP61 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                               62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CYTO-) CYTOKINETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nislow CE, Sakowicz R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-895513/82.
N-PSDB; ADG98861.
                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                enzymatic reaction
                                                                                                    Sequence 1066 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US6627408-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-SEP-2003.
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                                                                                                                                                                                                                                                                                                        183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADG98862;
                                                                                                                          Query Match
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The invention relates to a candidate agent that binds to a target protein. Identification of a candidate agent as a modulator of function of a target protein involves adding the candidate agent to a mixture comprising the target protein that directly or indirectly produces adenosine diphosphate (ADP) or phosphate, subjecting the mixture to an allow the production of ADP or phosphate under conditions which normally allow the ADP or phosphate as a substrate under conditions which normally allow the ADP or phosphate to be utilised, and determining the level of activity of the enzymatic reaction where a conditions which normally allow the ADP or phosphate to be utilised, and determining the level of activity of the enzymatic reaction where a conditions which normally allow the ADP or phosphate to be utilised, and determining the level of activity of the enzymatic reaction where a gent indicates modulation of the target protein. The method provides a high throughput system for target protein. The method provides a high throughput system for detecting modulators of blmC enzyme activity. This sequence represents the fruit fly KLDel polypeptide, which is a homologue of the kinesin related protein (KRP) bimC, a target protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----AGIVAGPFGL----IISYSIAAGVIEGKLIPELNNRL--KTVQNFFTSLSATVK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 326 KTSIIATISPGHKDIEETLSTLEYAHRAKNIQNK--PEVNQKLTKKTVLKEYTE---EID 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QSFNNASGK------LLALDSQLTN--DFSEKSSYFQSQVDRIRKEAYAGAA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LELYNBELCDLL---STDDTTK--IRIFDDSTKKGSVIIQGLEEIPVHSKDDVYKLLEKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214 KERRKTATTLMNA-----QSSRSHTVFSIVVHIRENGIEGEDMLKIGKLNLVDLAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 LDLYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVLVGDIKVLLMDSQDKYFEATQTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 YEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRILDDGVK-----KLNEAQKSLLTSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          231 QANKDIDAAKLKLATEIA--AIGEIKTETETTRFYVDYDDLMLSLLK 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            381 KLKRDLMAARDKNGIYLAEETYGEITLKLESQNRELNEKMLLLKALK 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein encoded by Prokaryotic essential gene #28838.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.2%; Score 108.5; DB 7; ilarity 21.6%; Pred. No. 8.1; Conservative 62; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABU43311 standard; protein; 3692 AA
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06-SEP-2001, 2001US-0094893.
25-OCT-2001, 2001US-0342921P.
08-FEB-2002, 2002US-0072851.
06-MAR-2002, 2002US-0362699P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
tes 62; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1066 AA;
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Staphylococcus epidermidis; open reading frame; ORF; bacterial infection; antibacterial; gene therapy.

Staphylococcus epidermidis.

Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5080.

(first entry)

24-JUL-2002

ABP40235;

screening

ABP40235 standard; protein; 3696 AA.

RESULT 32

ABP40235

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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the mucleic acid of a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide; (5) producing the polypeptide; (3) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for completed for that has an activity against a biological pathway in which a proliferation, or that thibits cellular proliferation; (8) required for proliferation, or that thibits cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the servent comprising strains in which the strains is present in a culture or collection of a compound a activity; (11) a culture comprising strains in which the strains is present in a culture or collection of compound's activity; (11) a culture comprising strains in which the strains or (13) identifying the target of a compound that inhibits the collection of an organism. The antisense mucleic acids are useful for proliferation of an organism. The antisense mucleic acids are useful for cellular proliferation in cells other than S. aureus, S. typhimurium, argument discorpty programs, or for serventnessed candidate molecules for proliferation in cells other than S. aureus, S. typhimurium, and the argument of the printed specification, but was obtained in electronic control of the present sequence are sequenc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 SVLVGDIKVLLM-----DSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OKDILIRILDDGVKKINEAQKSLLTSS-----QSFNNASGKLLALDSQLTNDFS 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQVNKDIIPSNYTLASYNKY-----NKLKERAQTVLDEETNNTPFNORYSQTQI 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SINI DDELTDDGVERVKEAGLHTLESDTPHPVTKPNARQVVNNRA-----DQQKTLIRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zyskind JW;
Xu HH;
                                                                                                                                    New antisense nucleic acids, useful for identifying proteins or scre
for homologous nucleic acids required for cellular proliferation to
isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 3692;
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    罚员
    Ohlsen K
Forsyth R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 EVVKSAIETADGALDLYNKYLDQVIPWKTFDETIKELSR-
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    Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                    Claim 25; SEQ ID NO 71235; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences
       Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 21.5%;
tes 71; Conservative 4
         Zamudio C,
Trawick JD,
                                                                             WPI; 2003-029926/02
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                                                                                                     N-PSDB; ACA47181
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Novel isolated nucleic acid encoding a Staphylococcus epidermis polypeptide, useful for diagnosing and treating bacterial infections.

(GENO-) GENOME THERAPEUTICS CORP.

Bush D;

WPI; 2002-381255/41. Doucette-Stamm LA,

N-PSDB; ABN92780.

97US-0055779P. 97US-0064964P. 98US-00134001.

13-AUG-1998; 14-AUG-1997; 08-NOV-1997;

30-APR-2002.

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NFFTSLSAT-VKQANKDIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDLMLSLLKGAA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   728 NHEATTEEÖNEAIROVEAHSSDÄLAKIGE------AETDTTVNEAR 767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   674 SNNIDDBELTDDGVERVKEAGLHTLESDTPHPVTKPNARQVVNRRA------DQQKTLIRN 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EKSSYFQSQVDRIFK-EAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNNRLKTVQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 SVLVGDIKVLLM-----DSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 QKDILIRILDDGVKKLNEAQKSLLTSS-----QSFNNASGKLLALDSQLTNDFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.2%; Score 108.5; DB 5;
21.5%; Pred. No. 40;
:ive 49; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, SEQ ID NO 5080; 267pp; English.
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Grandi P, Krause R, K
z JD, Superti-Furga GD;
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  in non-homologous recombination
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                                                                            Query Match
Best Local Similarity 17.2.
Best Local Similarity 17.2.
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Marzioch M, Schultz JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CELL-) CELLZOME AG.
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                                                      Sequence 1292 AA;
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preferably a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               c cukaryotic cell, or encodes a therapeutic proteinaceous substance or a substance conferring resistance for an antibiotic substance to a cell.

The method is useful for improving gene targeting efficiency. The method is useful in the replacement of an active gene by an inactive gene, for e.g. for the inactivation of genes controlling undesired side branches of metabolic pathways, to increase the quality of bulk products such as starch, or to increase the production of specific secondary metabolites or to inhibit formation of unwanted metabolites, and also to inactive genes or to inhibit formation of unwanted metabolites, and also to inactive genes controlling senescence in fruits and flowers or that determine flowers or the determine by an active gene. For e.g. the replacement of a defective p53 by an intact p53. Many tumours acquire a mutation in p53 during their development which renders it inactive and often correlates with a poor response to cancer therapy. By replacing the defect p53 by an intact p53.

C e.g. through gene therapy, conventional anti cancer therapy have better changes of succeeding. The method is also useful for therapeutic changes of succeeding. The method is also useful for therapeutic concer therapy as substance integration. A tumoricial gene can be delivered to a pre-determined site present only in e.g. proliferating cells, or present only in tumour cells, e.g. to the site where a tumour antigen is expressed form. ABB77984-86 represent RADSO homologues. RADSO is involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The specification describes a method for directing integration of a nucleic acid of interest to a pre-determined site, where the nucleic acid has homology at or around the pre-determined site, in a eukaryote with a preference for non-homologous recombination. The method comprises steering an integration pathway towards homologous recombination. The method is useful for directing integration of a nucleic acid of interest or a subtractomaric and/or telometric region in an eukaryote with a preference for non-homologous recombination. The nucleic acid of interest comprises an inactive gene to replace an active gene, or vice versa, is a portion of a gene delivery vehicle, confers a desired property to the
DNGTKLIATDVPNPTKKAEA----RAAVTNSANSKIKDINNNTQATLDERNDAIALVNRSK 824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Directing integration of nucleic acid of interest to a sub-telomeric region in an eukaryote with preference for non-homologous recombination, by steering an integration pathway towards homologous recombination.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid integration; homologous recombination; telomeric region;
                                                                                                                                                                                                                                                                                                                                                                                            Amino acid seguence of an Arabidopsis RAD50 homologue.
                                                   279 KKMINTCNEYQ-----QRHGKKTLFEVP 301
                                                                                  : | : | | : : | | DEALQNINTAQGNDDVTEAQNNGTNTIQQVP 855
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STICHTING BINAIR VECTOR SYSTEEM.
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                                                                                                                                                                                                                                                                                                                                                                 154
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                                                                                                                       42
                                                                                                                                                                                                                                            ---TIKELSRFKQEYSQEASVL--VGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAY 97
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                                                                                                                                                                                                                                                                                                                                                              98 ILLFDEYNEKKASAQKDILIRILDDGVKKLNEAQKSLLTSSQSFNNASGKLLALDSQ---
                                                               Gaps
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                                                        Indels 117;
Length 1292;
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                                                                                                                       2 TSIFAEQTVEVVKSAIETADGALDLYNKYLDQVIPWKT-FDE-
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7.1%; Score 107.5; DB 5;
17.2%; Pred. No. 13;
ive 77; Mismatches 138;
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1024 KIQND-----LDQQTIYANTAQNNYE-------QELQKHADVSKTİSELR 1061
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                                                                                                                                                                                                                                                                                                                                  The invention relates to multiprotein complexes from eukaryotes. Proteins of the invention and DNA sequences encoding them are given in records ABR52568-ABR53903 and ACC6610-ACC61944 respectively. The complexes are obtainable by using a protein as a bait and isolating the set of proteins which is attached thereto from cells. Such protein complexes may comprise up to 30 distinct proteins. Protein complexes of the invention are useful for diagnosing a disease or disorder, or as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder. Note: The sequence data for this patent is not represented in the printed specification, but is based on sequence information upplied by the Buropean Patent Office. The complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNNRLKTVQNFFTSLSA 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TVKQANKDIDAAKLKLATEIAAIGEIKTETETTR-----FYVDYDDLM----LSLL 274
                                                                                                                                                                                                                                                                                                                                                                                                                                       116 -LIRILDDGVKKIN----EAQKSLLTSSQSFNNASGKLLA---LDSQLTNDFSEKSSYFQ 167
                                                                                                                                                                                                                                                                                                              7 EQTVEVVKSAIETADGALDLYNKYLDQVIPWKTFDETI-----KELSRFKQEYSQEAS
                                                                                                                                                                                                                                                                                                                                                                          60 VLVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDI----
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Kruse U, Merino A, Bauch A;
                                                                                                                                                                                                                                                                               81;
                                                                                                                                                                                                                                                 DB 6; Length 1875;
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19.9%; Pred. No. 20;
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Marzioch M, Grandi P, Krause R,
Michon A, Leutwein C, Rick J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         275 KGAAKKMINTCNEYQQRHGKK 295
                                                                                                                                                                                      document is available on CD-ROM
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The invention relates to novel protein complexes comprising a first and a second protein, or its derivative, fragment, homologue or variant. The proteins are selected from given protein complexes, which are not defined in the specification. The variants are encoded by nucleic acids that the specification. The variants are encoded by nucleic acids that thybridize to the nucleic acids encoding the proteins under low stringency conditions. The protein complexes are useful as targets for an active conditions. The protein complexes are useful as targets for an active cuseful as drugs targets for the treatment or preventing of a disease or disorder. The complexes and methods above are useful in diagnosing or correcting for the presence of a disease or disorder or a predisposition of sortering for a drug for treatment or prevention of a disease or disorder. The molecule that modulates the amount, activity or protein components of the complex is useful for the manufacture of a medicament or prevention of a disease or disorder. This sequence of corresponds to a protein of the invention. (Note: the sequence data for this patent did not form part of the printed specification but was for corporatine from the EPO in electronic formath).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .062 EQLHTYKGQVKTLNLSRDQLENALKENEKSWSSQKESLLEQLDLSNSRIEDLSSQNKLLY 1121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1122 DQI-----QIYTAADKEVNNSTNG--------PGLNNILITLRRERDILDT 1159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1024 KIQND-----LDQQTIYANTAQNNYE---------QELQKHADVSKTISELR 1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        epidermidis; open reading frame; ORF; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 -LIRILDDGVKKIN----BAQKSLLTSSQSFNNASGKLLA---LDSQLTNDFSEKSSYFQ 167
                                              ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SQVDRIRKBAYAGAAAGIVAGPPGLIISYSIAAGVIEGKLIPELNNRLKTVQNFFTSLSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TVKQANKDIDAAKLKLATEIAAIGEIKTETTTR-----FYVDYDDLM-----LSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 VLVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 BQTVEVVKSAIETADGALDLYNKYLDQVIPWKTFDETI-----KELSRFKQEYSQEAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4820.
                                            New proteins and protein complexes from eukaryotes, useful as targ drug screening, or in diagnosing or screening for the presence of disease or disorder, or a predisposition for developing a disease disorder in a subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1875;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.1%; Score 107.5; 19.9%; Pred. No. 20;
                                                                                                                                             English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABP39975 standard; protein; 1211 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : : | | | : : | | | 1220 R---ESNITLRNELENNNNKK 1237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             275 KGAAKKMINTCNEYQQRHGKK 295
                                                                                                                                                 Disclosure; SEQ ID NO 2369; 13pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus epidermidis;
antibacterial; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64; Conservative
WPI; 2003-638460/61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1875 AA;
                    N-PSDB; ADK64381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-JUL-2002
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Best Local S
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Listeria monocytogenes protein #2424
                                                         Listeria monocytogenes
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                                                                                                                                                                                                                                                                                     Voss H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 927 AA;
                                                                                WO200177335-A2
                                                                                                                                                                                                                                                                                                                                                           polypeptides.
                                                                                                       18-OCT-2001
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                                                                                                                                                                                                                                                                     ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection. N.B. The sequence data for this patent did not form part of the princed specification, but was obtained in electronic format directly from the USPTO web site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             - KGKRQQN-----DYDIEKLN---YELVKATENYEQLSGKLNVLEERKKKNQSETNARYE 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNNRL----K 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 LVGDIKVLLMDSQDKYFEATQTVYEWC------GVVTQLLSAYILLFDEYNE 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107 KKASAQKDILIRILDDGVKKLNEAQKSLLTSSQSFNNASGKLLALDSQLTND-----FS 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     217 TVQNFFTSLSATVKQANKDIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDLMLSLLKG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVQELESLLYISDEQHDEKLEEIKNSYYTLMSEQSVVNNDIRFLEHTINENEAKKSRLDS 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---KLLADLKNKOKOLNK 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 EQTVEVVK-----SAIETADGALDLYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated nucleic acid encoding a Staphylococcus epidermis polypeptide, useful for diagnosing and treating bacterial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      82;
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 7.1%; Score 107; DB 5; Length 1211; Best Local Similarity 18.3%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     59; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAKKMINTCNEYQQ------RHGKKTLFEV 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RLVEAFNQLKDIQQNITQTQKEYQSSKKSMEKV 474
                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 4820; 267pp; English.
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                                                                                                                              (GENO-) GENOME THERAPEUTICS CORP
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                                                                                           97US-0055779P.
97US-0064964P.
                                                                      98US-00134001,
                                                                                                                                                      Doucette-Stamm LA, Bush D;
 Staphylococcus epidermidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     61; Conservative
                                                                                                                                                                            WPI; 2002-381255/41
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1211 AA;
                                                                                                                                                                                        N-PSDB; ABN92520
                                                                                                      08-NOV-1997;
                      US6380370-B1
                                              30-APR-2002
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ID ABB4
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(first entry)

05-FEB-2002

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The present invention relates to the genome sequence of Listeria

monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of
it are useful for selecting probes and primers for detecting genes in L.
monocytogenes and related organisms, and for studying genetic
color polymorphisms and other genomes. The present sequence is a protein
expensed from the genome sequence of the present invention. Proteins
expressed from the genome sequence are useful for raising specific
antibodies, identification of L. monocytogenes and related organisms, and
for blosynthesis and biodegradation, especially biosynthesis of vitamin
constructions that regulate gene expression and cell replication
and modulate L. monocytogenes related diseases. In addition, the genome
sequence and proteins encoded by it are useful in pharmaceutical and
vectines compositions for the treatment or prevention of infections by L.
monocytogenes and related organisms. Note: The sequence data for this
monocytogenes and related organisms. Note: The sequence data for this
content of not form part of the printed specification, but was obtained
in electronic format directly from WIPO at
the wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           277 VSTYTSGVDTL---AGGINQAYTGSTALSDGLNKMNGS-----VPTLASGITQLNNGQK 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SILISSOSFNNASGKILA----LDSQLTN-----DFSEKSSYFQSQVDRIRKEAYAGAA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         217 FKDGANTLEVGLKTYTDGVNTAAAGGDKLNAGVSTLAAGVGPLKDGVAALDGGATKLASG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 QDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRILDDGVKKLNEAQK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MTSIFAEQTVEVVKSAIETADG---ALDLYNKYLDQVIPW----KTFDETIKELSRFKQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amend A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P; Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart Daniels J, Goebel W, Kreft J, Kuhn M, Ng B, Vazquez-Boland JA; Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A; Chakraborty T, Domann B, Hain T, Berche P, Charbit A, Durant L; Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N; Haduenio B, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin B12; bacterial infection; disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 927;
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20.5%; Pred. No. 9.8;
:ive 44; Mismatches 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 6; SEQ ID NO 2425; 192pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                       11-APR-2001; 2001WO-FR001118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-APR-2000; 2000FR-00004629.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 YSQEASVL-----
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The present sequence represents a human homologue of the yeast S. cerevisiae gene RAD50. The present sequence has 35% overall homology to the yeast RAD50 gene, and is expressed in activated T-cells, testis, foctal liver and heart tissues. The specification also describes sequences encoding human homologues of the yeast RAD50, the Drosophila Septin-2 and Acyl-CoA synthetase. The proteins have immunomodulatory activity. The nucleic acids and proteins can be used to identify activated T-cells in a sample population. They can also be used to isolate and identify sequences encoding other proteins or other compounds isolate and identify sequences encoding other proteins or other compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human immunomodulatory poly:peptide(s) - have homology to the yeast RAD50 or Drosophila Septin-2 proteins.
                                                                                                                                                                                            VONFFTSLSATVKQANKDIDAAKLKLATEIAAIGBIKTETETT------RFYVDY 266
                                                                                                                                                                                                                     ------NRDİQRLKNDIBBQBTLLĞTİMPEBESAKVCLTDVTIMBRRQMBL 802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human homologue; yeast RAD50; Drosophila Septin-2; Acyl-CoA synthetase;
immunomodulatory activity; identification; activated T-cell.
                                                                                                         641 DLDRLKEBIEKSSKORAMLÅGÅTA--VYSOFITQLTDENQSCCPVCQRVFQTBABLQBVI
                                                                                                                                     -GLI-ISYSIAAGVIEGKLIPELNNRLKT
                                                                                                                                                      ||::||||:|||||:||
SDLQSKLRLAPDKLKSTESELKKKEKRRDEMLGLVPMRQSIID--LKEKEIPELRNKLON
                      115 ILIRILDDGVXKLINEAQKSLLTSSQSFNNASGKLLALDSQLTNDFSEK-----SSYFQS
                                        Length 1312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
----YFPNKKQLEDWLHSKSK---
                                                                                                                                                                                                                                                      267 DDLMLSLLKGAAK-----KMINTCNEYQQRHGKK 295
                                                                                                                                                                                                                                                                                 воз круеккі аодаакцоді рідрктуодуй декреконк взв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 106.5;
Pred. No. 15;
                                                                                    169 QVDRIRKE-----AYAGAAAGIVAGPF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 136-140; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                          AAW71295 standard; protein; 1312 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunomodulatory activity
                                                                                                                                                                                                                                                                                                                                                                                                                                            Human homologue of yeast RAD50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GENE-) GENELABS TECHNOLOGIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.0%;
18.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97WO-US003159.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97WO-US003159
                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
   560 SDELTSLLG-----
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N-PSDB; AAV59979.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                            AAW71295;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16;
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                                        -----KTVQNFFTSLSAT 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human tumour suppressor gene RAD50 - useful to detect predisposition to, decrease risk of and treat cancer, also Septin-2 homologues.
          SLATGLDSLVDGSNKLSAGLKELDGNLTDKQGKIAQLKQGMNDLQQGIDQLNQSVNGEDA 387
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                                                                  A------LAKQLAT----LQKSLSDLQNGLTFIKSNANFDAEAIKSKINATAGVSAE
                                                                                                                  ---ETETTRFYVDYDDLMLSL
                                                                                                                                                                                                                                                                                                                                                                      DNA repair; tumour suppression; cancer; Septin-2;
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18.9%; Pred. No. 15;
iive 54; Mismatches
                                                                                                 229 VKQ----ANKDIDAAKLKLATBIAAIGBIKT---
                                           AGIVAGPFGLIISYSIAAGVIEGKLIPELNNRL-
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                                                                                                                                                             274 LKGAAKKMINTCNEYQQRHG 293
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96US-00687080.
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central nervous system
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N-PSDB; AAT75237.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  solated nucleic acid detection reagent for detecting 1000 or more from Drosophila and for elucidating cell signaling and cell-cell
                                                                 -----DRLAKLN----KELASSEQNKNHINNELKRREEQLSS-YEDKLFDVCGSQDFES
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Gaps
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  169;
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  Indels
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98;
                                       VEVVKSAIETADGALDLYNKYLDQVIPWKTFDETIK---
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11-JUL-2000; 2000US-00614150.
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discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABR72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                              65;
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                                                                                                                                                                                              Length 2346;
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                                                                                                                                                                                            7.0%; Score 106.5; DB 4;
18.9%; Pred. No. 33;
tive 66; Mismatches 118;
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johnsonii, useful for binding bacteria to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 8; SEQ ID NO 25; 225pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NONENKK 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2004-111519/12.
                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                 Sequence 2346 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ADH62787
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JAN-2004
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Matches
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----IHFINLDDSKKAANSAIEDALTTKKDEINNASNLSDSEKAKLINQATEIANAAKA 4386
                                                                                                                                                                                                                                                                                                              4291 KTDLINO-----ATEIANAAKDAINSATT-------NTAVEAAEYKGVADINN- 4331
                                                                                                                                                              13;
                                                                                                                                                                                                                                                                                                                                                   214
                                                                                                                                                                                                                                                                                                                                                                                                      -----DAAKLKL---ATEIAAIGEI 253
                                                                                                                                                                                                                                            86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
sequences which encode them. In particular, the genes are derived from Lactobacillus johnsonii. The invention may allow a better understanding of the mechanism by which probiotics (such as L johnsonii) can bind to mucins, large glycoprotesins present on the surface of a large number of epithelial cells including those in the gastrointestinal tract, the lung or the uterine cervix. The present sequence is that of an L johnsonii mucin binding protein of the invention.
                                                                                                                                                                                       --KYLDQV-----IPWK 38
                                                                                                                                                                                                                                                                                                                                                  LINDFSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNNR
                                                                                                                                                                                                                                          TFDETIKELSRFKQEYSQEASVLVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYI
                                                                                                                                                                                                                                                             SIDLINKALNE-KQDEINNASNLSQDESTELIDQAKKI--ATEAINBAQTN-----
                                                                                                                                                                                                                                                                                             LLFDEYNEKKASAQKDI---LIRILDDGVKKLNEAQKSLLTSSQS-FNNASGKLLALDSQ
                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         developmental biology; cell signalling; insecticide;
                                                                                                                                                              87;
                                                                                                                                      Length 4734;
                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster polypeptide SEQ ID NO 40200.
                                                                                                                                       7.0%; Score 106.5; DB 8;
23.8%; Pred. No. 81;
tive 38; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                          215 LKTVQNFFTSLSATVKQANKDI-----
                                                                                                                                                                                          2 TSIFAEQTVEVVKSAIETADGALDLYN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; protein; 7201 AA.
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11-JUL-2000; 2000US-00614150.
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                                                                                                                                             Query Match 7.03
Best Local Similarity 23.83
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AINNATT 4393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                KTETETT 260
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                                                                                                                  Sequence 4734 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4387
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                                                                                                                                                                                                                                                                                                                                                      3564 KRIVEAVNEKAAALIGSAAPANADEISKAVAEVNKRYDQVGQDCAKLVADLDGAFDVYQQ 3623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3677 KSLEDHIEQQ-----ASNIPARSKEVMARDLANLHADFEKFGASLS-DVKSG-LENR 3726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L------IPELNNRLKTVQ------NFFTSLSATVKQANKDIDA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14;
                                                                                                                                                                                                                                                                                                                                                                                                                                         149 LALDSQLTNDFSEKSSYFQSQVDRIRKEAYAGAAAGIVAG--PFGLIISYSIAAGVIEGK 206
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13
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                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and insectioides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176, ABL30511), expressed DNA sequences (ABL16176, and the encoded proteins (ABB57737-Sequences (ABC)2072). The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                               3504 QEAQGVQLSSYQDILNQTVNWLDQVEKLIHNENPASWTSAQEIRSKLYKYKATNQDINSH
                                                                                                                                                                                                                                                                                                                             SRFKQBYSQBASVLVGDIKVLLMDSQDKYFBATQTVYBWCG-----VVTQLLSAYILL--
                                                                                                                                                                                                                                                                                                                                                                                  PDEYNEKKASAQKDILIRI-------LDDGVKKLNEAQKSLLTSSQSFNNASGKL
                                                                                                                                                                                                                                                                       -KTFDETIKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       239 AKLKLATEIAAIGE----IKTETETTRRYUDYDDLMLSLLKGAAKKMINTCNEYQQRHG
                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                            Indels 109;
                                                                                                                                                                                                                Length 7201;
 Disclosure; SEQ ID NO 40200; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster polypeptide SEQ ID NO 18846.
                                                                                                                                                                                                                ; Score 106.5; DB 4;
; Pred. No. 1.4e+02;
51; Mismatches 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Myers EW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; protein; 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Li PWD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
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Similarity 18.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                             Sequence 7201 AA
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                                                                                                                                                                                                                                                      68;
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Matches
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N-PSDB; ADA28871
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                                  Breton G,
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISAENRKOLLESKCNILDLKLESLNKNYDQELKNKIQILGTTPVKLSARNASEAQATRA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                         293 ELELKEERPCODYSVFVDKLOSKVYRFNGISLGDEENADELISDYLVQYNMRNFNRSONE 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----IEGKLIPELNNRLKTVQNFPTSLSATVKQANKDIDAAKLKLATEIAAIGEIKTET 257
                                                                                                                                                                                                                                                                                               3 SIFAEQTVEVVKSAIETADGALDLYNKYLDQVIPWK--TFDETIKELSRFKQEYSQEASV 60
                                                                                                 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidaring cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA BBC2072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                  detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                            -------VDRIRKEAYA--GAAAGIVAGPFGLIISYSIAAGV-----
                                                                                                                                                                                                                                                                                                                                           61 LVGDIKVLLMDSQDKYFEATQTVYEWC---GVVTQLLSAYILLFDEYNEKKASAQKDILI
                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Acinetobacter baumannii; bacterial disease; antibacterial; vaccine;
                                                                                                                                                                                                                                                                          64;
                                                                            ID NO 18846; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                   DB 4; Length 685;
                                                                                                                                                                                                                                                  7.0%; Score 106; DB 4; Length 68:
20.8%; Pred. No. 7.3;
Live 52; Mismatches 143; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ETTRFYVD - - YDDLMLSLLKGAAKKMI 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : | | : | | : 411 LFSRNMMKNLLDDMQAATOKONAKSOL 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Acinetobacter baumannii protein #158
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                                 isolated nucleic acid
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                                                                                                                                                                                                                                                              Best Local Similarity 20.8
Matches 68; Conservative
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2001-656860/75
           N-PSDB; ABL08123
                                                                              Disclosure; SEQ
                                                                                                                                                                                                                              Sequence 685 AA;
                                                        interactions
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New Acinetobacter baumanii proteins and nucleic acids, useful as reagents for diagnosing a bacterial disease, as components of antibacterial
                                                                                                                                                                                                                                                                                  for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDE--YNEKKASAQKDILIRILDDGV 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            280 LVTIDGEDARD---------313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 KKLNEAQKSLLTSSQSFNNASGKLLALDSQLTNDFSEK--SSYFQSQVDRIRKEAYAGAA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 AGIVAGPF-----GLIISYSIAAGVIEGKLIPELNNRLKTVQ--NFFTSL 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        226 SATVKQANKDIDAAKLKLATEIAAIGEIKT----ETETTRFYVDYDDL-----MLSLLK 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 354 CSL--NPHVDRLCMVCDLKLSRTGRVTGYEFYPAVMHSKA-----RLTYTQVGQYFEGA 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The A. baumannii nucleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. baumannii and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agents for plants. The present sequence represents the amino acid sequence of an A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to isolated Acinetobacter baumannii nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 TVEVVKSAIETADGALDLYNKYLDQVIPWKTFDETIKELSRFKQ--EYSQEASVLVGDIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alloiococcus otitidis, antigenic protein; immunogenic; immunisation; gene therapy; Gram-positive bacterium; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     otitis antigenic protein SEQ ID NO:2870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.0%; Score 106; DB 6; L
19.5%; Pred. No. 9.2;
iive 48; Mismatches 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 276 GAAKKMINTC-----NEYQORHGKKTLFEV 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NDAHKL I EECMLLANVAAAEYALEHDI PMLYRV
                                                                                                                                                                                                                                                                                                                                                                                                                           Example; SEQ ID NO 4284; 328pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ž
(GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     863
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alloiococcus otitis
                                                                                                                                            WPI; 2003-576092/54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
es 65; Conserv
                                                                      Bush D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          baumannii protein.
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Zagursky RJ;

Russell DP,

polynucleotide (I) of

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The present invention describes an isolateu polymucieculue (1), oct.

Alloiococcus otitidis genomic DNA, which encodes an antigenic protein.

Alloiococcus otitidis is a Gram-poslitive bacterium. Also described: (1)

Alloiococcus otitidis is a Gram-poslitive bacterium. Also described: (1)

an isolated polypeptide that is encoded by the polymucleotide (1), its expression vector comprising the novel isolated polymucleotide (1), its complement, degenerate variant or fragment; (3) a genetically engineered composition comprising the polypeptide of (1); (5) an immunogenic composition comprising the polypeptide, its complement, biological cquivalent or fragment, or the polymucleotide that is comprised in the expression vector; (6) a pharmaceutical composition comprising the expression vector; (6) a pharmaceutical composition comprising an array of the polymeptide of (1), their biological equivalent or fragment, of the polymeptide of (1), their biological equivalent or fragment, of immunising against Alloiococcus otitidis by administering to a host the immunogenic composition; (9) detecting and/or identifying Alloiococcus cultidis in the biological sample; (10) a kit comprising a container or the antibody of (4); and (11) producing a polymeptide by culturing the containing the novel polymucleotide, its degenerate variant or fragment, or the antibody of (4); and (11) producing a polymeptide by culturing the polymucleotides, polymeptides, antibodies and compositions of the present composition and be used for treating and diagnoshing diseases, frugal trials. The polymucleotides are useful for expressing and detecting Alloiococcus otitidis. The present sequence represents an Alloiococcus otitidis antigen protein from the present invention.
                                                                                                                                                                                                                                                                                                                 New Alloiococcus otitidis polynucleotides and polypeptides, useful for treating and diagnosing diseases, drug screening assays and monitoring effects during drug clinical trials.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present invention describes an isolated
                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 33; SEQ ID NO 2870; 1019pp; English
                                                                                      2001US-0333777P.
2002US-0426742P.
                                           25-NOV-2002; 2002WO-US036123
                                                                                                                                                                                                             Mcmichael JC,
                                                                                                                                                             (AMHP ) WYETH HOLDINGS CORP
                                                                                                                                                                                                                                                              WPI; 2003-505284/47.
                                                                                                                                                                                                                                                                                     N-PSDB; ADB08929
                                                                                                                                                                                                                Fletcher LD,
                                                                                                                  18-NOV-2002;
                                                                                              29-NOV-2001;
12-JUN-2003
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638 184 639 GÓ-----AĞLLKLLIYLYKN--GEKYDWIKEGVINIQSIIIDKINSNEVLHKKYLGYSHG 691 185 IVAGPFGLIISYSIAAGVIEGKLIPELNNRLKTVQNFFTSLSATVKQANKDIDAAKLKLA 244 579 137 --FKQEYSQEASVLVGDIK--VLLMDSQDKYF 77 -----DGALDLYNKYLD-----Q 33 :|: :|| : : :: 460 MFSREDMEIQRQLIKSSINFELFENQMVNHNHNSSSNEKDYYLYLYKELIEATSELFWID 78 BATQIVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRILDDGVKKLNEAQKSLLTŞ 138 SQSFNNASGKLLALDSQLTNDFSEKSSYFQSQV-----DRIRK-----EAYAGAAAG Gaps 78; 7.0%; Score 106; DB 6; Length 863; 20.3%; Pred. No. 9.9; ive 54; Mismatches 107; Indels 7 4 IFAEQTVEVVKSAIETA--------34 VIPWKTFDETIKELSR-------Query Match Best Local Similarity 20.39 Matches 61; Conservative Sequence 863 AA; 692 LV-

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87 61

Gaps

DB 4; Length 885;

7.0%; Score 106; DB 4; Length 88 18.5%; Pred. No. 10; ive 51; Mismatches 111; Indels

Similarity 18.5%;

Conservative

54;

Matches

Query Match Local 148 LLALDSQLTND-----FSEKSSYFOŞQVDRİRKEAYAGAAAGIVAGPFGLIISYSIAAG 201

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88 GVVTOLLSAYILLFDEYNEKKASAQKDILIRILDDGVKKLNEAQKSILTSSQSFNNASGK 42 ETIKELSRFKQEYSQEASVLVGDIKVLLMDSQDKYFEATQTVYEWC-------

AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides CC (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (I) and have antibacterial activity and therefore can be used in and (II) can have antibacterial activity and therefore can be used in epidermidis polypeptides (I) may be used to produce the S. the molypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides may also be used to mucleic acids) may then be polypeptides may also be used to assay for other inhibitors of their or the polypeptides may also be used to assay for other inhibitors of their creatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to treatment of S. epidermidis infections, e.g. endocarditis. AAH55091 co polymucleotide sequences from the present invention. AAH55091 to AAH55091 co polymucleotide sequences and primers which are used in the cemplification of the present invention. N.B. The present invention examplification of the present invention. N.B. The present invention examplification of the present specification, however the sequence specifically claims all the polymucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4455 so even though sequences are given in the form the present specification, nower though sequences are present for the present the present present present contains and present present present present present present contains and present present contains and present present contains and present contains and present contains and present present contains and present present contains and present present contains and present contains and present contains and present present contains and present contains and present contains and present contains and present contains and present contains and present contains and present contains and present contains and present contains and present contains and present contains and present Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination; Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis. frame protein sequence SEQ ID NO:1660. Claim 18; Page 462; 2188pp; English. AAG82283 standard; protein; 885 AA. 09-NOV-2000; 2000WO-US030782. 99US-0164258P. S. epidermidis open reading for SEQ ID NO:4455 to 4464 Staphylococcus epidermidis. (first entry) (GLAX) GLAXO GROUP LTD 2001-316495/33. Sequence 885 AA; N-PSDB; AAH53133 WO200134809-A2 endocarditis. 09-NOV-1999; 17-MAY-2001. Kimmerly WJ; 03-SEP-2001 AAG82283;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The proteins are soluted by the protein complex comprises; proteins. The protein complex delta sub-unit; MaPKAP-K3 and amyloid A4 precursor adaptor complex delta sub-unit; MaPKAP-K3 and amyloid A4 precursor protein, APP-695; MAPKAP-K3 and heat shock protein (Hap) 8; leucine rich injo and NY-REN-58; P38 Alpha and P38 Beta; protein (Hap) 8; leucine rich injo and NY-REN-58; P38 Alpha and cell cycle dependent kinase (CDK) 9; ERK3 and protein kinase CLK; C-NAP-1 and Cathrin heavy chain; C-NAP-1 and Amphiphysin; C-NAP-1 and novel protein PN9109 or C-NAP-1 and KIAAl106 (unknown function) interactions. The protein complexes are useful for chair modulate the interaction of the proteins (thus identify drug targets), and identifying additional proteins in the pathway common to the proteins. These physiological disorders include non-insulin dependent chabetes mellitus (NIDDM), neurodegenerative disorders (e.g. Alzheimer's disease), inflammatory diseases (e.g. rheumatoid arthritis and cite inflammatory bowel disorder) and other human disease such as
                                                  New protein complexes comprising protein-protein interactions (e.g. MAPKAP-K3/AP-3 delta or C-NAP-1/Clathrin HC), useful for diagnosing physiological generative disorders or screening drugs for these diseases.
                               202 VIEGKLIPELNNRL----KTVQNFFTSLSATVKQANKDIDAAKLKLATEIAAIGEIKTET 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         atherosclerosis, cardiac hypertrophy and hypoxic brain injury. This is the amino acid sequence of novel protein PN9109, found to bind C-NAP1 in a yeast two-hybrid assay used to determine components of signal
                                                                                                                                                                                                                                                                                                                                   MAPKAP-K3; AP-3 delta; APP-695; amyloid A4; Hsp8; heat shock protein 8; L130; NY-REN-58; P38 Alpha; P38 Beta; ERK3; KIAA0934; CDK9; cell cycle dependent kinase 9; CLK; C-NBP-1; clathrin heavy chain; amphiphysin; PN9109; KIAA1106; neurodegenerative disorder; non-insulin dependent diabetes mellitus; NIDDM; Alzheimer's disease; inflammatory disease; rheumatcid arthritis; inflammatory bowel disorder; atherosclerosis; cardiac hypertrophy; hypoxic brain injury; yeast two-hybrid; signal transduction pathway; human; mitogen activated protein kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention describes an isolated protein complex, comprising two
                                                                                                                  RFLEHTINENEAKKSRLDSRLVEAFNQLKDIQQNITQTQKEYQSSKKSMEKV 250
                                                                                             258 ETTRPYVDYDDLMLSLLKGAAKKMINTCNEYQQ------RHGKKTLFEV 300
LNVLEERKKNQSETNARYEEELDNLESQIDSIKNEKAQNE---
                                                                                                                                                                                                                                                                                                         Novel signal pathway protein protein PN9109.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 12; Page 31-32; 60pp; English.
                                                                                                                                                                                                           AAU75100 standard; protein; 2835 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUN-2001; 2001WO-US019762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-JUN-2000; 2000US-0213245P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MYRI-) MYRIAD GENETICS INC.
                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bartel PL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-122287/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ABK13224.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200198524-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                         09-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heichman K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-DEC-2001
                                                              143
                                                                                                                             199
                                                                                                                                                                                                                                          AAU75100;
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986 --WIDKVEVELLSYETQVLK--GEBASQAQMRPKELKKEAKNNKA-------LLDSLN 1032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17;
                                                                                                                                                                                                                                                                                                             -IAAGVIE------GKLIPELNNRLKTVQNFFTSLSATVKQANKDIDA----- 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----AKLKLATE----IAAIGEIKTETETTRFYVD------YDDLMLSLLKGAA 278
                                                                                                                                                                                                                                807 KSTVEVIKREGEKIATTAEPADKVKILKOLSLLDSRWEALLNKAETRNROLEGISVVAQQ 866
                                                                                                                                                                                                                                                                                                                                                                       87 CGVVTQLLSAYILLFDEYNEKKASAQKDI-----LIRILDDGV---KKLNEAQKSLLTS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                138 SOSFNNASGKLIALDSQLTNDFSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYS 197
                                                                                                                                                                                     -----GALDLYNKYLDQV-IPWKT 39
                                                                                                                                                                                                                                                                              40 PDETIKELSRFK------QEYSQEASVL---VGDIKVLLMDSQDKYFEATQTVYEW 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Directing integration of nucleic acid of interest to a sub-telomeric region in an eukaryote with preference for non-homologous recombination, by steering an integration pathway towards homologous recombination.
                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid integration; homologous recombination; telomeric region;
                                                                                                                                         Gaps
transduction pathways, described in the method of the invention
                                                                                      7.0%; Score 106; DB 5; Length 2835;
19.4%; Pred. No. 46;
Live 76; Mismatches 122; Indels 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence of a human RAD50 homologue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bundock P;
                                                                                                                                                                                     7 EQTVEVVK-----SAIETAD-----
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STICHTING BINAIR VECTOR SYSTEEM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KKMINTCNEYQQRHGKKTLFEV 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB77985 standard; protein; 1318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 5; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Van Attikum H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-DEC-2000; 2000EP-00204693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-DEC-2000; 2000EP-00204693
                                                                      Ouery Match
Best Local Similarity 19.%
The 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-550409/59.
                                                  Sequence 2835 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hooykaas PJJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP1217074-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 48
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(first entry)

06-MAY-2004

The specification describes a method for directing integration of a nucleic acid of interest to a pre-determined site, where the mucleic acid has homology at or around the pre-determined site, in a eukaryote with a preference for non-homologous recombination. The method comprises compared is useful for directing integration of a nucleic acid of interest to a subtelomeric and/or telomeric region in an eukaryote with a to a methologous recombination. The mucleic acid of interest comprises an inactive gene for replace an active gene, or vice versa, is a comprises an inactive gene for replace an active gene, or vice versa, is a portion of a gene delivery vehicle, confers a desired property to the cukaryotic cell, or encodes a therapeutic proteinaceous substance or a substance cornferring resistance for an antibiotic substance to a cell.

The method is useful for improving gene targeting efficiency. The method is useful for improving gene targeting efficiency. The method is useful for improving gene targeting efficiency. The method is useful for increase the quality of bulk products such as earth, or to increase the quality of bulk products such as earth, or to increase the production of specific secondary metabolites or to inhibit formation of unwanted metabolites, and also to inactive gene critical products on the flowers or that determine to the method is also useful for replacing and inactive gene flower pigments. The method is also useful for replacing with a poor cereponse to cancer therapy. By replacement of a defective p33 by an intact b3. Many tumours acquire a mutation in p53 during their capcapeutic cengonse to cancer therapy. By replacement of a defective p33 by an intact b3 through gene therapy, conventional anti cancer therapy have batter changes of succeeding. The method is also useful for therapeutic cengons to a pre-determined site present only in e.g. proliferating or present only in tumour cells, e.g. to the site where a tumour aniegance processed form. Abbaryage and expressed form. Abbaryage of s Indels 161; Length 1318; 7.0%; Score 105.5; DB 5; 18.4%; Pred. No. 19; tive 53; Mismatches 106; 10 VEVVKSAIETADGALDLYNKYLDQVIPWKTFDETIK---203 IEGKL------169 QVDRIRKE-----AYAGAAA-Local Similarity 18.4% nes 72; Conservative Seguence 1318 AA; 707 Query Match Best Loc Matches 셤 g ò 유 셤 ð 유 ઠે ठे ð

14; 812 763 FISLSATVKQANKDIDAAKLKLATEIAAIGEIKTETETT-------RFYVDYDDLM 270 646 202 647 DLDRIKEEIEKSSKQRAMLAGATAVYSQFITQLIDENQSCCPVCQRVFQTEAELQEAISD 706 508 MEVISLONEKAD--LDRILRKLDDEMEQLNHHTTTRTOMEMLTKDKADKDEQIRKIKSRH 565 55 SQEASVLVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKD 114 -----IPELNNRLKTVQNF 221 ---ELSRFKQEY 54 115 ILIRILDDGVKKLNEAQKSLLTSSQSFNNASGKLLALDSQLTNDFSEK-----SSYFQS ---GIVAGPFGLIISYSIAAGV LOSKLRLAPDKLKSTESELKKKEKRRDEMLGLAPWROSIIDLKEKEIPELRNKLONV---566 SDELTSLLG------YFPNKKQLEDWLHSKSK------BINQTR-----LSLLKGAAK-----KMINTCNEYQQRHGKK 295 813 RKIAQQAAKLQGIDLDRTVQQVNQEKQEKQHK 222 271 764 ò g 8

Huntington's disease; osteoarthritis; Leber's hereditary optic neuropathy; LHON; mitochondrial encephalopathy lactic acidosis and stroke; MELAS; mycolonic epilepsy ragged red fibre syndrome; MERRF; cancer; neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic; osteopathic; ophthalmological; cytostatic. Identifying a mitochondrial target for drug screening assays and for treating diseases associated with altered mitochondrial function, comprises detecting a modified polypeptide in a sample and correlating Human heat mitochondrial protein as a therapeutic target SeqID666 GM; Glenn mitochondrial; human; screening assay; diabetes mellitus; SW, Taylor Gibson BW, Fahy ED, Zhang B, 12-APR-2002; 2002US-0372843P. 17-JUN-2002; 2002US-0389987P. 20-SEP-2002; 2002US-0412418P. 04-APR-2003; 2003WO-US010870. (BUCK-) BUCK INST AGE RES. WPI; 2003-845369/78. with the disease. WO2003087768-A2. (MITO-) MITOKOR. Homo sapiens. 23-OCT-2003 Warnock DE; Ghosh SS,

the foreign of the fo This invention relates to novel mitochondrial targets that

Claim 1; SEQ ID NO 666; 180pp; English.

115 ILIRILDDGVKKLANEAQKSLLTSSQSFNNASGKLLALDSQLTNDFSEK-----SSYFQS 168 114 566 SDELTSLIG------YPPNKKQLEDWLHSKSK------EINQTR----- 597 55 SQEASVLVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKD 10 VEVVKSAIETADGALDLYNKYLDQVIPWKTFDETIK-------BLSRFKQEY Length 1318; Indels DB 7; Pred. No. 19; 3; Mismatches 106; 7.0%; Score 105.5; 53; 18.4%; Query Match
Best Local Similarity 10.Take 72; Conservative 8 g 8 g 8 셤

ADJ68860 standard; protein; 1318 AA.

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Sequence 1318 AA;

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are useful in diagnosing or treating diseases and disorders, preferably neurodegenerative diseases. These may also be used as a drug target or in manufacturing a medicament for the treatment or prevention of the abovementioned diseases or disorders. The composition may also be used for treating cancer. This sequence represents one of the proteins of the complex of the invention.
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Sequence 5150, Ap
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Sequence 18, Appli
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Sequence 1820, Ap
Sequence 51, Appli
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Sequence 148, App
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Sequence 6
Sequence 8
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Fatent No. 5731151
FATENT NOTATION:
APPLICANT: Sthish, Mundayoor
APPLICANT: Sthish, Mundayoor
ITLE OF INVENTION: Regulator of Contact-Mediated Hemolysin
VUMBER OF ENQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEB: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A.
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,115
FILING DATE: 26-UN-1996
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Greene, Jamie L.
REGISTRATION NUMBER: 32,467
REFERENCE/DOCKET NUMBER: 03063-0171US
TELEPAN: (404) 818-3700
TELEPAN: (404) 818-3700
TELEPAN: (404) 818-3700
TELEPAN: (404) 818-3700
TELEPAN: (309-31)
SEQUENCE CHARACTERISTICS:
TENORMATION FOR SEC ID NO: 3:
SEQUENCE CHARACTERISTICS:
THORYATION FOR SEC ID NO: 3:
COUNTY.
                                                                                          US-09-538-092-956
US-09-134-001C-3159
US-09-134-001C-5178
US-09-134-001C-5178
US-09-328-32-5599
US-09-318-32-5599
US-09-252-991A-31794
US-09-199-677A-170
US-09-917-244-91
US-09-917-24-91
US-09-538-092-1084
US-08-538-254-6
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US-09-914-259-66
US-09-489-039A-8352
US-08-924-629C-6
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APPLICANTION:
TITLE OF INVENTION:
DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION:
DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION:
APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
FRICE APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 7736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 GIVAGPFGLIISYSIAA--GVIEG-----KLIPELNNRLKTV------QNFFTS- 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  397 ASTÄSLIGAPISALVGÄITGIISGILEASKOSMFEHVANRMANTIAEWEKTHGKNFFENG 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------EIAATVK---QANKDIDAAKLKLAT-------FIAAIGBIKTETETTRFYV 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54 YSQEASVI.-----VGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAXILL-FDEY 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AIADQFKRANKIBĖYSORPKKFGYBGDSLLAAFRKĖTGAIDASLTTINTALGTISAGISA 396
                                                                                                                                                                                                                                                                                 61 LVGDIKTLIMDSQDKYFEATQTVYEWCGVATQLLAAYILLFDEVNEKKASAQKDILIKVL 120
                                                                                                                                           DDGVKKLNEAQKSLLISSQSPNNASGKLLALDSQLINDFSEKSSYFQSQVDRIRKEAYAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   105 NEKKASAQKDILIRILDDGVKKLNE------AQKSLLTSSQSFNNASGKLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 AAAGIVAGPFGLIISYSIAAGVIEGKLIPELNNRLKTVQNFFTSLSATVKQANKDIDAAK
                                                                                                                                                                                                                        LKLATBIAAIGBIKTETETTRFYVDYDDLMLSLLKGAAKKMINTCNEYQQRHGKKTLFEV
                                          61 LVGDIKVILMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRIL
                         1 MISIFABQTVEVVKSAIETADGALDLYNKYLDQVIPWKTFDBTIKELSRFKQBYSQEASV
Indels
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20.7%; Pred. No. 0.0068;
tive 66; Mismatches 126;
 11;
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7736, Application US/09543681A Patent No. 6605709
    15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Proteus mirabilis US-09-543-681A-7736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.0%
Best Local Similarity 20.7%
Matches 80; Conservative
    275; Conservative
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         Matches
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                                                                                                                                                                                             61 LVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRIL 120
                                                                                                                                  DDGVKKINBAQKSILITSSQSFNNASGKLIALDSQLTNDFSEKSSYFQSQVDRIRKEAYAG 180
                                                                                                                                                                                                                                      240
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                                                       1 MTSIFAEQTVEVVKSALETADGALDLYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: King, C. H.
APPLICANT: Sathish, Mundayoor
APPLICANT: Shinnick, Thomas M.
TITLE OF INVENTION: REGULATOR OF CONTACT-WEDIATED HEMOLYSIN
TITLE OF INVENTION: OF MYCOBACTERIUM TUBERCULOSIS
TITLE OF INVENTIORS: 3
CORRESPONDENCE ADDRESS:
                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 30303-1811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1396; DB 5;
Pred. No. 3e-130;
              Pred. No. 3e-130;
; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Suite 1200, The Candler Building 127 Peachtree Street, N.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application PC/TUS9405869
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
ATTORNEY/AGENT INPORMATION:
NAME: PETTYMEN, DEA'LD G.
REGISTRATION NUMBER: 33,438
REPERENCE/DOCKET NUMBER: 1414,
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 688-970
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92.1%;
91.4%;
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amino acid
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                    Best Local Similarity 91.4
Matches 275; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                  P 301
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STREET: 12
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PCT-US94-05869-3
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PCT-US94-05869-3
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 10796-132
CURRENT PEDLICATION UNMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR PILING DATE: 1999-02-13
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR PILING DATE: 1999-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR PELING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 28208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5150, Application US/09107532A

Patent No. 6583275

GENERAL INPORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
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                                           230 RGYEEYIRSQGEVRDG-----VTTVNAAAVVPEEVIGEVFDLKRS--NYNLAQYATVKTV 282
                                                                                                                        93 L-------LSAYILLFDEYNEKKASAQKDILI--RILDDGVKKLNEAQKS 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 LLTSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLI 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    194 ISYSIAAGVIEGKLIPE-LMNRLKTVQN--FFTSLSATVKQANKDIDAAKLKLATEIAAI 250
                   ---EAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNNRLKTVQNFFTSLSATVKQA 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38 KIFDETIKELSRFKQEYSQEASVLVGDIKVLLMDSQDKYFEATQ-----TVYEWCGVVTQ 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       330 LLLVRBE-----LRTTQILIKDFRIKVENLEATIEE------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 722;
                                                                                                                                                                                                          267 DDLMLSLLKGA----AKKMINTCNEY----QQRHGKKTLFEVPDV 303
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                                                                                                ----EIAAIGEIKTETETTRFYVDY
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CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESS THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 112.5; DB 4;
; Pred. No. 0.031;
40; Mismatches 90;
                                                                                                                                                                                                                                                                                                                      Sequence 20613, Application US/09248796A Patent No. 6747137 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - | | : :||:|::|
-ETKLIKENKKLQLDYEDVLL 432
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                                                                                                   233 NKDIDAAKLKLAT----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                         US-09-248-796A-20613
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LENGTH: 722
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                                                                                                                                                                                                                                                                TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ::| | : : : | | : : : | | : 229
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457 YDARHSAFLEDNFKLLSQYNKEYSVERSVLITQQHWDELIGELASVTKNGAKTLSGKSYI 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 YLDQVIPWKTFDETIKELS-----RFKQEYSQE-ASVLVGDIKVLLMDSQDKYFEATQT 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.5%; Score 114; DB 4; Length 515; 23.5%; Pred. No. 0.013; tive 61; Mismatches 107; Indels 5
                                                                                                                                                                                                                                               and David Bush
                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 14 MAY 1998
FILING DATE: 14 MAY 1998
APPLICATION UNDBER: 60/05551
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...515
; SEQUENCE DESCRIPTION: SEQ ID NO: 5317:
US-09-107-532A-5317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Arintello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
                                                                    DYDDLMLSLLKGAAKKMINTCNEYQQR 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                            APPLICANT: Lynn A Doucette-Stamm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
                                                                                                                                                                              Sequence 5317, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                     STREET: 100 Beaver Street CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (781)893-5007
TELEPRA: (781)893-8277
INFORMATION FOR SEQ ID NO: 5317:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 515 amino acids
                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 7310
                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | Similarity 23.54
81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 02354
                                                                                                                                                               US-09-107-532A-5317
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Best Local 9
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us-09-993-292b-2.rai

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84 YEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRILDDGVK-----KLNEAQKSLLTSS 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          139 QSFNNASGK------LLALDSQLTN--DFSEKSSYFQSQVDRIRKEAYAGAA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  266 ENVSKAGNEKGIRVRETVNINQSLLTLGRVITALVDRAPHVPYRESKLTRLLQESLGGRT 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 ----AGIVAGPFGL----IISYSIAAGVIEGKLIPELNNRL--KTVQNFFTSLSATVK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 IDLYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVLVGDIKVLLMDSQDKYFEATQTV
                                                                                                                                                                                                                                                                                                                                                           84 YEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRILDDGVK-----KLNEAQKSLLTSS
                                                                                                                                                                                                                                                                                                                                       24 LDLYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVLVGDIKVLLMDSQDKYFEATQTV
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                                                                                                                                                                                                                                                                                                    53;
                                                                                                                                                                                                                                                                Length 1066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 231 QANKDIDAAKLKLATEIA--AIGEIKTETETTRFYVDYDDLMLSLLK 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 7.2%; Score 108.5; DB 3; Length Best Local Similarity 21.6%; Pred. No. 0.14; Matches 62; Conservative 62; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Nielow, Corey
APPLICANT: Sakowicz, Roman
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: Antifungal Assay
FILE REFERENCE: 1015
CURRENT APPLICATION NUMBER: US/09/723,820
CURRENT APPLICATION NUMBER: 09/541,782
PRIOR APPLICATION NUMBER: 09/541,782
PRIOR PILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 8
APPLICANT: Sakowicz, Roman
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: Antifungal Assay
TILLE REPERENCE: 1015
CURRENT APPLICATION NUMBER: US/09/541,782
CURRENT FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FASTERO FOR Windows Version 4.0
SEQ ID NO 8
                                                                                                               SEQ ID NOS: 10
FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-723-820-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 8, Application US/09723820; Patent No. 6468760; GENERAL INFORMATION:
                                                                                                                                                                       LENGTH: 1066
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-541-782-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LALDSQLTNDFSEKSSYFQSQ-----VDRIR-----KEAYAGAAAGIVA--GPFGLII 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : : | : :: | : | : | : 439 IKIIGDHTDKYAQGYFYYDSKKSGGLTVSHLRFGDTPIRSAYLVEHADLVACHTP-AYLH 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SYSIAAGVIEGKLIPELNNRLKTVQNFFTSLSATVKQ--ANKDI----DAAKLKLATEIAA 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49 RFKQEYSQEASVLVGDIKVLLMDSQ-----DKYFEATQTVYEWCGVVTQLLSAYILLF 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          250 IGEIKTETETTRF----YVDYDDLMLSLLKGAAKK 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
FILING DATE: 30-Jun-1998
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/081571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Arinfello, pamela Deneke
REGISTRATION NUMBER: 40,489
TELCOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...1231
SEQUENCE DESCRIPTION: SEQ ID NO: 5150:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Enterococcus faecium
                                                                  COMPUTER READBALE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 8, Application US/09541782; Patent No. 6284480; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1231 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 5150:
                STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                     SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-107-532A-5150
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US-09-541-782-8
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Sequence 4820, Application US/09134001C

Sequence 4820, Application US/09134001C

Sequence 4820, Application US/09134001C

Sequence 4820, Application US/09134001C

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE:
GURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-08-14

NUMBER: OF SEQ ID NOS: 5674

SEQ ID NO 4820

LENGTH: 1211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     220 NPFISLSAT-VKQANKDIDAAKLKLATEIAAIGBIKTETETTRFYVDYDDLMLSLLKGAA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                768 DNGTKLIATDVPNPTKKAEA---RAAVTNSANSKIKDINNNTQATLDERNDAIALVNRSK 824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -GVVTQLLSAYILLFDEYNE 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    568 EQVNKDIIPSNYTLASYNKY------NKLKERAQTVLDEETNNTPFNORYSQTQI 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 SVLVGDIKVLLM-----DSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             617 DDLLHELQTTLINRVSASREINDKAQEMTDAVYDSTELTTEEKDT---LVDQIENHKNEI 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 QKDILIRILDDGVKKLNEAQKSLLTSS-----QSFNNASGKLLALDSQLTNDFS 160
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                                                                                                                                                                                                                                                                                                                                                                                                                  Length 3696;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  7.2%; Score 108.5; DB 3;
llarity 21.5%; Pred. No. 0.95;
Conservative 49; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           279 KKMINTCNEYQ-----QRHGKKTLFEVP 301
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                            PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
SEQ ID NO 5080
LENGTH: 3696
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US-09-134-001C-4820
                                                                                                                                                                                                                                                                                                                 ORGANISM: Staphylococcus epidermidis
1998-08-13
   CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
les 71; Conserv
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Best Local Similarity
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Matches
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APPLICANT: LYND DOUGETGE-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
                                                                           ::: | : | : | : | : | : | ENVSKAGNEKGIRVRETVNINQSLLTLGRVITALVDRAPHVPYRESKLTRLLQESLGGRT 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214 KERRKTATTLMNA-----QSSRSHTVFSIVVHIRENGIEGEDMLKIGKLNLVDLAGS 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----LLALDSQLTN--DFSEKSSYFQSQVDRIRKEAYAGAA 182
                                                                                                                                                                            ----AGIVAGPFGL----IISYSIAAGVIEGKLIPELNNRL--KTVQNFFTSLSATVK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 YEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRILDDGVK-----KLNEAQKSLLTSS 138
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                                                                                                                                                                                                                                         326 KTSIIATISPGHKDIEETLSTLEYAHRAKNİQNK--PEVNOKLTKKTVLKEYTE---EID 380
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                                                                                                                                                                                                                                                                                                              231 QANKDIDAAKLKLATEIA--AIGEIKTETETTRFYVDYDDLMLSLLK 275
                                                                                                                                                                                                                                                                                                                                                            231 QANKDIDAAKLKLATEIA--AIGEIKTETETTRFYVDYDDLMLSLLK 275
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Best Local Similarity 21.6%; Pred. No. 0.14;
Matches 62; Conservative 62; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | Sequence 8, Application US/10270085 | Patent No. 6627408 | GENERAL INFORMATION: APPLICANT: Nislow, Corey APPLICANT: Sakowicz, Roman APPLICANT: Baraud, Christophe | TITLE OF INVENTION: Antifungal Assay FILE REFERENCE: 1015 | CURRENT APPLICATION NUMBER: US/10/270,085 | CURRENT APPLICATION NUMBER: US/09/723,820 | PRIOR FILING DATE: 2000-11-28 | PRIOR FILING DATE: 2000-11-28 | PRIOR FILING DATE: 2000-11-28 | PRIOR FILING DATE: 2000-10-3 | NUMBER OF SEQ ID NOS: 10 | SOFTWARE: PRESEQ FOR WINGOWS VERSION 4.0 | SEQ ID NOS: 10 | SEQ ID NOS: 10 | SEQ ID NOS: 10 | SEQ ID NOS | SEDESTER OF SEQ ID NOS: 10 | SEDESTER OF SEQ ID NOS: 10 | SEDESTER OF SEQ ID NOS: 10 | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NOS | SEDESTER OF SEQ ID NO
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; ORGANISM: Drosophila melanogaster
US-10-270-085-8
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US-10-270-085-8
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115 ILIRILDDGVKKLINBAQKSLLTSSQSFNNASGKLLALDSQLTNDFSEK-----SSYFQS
                                                                                                    641 DLDRLKEEIEKSSKQRAMLAGATA--VYSQFITQLTDENQSCCPVCQRVFQTEAELQEVI
                      ---RFYVDY
                                                                                                                                          -----GLI-ISYSIAAGVIEGKLIPELNNRLKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human RAD50 Gene and Methods of Use Thereof
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                                                                                                                                                                                                                 218 VONFFISLSATVKQANKDIDAAKLKLATEIAAIGEIKTETETT
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                                                                                                                                                                                                                                                                                      267 DDLMLSLLKGAAK-----KMINTCNEYQQRHGKK 295
                                                                                                                                                                                                                                                                                                                7.0%; Score 106.5; L
18.9%; Pred. No. 0.3;
:ive 54; Mismatches
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STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REPERENCE, DOCKET NUMBER: 4600-0111.30
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
                                                                            169 QVDRIRKE-----AYAGAAAGIVAGPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,080
FILING DATE: 17-ULL-1996
CLASSIFICATION A 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/592,126
FILING DATE: 26-JAM-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 51, Application US/08687080;
Patent No. 5965427;
GENERAL INFORMATION:
APPLICANT: GREGOTY Dolganov
TITLE OF INVENTION: Human RAD50 Gen
NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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Matches 75; Conserv
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                                     160
                                                           -KGKRQQN-----DYDIEKLN---YELVKATENYEQLSGKLNVLEERKKNGSETNARYE 345
                                                                                                    EKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNNRL----K 216
                                                                                                                             217 TVONFFTSLSATVKQANKDIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDLMLSLLKG 276
                                                                                                                                                                                                502 MEVISLQNEKAD-LDRTLRKLDQEMEQLNHHTTTRTQMEMLTKDKADKDEQIRKIKSRH
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                                 107 KKASAQKDILIRILDDGVKKLNEAQKSLLTSSQSFNNASGKLLALDSQLTND----FS
 245 MEQSDVIVTVSDIDHYTEDNQRLDERLNHLKSQQAEKEGQQAQINQLLQKY----
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                                                                                                                                                                                                                                                                                                                                                               US-08-592-126-148

Sequence 148, Application US/08592126

Patent No. 2821091

Patent No. 2821091

Patent No. 2821091

Patent No. Transcripts Encoding Immunomodulatory

TITLE OF INVENTION: Transcripts Encoding Immunomodulatory

TITLE OF INVENTION: 191/peptides

NUMBER OF SEQUENCES: 151

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98;
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                                                                                                                                                                                                                                                                                    442 RLVEAFNOLKDIQONITQTQKEYQSSKKSMEKV 474
                                                                                                                                                                                                                                                      -----RHGKKTLFEV 300
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18.9%; Pred. No. 0.3;
iive 54; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
STREE Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0111
TELEPHONE: (415) 324-0880
INFORMATION FOR SEQ ID NO: 148:
SEQUENCE CHARACTERISTICS:
LENGTH: 1312 amino acids
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                                                                                                                                                                                                                                                          277 AAKKMINTCNEYQQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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3Y: linear
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Best Local Similarity
Matches 75; Conserv
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Sequence 4284, Application US/09328352

Sequence 4284, Application US/09328352

Patent No. 6562958

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 4284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             354 CSL--NPHVDRLCMVCDLKLSRTGRVTGYEFYPAVMHSKA-----RLTYTOVGQYPEGA 405
                                                                                                                                                              :||:::|
641 DLDRLKEBIEKSSKQRAMLAGATA--VYSQFITQLTDENQSCCPVCQRVFQTEAELQEVI 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 VILIMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDE--YNEKKASAQKDILIRILDDGV 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125 KKINEAQKSLLTSSQSFNNASGKLLALDSQLTNDFSEK--SSYFQSQVDRIRKEAYAGAA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183 AGIVAGPF-------GLIISYSIAAGVIEGKLIPELNNRLKTVQ--NFFTSL 225
                                                                                                                                                                                                                 55 SQEASVLVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKD 114
                                                                                                                                                                                                                                                                                           115 ILIRILDDGVKKLNEAQKSLLTSSQSFNNASGKLLALDSQLTNDFSEK-----SSYFQS 168
                                                                                                                                                                                                                                                                                                                                                                          ---- 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                        699 SDLQSKLRLAPDKLKSTESELKKKEKRRDEMLGLVPMRQSIID--LKEKEIPELRNKLQN 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    218 VQNFFTSLSATVKQANKDIDAAKLKLATEIAAIGEIKTETETT-------RFYVDY 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----VSHYVRLDSALNEEAEERGTSVYFPHFVLPMLPEALSNGL 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 TVEVVKSAIETADGALDLYNKYLDQVIPWKTFDETIKELSRFKQ--EYSQEASVLVGDIK
                                                                                                                                   ---ELSRFKQEY
                                                                                                                                                                                                                                                    560 SDELTSLLG------YPPNKKOLEDWLHSKSK------EINOTR----
                                                                                                Gaps
                                                                                              Indels 169;
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                                                         Length 1312;
SEQ ID NO:54
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                                                                                                                                   10 VEVVKSAIETADGALDLYNKYLDQVIPWKTFDETIK------
                                                         DB 4,
                                                                                            98;
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Rad50.pro-translation of
                                                     Query Match 7.0%; Score 106.5; D
Best Local Similarity 18.9%; Pred. No. 0.3;
Matches 75; Conservative 54; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , OKGANISM: Acinetobacter baumannii
US-09-328-352-4284
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; INDIVIDUAL ISOLATE:
US-09-168-595-148
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Matches 65; Conserv
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                                             641 DLDRLKEBIEKSSKORAMLAGATA--VYSOFITQLTDENOSCCPVCORVFOTEABLOEVI 698
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                                                                                                                                                                                                                                                                                                                                                                                                                   VONFFISLSATVKQANKDIDAAKLKLATEIAAIGEIKTETETT------RFYVDY 266
                                                                                                                                                                                                                                                                                                                                                                                                                                            SQEASVLVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKD 114
                                                                                                                                                                                                   ------DRLAKLN----KELASSEQNKWHINNELKRKEEEQLSS-YEDKLFDVCGSQDFES
                                                                                                                                   SDELTSLIG------YPPNKKQLEDWLHSKSK------EINOTR----
                                                                                                                                                                          115 ILIRILDDGVKKLNEAQKSLLTSSQSFNNASGKLLALDSQLTNDFSEK-----SSYFQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
US-09-168-595-148

Sequence 148, Application US/09168595
Sequence 148, Application US/09168595
Parent No. 6555666
Trible OF INVENTION:
TITLE OF INVENTION: Polypeptides
NUMBER OF SEQUENCES: 151
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    803 KDVERKIAQQAAKLQGIDLDRTVQQVNQEKQEKQHK 838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 267 DDLMLSLLKGAAK-----KMINTCNEYQQRHGKK 295
                  VEVVKSAIETADGALDLYNKYLDQVIPWKTFDETIK-
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NAME: Sholtz, Charles K.
REGISTATION NUMBER: 38,615
REPERENCE/DOCKET NUMBER: 4600-0111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-080
TELEPHONE: (415) 324-080
INFORMATION FOR SEQ ID NO: 148:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/168,595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,126
FILING DATE:
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IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1312 amino acids
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HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53 EYSQBASVLVGDIKVLLMDSQDK--YFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKAS 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | : :|:| : |: |: |: | | 282 TRAD---QIKELVSEHELQIEKISKDLTEKFKLVETQLLSKHESHVQQFTKELIAESESK 338
                                                                                                                                                                                                                                                                                                                                               142 NNA-------SGKLIALDSQLTNDFSEKSSYFQSQVDRIRKEAYAGAAAGIVA 187
                                                                                                                                                                                                                                                                                                                                                                                                                         188 GPFGLIISYSIAAGVIEGKLIPELNNRLKTVQNFFTSLSATVKQANKDIDAAKLKLATEI 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                 383 ------EEEREIQNKKLDQVSEL 421
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                                                                                                                                                                                                                       82 TVYEWCGVVTQILSAYILLFDEYNEKKASAQKDILIRILDDGVKKLNEAQKSLLTSSQSF
                                                                                                                                                                                                                                                                                                                                                                       339 QQVEBELENLKTIHAKDSARILELETQLSDAAKEKSESDYKLTD--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same FILE REPERENCE: 15966-542

CURRENT APPLICATION NUMBER: US/09/538,092

CURRENT FILING DATE: 2000-03-29

PRIOR FILING DATE: 1999-04-01

PRIOR FILING DATE: 1999-04-01

NUMBER: CLICATION NUMBER: 60/178,965

PRIOR FILING DATE: 2000-02-01

NUMBER OF SEQ ID NOS: 1387

SOFTWARE: CLICATORALS—COMMETTER VETBION 0.9
                                                                                                                                                                                               26 LYNKYLDQVIPWKTFDETIKELSR----FKQEYSQEASVLVGDIKVLLMDSQDKYFEATQ
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                                                                                                                         Length 924;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             422 KELKELKVE-----ELSNNILKIQQELHRKEIELNEQLEKIHG 459
                                                                                                                                                                 Indels
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NAME/KRY: misc_feature
LOCATION: (0) ... (0)
OTHER INFORMATION: Polypeptide Accession Number YPR070W
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Similarity 25.4%; Pred. No. 0.13;
57; Conservative 29; Mismatches 91;
                                                                                                                               DB 4;
                                                                                                                                             ; Pred. No. 0.22; 58; Mismatches 100;
                                                                                                                               7.0%; Score 105.5;
17.8%; Pred. No. 0.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 807, Application US/09538092; Patent No. 675314; GENERAL INFORMATION: APPLICANT: Mansfield, Traci A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 SAIETADGALDLYNKY----
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 18798
LENGTH: 924
                                                                                                                                                                     51; Conservative
                                                                           : Candida albicans
                                                                                                                                                       Similarity
                                                                           ORGANISM: Candida
US-09-248-796A-18798
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US-09-538-092-807
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LENGTH: 566
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Best Local
                                                               TYPE: PRT
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Best Local
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Matches
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Sequence 18798, Application US/09248796A
Batent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT PILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
                                                                                                                                                                                                     RESULT 16
US-09-710-279-1660
Sequence 1660, Application US/09710279
Sequence 1660, Application US/09710279
Patent No. 6703492
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
TILE REFERENCE: PUJ480US
CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1660
: LENGTH: 885
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88 GVVTQLLSAYILLFDEYNEKKASAQKDILIRILDDGVKKINEAQKSLLTSSQSFNNASGK 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLALDSQLTND-----FSEKSSYFQSQVDRIRKEAYAGAAAGIVAGFFGLIISYSIAAG 201
                             226 SATVKQANKDIDAAKLKLATEIAAIGEIKT-----ETETTRFYVDYDDL-----MLSLLK 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 EPLKEEAAIAKEYKQLSKEMEQSDVIVIVSDIDHYTEDNQRLDERLNHLKSQQAEKEGQQ 61
                                                     406 TDAIPK-DRDIHKSLNTLFQLYQILKNLRYDRHAMEFËTIETYMTFDELGGIKEILPRTR 464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 7.0%; Score 106; DB 4; Length 885; Best Local Similarity 18.5%; Pred. No. 0.19; Matches 54; Conservative 51; Mismatches 111; Indels
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                                                                                                           276 GAAKKMINTC-----NEYQORHGKKTLFEV 300
                                                                                                                                               465 NDAHKLİEECMLLANVAAABYALEHDIPMLYRV 497
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GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR:
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REPERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT PILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 KKASAQKDILIRILDDGVKKINEAQKSLLTSSQSF-NNASGKL----LALD--SQLTND 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        159 FSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNNRLKTV 218
                                                                                                   ---KHTQKSSQEYQTSLAEAQ 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         150 ASDKVETTKAEAQSLKDDATQTFESAKQAVEGKVEAIKEQVLDQVDSLKDDTDQDNTDQD 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      210 QEKQTLKDKAVQAATAAKRKVEDVVDDVKHTTESFKNTÄSGKIDEIKQAAVDKTEEVKSQ 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----DSAQSTA 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---- DLATQVIKEEA 371
                                 170 VDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNNRLKTVQNFFTSLSATV 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                             230 KOAN--KDIDAAKLKLA----TEI--AAIGEIKTETETTRFYVDYDDLMLSL 273
                                                                                                                                                                                                                                            333 KKVKHFEKLQESLMKAAAEKETEIQKAEANLIKTQQELEKYQKSTKELLAEL 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 AEQTVEVVKSAIETADGALDLYNKYLDQVIPWKTFDETIKELSRFKQE-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 6.8%; Score 103.5; DB 4;
Best Local Similarity 20.0%; Pred. No. 0.24;
Matches 66; Conservative 57; Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2. Application US/08477831C
Patent No. 6429291
GENERAL INFORMATION:
APPLICANT: TURLEY, EVA A.
APPLICANT: SHUWEN, ZHANG
APPLICANT: BYTWISTLE, JOYCELYN
TITLE, OF INVENTION: HYALURONAN RECEPTOR PROTEIN
NUMBER OF SEQUENCES: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  279 KKMINTC-----NEYQQRHGKKTL 297
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ADDRESSEE: FISH & NEAVE
STREET: 1251 AVENUE OF THE AMERICAS
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2753, Application US/09540236
Patent No. 6673910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: M.catarrhalis
US-09-540-236-2753
                                                                                                       307 KDVLQERT----
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                                                                                                                                                                                                                                                                                                                                                           RESULT 20
US-09-540-236-2753
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LENGTH: 718
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                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54 YSQ-EASVLVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQ 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KDILIRILDDGVKKLNEA---QKSLLTSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQ 169
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125 YLLDAYSHIESDSTSHNNGSSDKSLDSSNASFNN-QGKL-----DLFKYFTELSHYIRQC 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 EQTVEVVK------SAIETADG---ALDLYNKYLDQVIPWKTFDETIKELSRFKQE 53
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                                                                      FQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIP 209
                                                                                                                                        -----YILTQG-İNGKEVP 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...1196
; SEQUENCE DESCRIPTION: SEQ ID NO: 3944:
US-09-107-532A-3944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
                                                                                                                                                                                                                                                                                                               Sequence 3944, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: <Unknown>
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INFORMATION FOR SEQ ID NO: 3944:
                                                                                                                                        179 PODNCCDFKVRTNLNDKFGI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 7310
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COUNTRY: USA
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MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
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                                                                                                                                                                                                                                                RESULT 19
US-09-107-532A-3944
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          177 AYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNNR-----LKTVONFF----TSL 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   394 ILTAESTN-----QEYA-----RMVQDLQNRSTLKEEEIKEITSSFLEKITDL 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ::| ::| ::| | : | 437 KNQLRQQDEDFRKQLEEKGKRTAEKENVMTELTMEINKWRLLYDELYEKTKPFQQQLDAF 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRIL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               285 L-RDVTAQLESEQEKYNDTAQSLRD---VTAQLESEQ----EKYND-TAQSLRDVTAQ-L 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .---- 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        228 LDNLLREKEVELEKHIAAHAQAILIAQEKYNDTA---OSLRDVTAQLESVQEKYNDTAQS 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MTSIFAEQTVEVVKSAIETADGALDLYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASV 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   226 SATVKQANKDIDAAKLKLATEIAAIGEIKTE--TETTRFYVDYDDL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: TUTLEY, EVA A.
APPLICANT: SHUWEN, ZHANG
APPLICANT: SHUWEN, ZHANG
APPLICANT: ENTWISTLE, JOYCELYN
ITILE OF INVENTION: HYALURONAN RECEPTOR PROTEIN
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEB: FISH & NEAVE
STREET: 1251 AVENUE OF THE AMERICAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     270 ---MLSLLK--GAAKKMINTCNE-YQQRHGKKTL 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :|| | | : : | | | : : | 497 EAEKQALINEHGATQEQINKIRDSYAQILGHQNL 530
                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
STRANDEL TYPE: protein
DESCRIPTION: /desc = "RHARM I protein"
                                             COMPUTER REALANDLE FORMY

COMPUTER: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

SOFTWARE: Patentin Rel. #1.0, ASCII

CURRENT APPLICATION DATA: US/08/477, 831C

PILING DATE: 07-UN-1995

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: PIERRI, MARGARET A.

REGISTRATION NUMBER: 30,709

REFERENCE/DOCKET NUMBER: SIM-10

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFRAX: 212-596-9000
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                             606 amino acids
                               COMPUTER READABLE FORM:
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RY: U.S.A.
10020-1104
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ZIP: 1002
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61 LVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRIL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    462 KNOLRÒQDEDFRKOLEEKGKRTAEKENVMTELTMEINKWRLLYDELYEKTKPFQQOLDAF 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MTSIFAEQTVEVVKSALETADGALDLYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               177 AYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNNR-----LKTVQNFF----TSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.8%; Score 103; DB 4; Length 631;
19.8%; Pred. No. 0.22;
tive 69; Mismatches 131; Indels
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PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CURAPALSEGFORMATTER Version 0.9
SEQ ID NO 1078
                                                                                                                      SOFWARE: PATENTIA NO.

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,831C
FILING DATE: 07-4UN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: PIERI, MARGARET A.
REGISTRATION NUMBER: 30,709
REFERENCE/DOCKET NUMBER: SIM-10
TELECOMMUNICATION:
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/desc = "RHAMM I-2a"
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 631 amino acids
TYPE: amino acids
STRANDEDNESS: single
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Best Local Similarity
Matches 66; Conserv
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DESCRIPTION:
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us-09-993-292b-2.rai

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308 KNQLRQQDEDFRKQLEEKGKRTAEKENVMTELTMEINKWRLLYEELYEELYEFLOQQLDAF 367
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                                                                                                                                                                                                                                                                                                                                                                                                            206 ESVQEKYNDTAQSLRDVSAQLESYKSSTLKEIE-DLKLENLTLQEKVAMAEKSVEDVQQQ 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 SATVKQANKDI------DAAKLKLATEIA-----AIGEIKTETETTRFYVD-Y 266
                                                                                                                                                                                                                                                                                                                            99 LDNLLREKEVELEKHIAAHAQAILIAQEKYNDTA---QSLRDVTAQLESVQEKYNDTAQS 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 DDGVKKLNEAQKSLLTSS---QSFNNASGKLLALDSQLTN-DFSEKSSYFQSQVDRIRKE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177 AYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNNR-----LKTVQNFF----TSL 225
                                                                                                                                                                                                                                                                              1 MTSIFAEQTVEVVKSAIETADGALDLYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASV 60
                                                                                                                                                                                                                               68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Hawkins, Phillip R.
APPLICANT: Wilde, Craig G.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: HYALURONAN RECEPTOR EXPRESSED IN HUMAN
TITLE OF INVENTION: UMBILICAL VEIN ENDOTHELIAL CELLS
                                                                                                                                                                            Query Match 6.7%; Score 101; DB 1; Length 477; Best Local Similarity 20.1%; Pred. No. 0.22; Matches 67; Conservative 72; Mismatches 127; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,178
FILING DATE: August 20, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/402,217
PTITNE NAME: US 08/402,217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 267 DDLMLSLLK--GAAKKMINTCNE-YQQRHGKKTL 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : :|| || : : || 368 EAEKQALLNEHGATQEQLNKIRDSYAQLLGHQNL 401
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CORRESPONDENCE ADDRESS:
ADDRESSE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 POXTER Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF-0028-1 DIV
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Patent No. 5783669
Patent No. 5783669 5700912
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: MATCH 10, 11
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
; TOPOLOGY: linear; MOLECULE TYPE: protein; IMMEDIATE SOURCE: LIBRARY: mouse; CLONE: GI 53979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  168 SQVDRI-----KKEAYAGAAAGIVAGPFGLIISYSIAAGVIEG-----KLIPELNNR 214
                                                                                                                                                                                                                                                                                                                                 52 QEYSQEASVLVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    215 LKTVQNFFTSLSATVKQANKDIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDLMLSLL 274
                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08402217A; Sequence 3, Application US/08402217A; Sequence 3, Application US/08402217A; Sequence 3, Application US/08402217A; Seant No. 5587301; APPLICANT: Hawkins, Phillip R. APPLICANT: Seilhame, Carig G. APPLICANT: Seilhame, Jeffrey J. TITLE OF INVENTION: HYALURONAN RECEPTOR EXPRESSED IN HUMAN TITLE OF INVENTION: UMBILICAL VEIN ENDOTHELIAL CELLS NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS: ADDRESSE: INCTE PHARMACEUTICALS, INC. STREET: 3174 Porter Drive CITY: Palo Alto
                                                                                                                                                                                                                                                                                68;
                                                                                                                                                                                                                             Query Match 6.7%; Score 102; DB 4; Length 1976; Best Local Similarity 21.1%; Pred. No. 1.6; Matches 56; Conservative 53; Mismatches 88; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1120 IAELQEDFESEKASRNKAEKQ----KRDLSEELEA---LKTELEDT
                                                                                                      NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number P35580
US-09-538-092-1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/08/402,217A
FILING DATE: 10-MAR-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   275 KGAAKKMINTCNEYQQRHGKKTLFE 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF-0028US
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COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Luther, Barbara J.
REGISTRATION NUMBER: 33954
REPRERNCK/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELERPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 415-802-2013:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 477 amino acids
TYPE: amino acid
                                                        ORGANISM: Homo sapiens
          LENGTH: 1976
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   265 ILTABSTN------QBYA-------RMVQDLQNRSTLKEBEITKBITSSFLBKITDL 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           308 KNOLRÒQDEDFRKOLEEKGKRTAEKENVMTELTWEINKWRLLYEELYEKTKPFQQQLDAF 367
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APPLICANT: Hawkins, Phillip R.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Wilde, Craig
APPLICANT: Seilhamer, Jeffrey
APPLICANT: Seilhamer, Jeffrey
TITLE OF INVENTION: HYALURONAN RECEPTOR EXPRESSED IN HUMAN
TITLE OF INVENTION: UMBILICAL VEIN ENDOTHELIAL CELS
NUMBER OF SEQUENCES:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                68;
                                                                                                                                                                                                                                            6.7%; Score 101; DB 1; Length 477; ilarity 20.1%; Pred. No. 0.22; Conservative 72; Mismatches 127; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastERG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/995,654
FILING DATE: December 22, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            267 DDLMLSLLK--GAAKKMINTCNE-YQQRHGKKTL 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/700,178
FILING DATE: August 20, 1996
PRIOR APPLICATION DATA:
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; Sequence 3, Application US/08995654
; Patent No. 6025138
                 TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 477 amino acids
                                                                                     TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
LIBRARY: mouse
CLONE: GI 53979
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Best Local Similarity
Matches 67; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 LVGDIKVLLAMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRIL 120
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Sequence 1, Application US/09310187A;
Patent No. 6358751
GENERAL INFORMATION:
APPLICANT: Benichou, Gilles
TITLE OF INVENTION: Involvement of Autoantigens in Cardiac
TITLE OF INVENTION: Involvement of Autoantigens in Cardiac
TITLE REFERENCE: UCSF-090
CURRENT APPLICATION NUMBER: US/09/310,187A;
CURRENT FILING DATE: 1999-05-12
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.7%; Score 101; DB 3; Length 1939;
22.5%; Pred. No. 1.9;
ve 44; Mismatches 128; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 6.7%; Score 101; DB 3; Length 477; Best Local Similarity 20.1%; Pred. No. 0.22; Matches 67; Conservative 72; Mismatches 127; Indels Matches
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REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0028-2 DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
FILING DATE: March 10, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
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Best Local Similarity 22.5%;
Matches 75; Conservative 4
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                                                                                                                                                                           TELEFAX: 650-845-4166
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ORGANISM: Homo sapiens
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Length 643;
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OTHER INFORMATION: Polypeptide Accession Number P04264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58; Mismatches 124;
                                           6.6%; Score 100.5; E 22.2%; Pred. No. 0.4;
                  267 DDLMLSLLKGAAKKMINTCNEYQQRHGKKTLFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             472 LALDLEIATYRTLLEGEESRMSGEC 496
                                                                                                                                                      Sequence 844, Application US/09538092
Patent No. 6753314
                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.
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Matches 72; Conservative
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LOCATION: (0)...(0)
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                                                                                                                                                                                                                            1316 DLKRQLEEEGKAKNALA-----HALQSARHDCDLIREQYEEBTEAKAELQRVLSKAN 1367
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------KAKANLEKVSRTLEDQA 1258
                                                                                                                                                        1259 NEYRVKLEEAQRSLNDFTTQRAKLQTENGELARQLEEKEALISQLTRG---KLSYTQQME 1315
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                                                                                                                   125 K----KLNEAQKSL---LTSSQSFNNASGKLL-----ALDSQLTNDFSEKSSYFQSQV 170
                                                                                                                                                                                               DRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPE-------LINRL 215
                                                                                                                                                                                                                                                                            KTVONFFISLSATVKQANKDIDAAKLKLATE-----IAAIGEIKTETETT--RFYVDY 266
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                                     65 IKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRILDDGV 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 FAEQTVEVVKSAIETADGALDLYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVLVGD 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 00/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION: (0)...(0); OTHER INFORMATION: Polypeptide Accession Number P13533 US-09-538-092-917
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1.9;
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                                                                            --VISNMEQII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuraPatSeqFormatter Version 0.9
SEQ ID NO 917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 917, Application US/09538092 Patent No. 6753314 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Traci A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
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                                                                            1226 FKLELDD
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Sequence 5793, Application US/09328352
| Patent No. 6562958
| GENERAL INFORMATION:
| TITLE OF INVERTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
| TITLE OF INVERTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF TOPERCE: GTC99-03PA |
| FILE REFERENCE: GTC99-03PA |
| CURRENT APPLICATION NUMBER: US/09/328,352 |
| CURRENT FILING DATE: 1999-06-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      365 KAEAESLYQSKYEELQ------ITAGRHGDSVRNSKIEISELNRVIQ-RLRSEIDN 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  214 RIKTVONFFTSLSATVKOANKDIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDLM--- 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 VGDIK---VLLMDSQDKYFE----ATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKD 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----SYFQSQVDRIRKBAYAGAAAGIVAGPFG-----LIISYSIAAGVIEGKLIPELNN 213
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REPERENCE: 15966-54.
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION UNBER: 60/127,352
PRIOR PLLING DATE: 1999-04-01
PRIOR PILING DATE: 1200-04-01
PRIOR PILING DATE: 2000-03-01
SPRIOR FILING DATE: 2000-03-01
SPRIOR FILING DATE: 2000-03-01
SPRIOR FILING DATE: AND NOS: 1387
SOFTWARE: CuraPatSeqFormatter Version 0.9
SEQ ID NO 844
: LENGTH: 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 PAEQTVEVVKS---AIBTADGALDLYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     1257 LQVKFNEGERVRTELADKVTKLQVELDNVTGLLSQSDSKSSKLTKDFSALESQLQDTQEL 1316
1166 EQEVNILKKTLEBERAKTHEAQIQEMRQKHSQAV--EELAEQLEQTKRVKANLEKAKQTLE 1223
                                                                                                                    ----SEHKRKKVEAQLQE 1256
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APPLICANT: Glot, Loic
APPLICANT: Mansfield, Traci A.
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Proctein-Protein Complexes and Method of Using Same
TILE REPERENCE: 15966-542
CURRENT PILING DATE: 0200-03-22
CURRENT FILING DATE: 0200-03-22
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR FILING DATE: 1999-04-01
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SEQ ID NO 936
LENGTH: 2871
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1262 QATEQRRRABENALQQKACG------SEIMQKKQHLEIELKQVMQQRSEDNAR
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                                                                                                                                                                                                                                                                                                 IRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNNRLKTVONFFTSLSATVKOA
                                                                                                                                                                                                                                                                                                                                                56 QEASVIVGDIKVILMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDI
                                                                                                                                                                                116 LIRILDDGVKKLNEAQKSLLTSSQSFNNASGKLLALD---SQLTNDFSEKSSYFQSQVDR
                                                                                                                                                                                                                                                                                                                                                                                                                  233 NKDIDAAKLKLATELAAIGEIKTETETTRFYVDYDDL-MLSLLKGAAKKMINTCNEYQQR
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ilarity 17.8%; Pred. No. 4.5;
Conservative 57; Mismatches 93; Indels 12
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CTHER INFORMATION: Polypeptide Accession Number P15924
US-09-538-092-936
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Patent No. 6753314
GENERAL INFORMATION:
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                                                                                                                                1224 NERGELANEVKVLLOGKGD-----
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Best Local Similarity
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| Sequence 1077, Application US/09538092
| Patent No. 6753314
| GENERAL INFORMATION:
| APPLICANT: Glot, Loic
| APPLICANT: Mansfield, Traci A. APPLICANT: Mansfield, Traci A. APPLICANT: Mansfield, Traci A. APPLICANT: Mansfield, Traci A. APPLICANT: MANSFINCE: 12966-542.
| TITLE OF INVENTION: Procein-Protein Complexes and Method of Using Same TITLE OF INVENTION NUMBER: US/09/538,092
| CURRENT APPLICATION NUMBER: 60/127,352
| PRIOR APPLICATION NUMBER: 60/127,352
| PRIOR APPLICATION NUMBER: 60/178,965
| PRIOR PILING DATE: 2000-02-01
| NUMBER OF SEQ ID NOS: 1387
| SOFTWARE: CuraPatSegFormatter Version 0.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              395 IKLNTATSIAGRLAKGAFGLIGGWAGVATLGVMGLAAAYSYFNNKAEEAKQKLAEQAKVA 454
                                                                                                                                                                                                                                                                                                                                                                                                                     278 OVLAGSVQTLASNLDLIADGALVVGIGYITRAILMKS--AAİKEGMASTLASRQASVLNA 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KQEYSQEASVL-----VGDIKVLLMDSQDKYFEAT-------QTVYE 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           173 IRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNNRLKTVONFFTSLSATVKQ-
                                                                                                                                                                                                                                                                                                              Gaps
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1 Similarity 19.6%; Bred. No. 1.4;
80; Conservative 57; Mismatches 133; Indels 139;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             613 AKQKDSVIDSIYKSGWLDKGYTVAQANAILELQKAKGMSAILSKDBIDS 661
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Best Local Similarity 19.1%; Pred. No. 2.5;
Matches 58; Conservative 46; Mismatches 120; Indele 80
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                                                                                                                                                   TYPE: PRT ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            232 ----ANKDIDAAKLKL----
                                                  NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5793
LENGTH: 1454
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US-09-328-352-5793
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Best Local S
Matches 80
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APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES AND THERAPEUTICS TITLE OF INVENTION: ENTERCOCCUS FARCALIS FOR DIAGNOSTICS AND THERAPEUTICS CURRENT APPLICATION NUMBER: US/09/134,000C CURRENT FILING DATE: 1996-08-13 FRIOR APPLICATION UNMBER: US 60/055,778 PRIOR APPLICATION UNMBER: US 60/055,778 NUMBER OF SEQ ID NOS: 6812
                                                                                                                                                                                                                                                                                                                  518
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                                                                                                                                                                                                                                                                                                                                                                                                 -----NDFSEKSSY----FQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAA 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201 GVIEGKLIPELNNRLKTVQNFFTSLSATVKQANKDIDAAKLKLATEIAAIGEIKTETETT 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133 ITPKKEKYVIASDSTFAPFEFONAQGDYVGIDVDLVKRAABLQGFTVEFKFIGFSSAVQA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----KKLNEAQK-----SLLTSSQSFN------NASGKLLALDSQLT-- 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 YDYTIKNFDDATGLYKALENGEADAIVDDYPVLGYAVKNGQKLQLVGDKETGSSYGFAVK 83
                                                                                                                                                                                                                                                                                                          459 KLFDKLQLDKSSYLSKLKEKKEQLNEIESSITNIDATLIDLNDKKDFVNEIKSAMSIGDT
                                                                                                                                                                                                                                                                 38 KTFDETIKELSRF-----KQEYSQEASVLVGDIKVLLMDSQDK-----YFEATQTVYEW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            679 EKTKDKL-NELNNKLKIEMNDQKHLTENLTQTSKEINNLELKMEKEMQQLG-----
                                                                                                                                                                                                               125;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   261 RFYYDYDDLM----LSLLKGAAKKMINTCNEYQQRH------GKKTL
                                                                                                                                                                                                                                                                                                                                                                      CGVVTQLLSAYILLFDEYNEKKASAQKDILIRILD-----DGV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.5%; Score 98; DB 4; Length 284; ilarity 21.4%; Pred. No. 0.2; Conservative 42; Mismatches 96; Indels
                                                                                                                                                                                                             Indels
                                                                                                                                                         6.5%; Score 98.5; DB 3;
19.3%; Pred. No. 1.3;
tive 51; Mismatches 109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3594, Application US/09134000C Patent No. 6617156 GENERAL INFORMATION:
; SEQ ID NO 5178
; LENGTH: 1010
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enterococcus faecalis
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SEQ ID NO 3594
LENGTH: 284
                                                                                                                                                                                 Best Local Similarity 19.3
Matches 68, Conservative
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Best Local Similarity
Matches 63; Conserv
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                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                      GENERAL INCORMATION:

APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: NUCLEIC AZID AND AMINO AZID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: NUCLEIC AZID AND AMINO AZID SEQUENCES
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-10-10
RIOR PILING DATE: 1997-10-14
RIOR PILING DATE: 1997-10-14
RIOR PILING DATE: 1997-10-14
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Sequence 5178, Application US/09134001C

GENERAL No. 5380370

GENERAL NO. 5380370

GENERAL STAIN DOUGE TE-Stamm et al

TITLE OF INVENTION: BFIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: BFIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: BFIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3692 QVPSTEGMTQQTK------DDYNSKQQAAQQEISKAQQVIDNGDATTQQISNAKTNVER 3744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------KENNAL 3849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3632 KTNTDRILKEONPSVADVNNALNKVREVOOKLNEARALLONKEDNSALVRAKEOLOOAVD 3691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       137 SSQSFNNASGKLLALDSQLTN------DFSEKSSYFQSQVDRIRKE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82 TVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDI--LIRILDDG----VKKLNEAQKSLLT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177 AYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELMNRLKTVQNFFTSLSATVKQANKDI 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57; Mismatches 105; Indels 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 VEVVKSAIETADGAL----DLYNKYLDQVIPWKTFDETIKELSRFKQEYSQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 10182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3805 ANS----ILTNDNPQVSQVTAALNKIKA-VQPELDKAIAMLKN
                                                         KTETETTRFYVDYDDLMLSLLKGAAKKMINTCNEYQQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 6.6%; Score 100; Di
Similarity 18.8%; Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3850 VQAKQQLQ-----QIVNEVDPTQ 3867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    237 DAAKLKLATEIAAIGEIKTETETTR 261
                                                                                                                                                                                                       Sequence 3159, Application US/09134001C
Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3159
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                                                                                                                                                         RESULT 33
US-09-134-001C-3159
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US-09-134-001C-5178
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Best Local S:
Matches 61
                           254
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US-09-252-991A-31794

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SECOND OF 252-991A-31794

SECOND OF 251795

GENERAL INFORMATION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ARROGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ARROGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ASSOCIATION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

SECOND NUMBER: US 60/094,190

NUMBER OF SEQ ID NOS: 33142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1206 NEYRVKLBEAQRSL----NDFTTQRAKLQTENGELARQLEEKEALIWQLTRGKLSYTQQM 1261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  215 LKTVQNFFTSLSATVKQANKDIDAAKLKLATE-----IAAIGEIKTETETT--RFYVD 265
                                                                                                                                                                                                                                                                                                                                                                                                           12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    170 VDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPE------LANNR 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 K----KLINEAQKSILITSSQSFNNASGKILALDSQLINDFSEKS-----SYFOSQ 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 IKVLLANDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRILDDGV 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 FABQTVEVVKSAIBTADGALDLYNKYLDQVIPWKTFDBTIKBLSRFKQBYSQBASVLVGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63;
                                                                                                                                                                                                                                                                                                                                                                                                                88;
                                                                                                                                                                                                                                                                                                                                                                    6.5%; Score 98; DB 3; Length 1886; 11.3%; Pred. No. 3.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                              44; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94;
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21.8%; Pred. No. 0.84;
iive 48; Mismatches 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       266 YDDLMLSLLKGAAKKMINTCNEYQQRHGKKTLFE 299
                   FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CTOOK, Wannell M.
REGISTRATION NUMBER: 3595-4
REFERENCE/DOCKET NUMBER: 3595-4
TELECHONE: (303) 863-9700
TELEPAX: (303) 863-9700
TELEPAX: (303) 863-9700
TELEPAX: (303) 863-9700
SEQUENCE CHARACTERISTICS:
APPLICATION NUMBER: US/08/938,105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                   21.3%;
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 21.3%
Matches 71; Conservative
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                                                                                                                                                                                                                                                       LENGTH: 1886 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                               , MOLECULE TYPE: protein US-08-938-105-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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IIILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF TOWN BAUMANII FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT APPLICATION DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 IKVILMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRILDDGV 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   245 ILGINYQGYDKEH------ITQVINAILVIYGAQNVERRSABSAQTLKFLDEQL 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 ----KKLNBAQKSLLTSSQSFNNASGKLLALDSQLTNDFSBKSSYFQSQVDRIR----- 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNNRLKTVONFFTSLSATVKOANK 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    201 VWKVAİFİKD---QLDSKY------NİKKLSIPPAVDNISSNYSVAERGKLTG- 244
             235 DIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDLMLSLLKGAAKKMINTCNEYQQ 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 VVKSAIETADGALDLYNKYLDQVIPWKTFDETIKELS-----RFKQEYS-QEASVLVGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86; Indels 102; Gaps
                                                                        229 VKQAN---KDIDAAK----LKLATEIA-AIGEIKTETETTRFYVDYDDLMLSLL 274
                                                                                                 6.5%; Score 98; DB 4; Length 733; 22.0%; Pred. No. 0.86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/08938105
Sequence No. 6353151
GENERAL INFORMATION:
APPLICANT: Lieinwand, Leslie A.
APPLICANT: Vikerrom, Karen L.
TITLE OF INVENTION: TRANSGENIC MODEL FOR HEART FAILURE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | : | : | | : | | : | | DVQRQYLQLYREV----EVKTQ-----LYTALL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln St., Suite 3500
CITY: Denver
                                                                                                                                                                                                                          Sequence 5599, Application US/09128352
Patent No. 6562958
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 22.09
Matches 65; Conservative
                   340 EQKQAEMAAKYTA-
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US-09-328-352-5599
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COUNTRY:
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GENERAL INFORMATION:

APPLICATION: Application US/09248796A

REQUENCE 16013, Application US/09248796A

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: WICLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANF
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
PRIOR FILING DATE: 1998-08-13
PRIOR FILING DATE: 1998-08-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 QDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRILDDGVKKLNEAQK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 SILTSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDRIRKEA--YAGAAAGIVAGPF 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            239 VKSAI--AEQAILAFFKNKPEVL-----ETIKIDESYWKNLTTE------KAFLM-- 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              191 GLIISYSIAAGVIEGKLIPELNNRLKTVONFFT-------SLSATVKQANK 234
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; Sequence 91, Application US/09917254
; Partent No. 6703204
; GENERAL INFORMATION:
    APPLICANT: Mutter: George
; APPLICANT: Baak, Jan
    TITLE OF INVENTION: Prognostic Classification of Breast Cancer;
    TILE REFERENCE: B0801/7224(JRV)
; CURRENT APPLICATION NUMBER: US/09/917,254
; CURRENT FILING DATE: 2001-07-28
; PRIOR PILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SEQ ID NOS: 102
; SEQ ID NO 91
LENGTH: 1857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89;
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21.0%; Pred. No. 4.1;
tive 51; Mismatches 108;
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Best Local Similarity 21.8%; Pred. No. 1.2;
Matches 65; Conservative 59; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 21.0% Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Candida albicans
US-09-248-796A-16013
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                                                                    JS-09-248-796A-16013
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LENGTH: 862
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                                                                                                                                                                                                                                                                                                                  228 EERKQNLTYPEQTIIVSEELSPAMLGEVPEGRLVGLVSVLGSG-----NSHVAILAR 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | | | : : | | : : | | : : | | 370 AMGIPTVMGAVDLPYSKVDGIDLIVDGYHGEV------YTNPSAELVRQXSD 415
                                                                                                                                                                             EAQKSLLT-----SSQSFNNA----SGKLLALDSQLTNDFSEKSSYFQSQVDRIRK 175
                                                                                                                                                                                                                                                                                                                                                                                                                176 EAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELMNRLKTVQNFFTSLSATVKQANKD 235
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                                           :|:| |: :::| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: ::::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: :::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: ::|| |: :|| |: :|| |: :|| |: :|| |: :|| |:
                                                                                                                                 76 YFEATQTVY--EWC-GVVTQLLSAYI----LLFDEYNEKKASAQKDILIRILDDGVKKLN 128
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----SQEASVL-----VGDIKVLLMDSQDK 75
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TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
TITLE OF THE REPERENCE: 00786/36.002
CURRENT APPLICATION NUMBER: 05/066,517
PRIOR APPLICATION NUMBER: 60/066,517
PRIOR FILING DATE: 1997-11-25
NUMBER OF SEQ ID NOS: 437
SEQ ID NO 170
LENGTH: 759
OVIPWKTFDETIKELSRFKOEY----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         236 IDAAKLKLATEIAAIGEIKTET 257
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Goodman, Howard M.
Rahme, Laurence G.
Mahajan-Miklos, Shalina
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Drenkard, Eliana
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US-09-199-637A-170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELNNRLKTVQNFFTSLSATVKQANKDIDAAKLKLATEIAALGEIKTETETTRFYVD-YDD 268
108 KASAQKDILIRILD-----DGVKKLNEAQKSLLTSSQ-----SFNNASGKLLALDSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     155 LINDFSEKSSYFQSQVDRIRK-----EAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --DLYNKYLDQVIPWKTFDETIKELSRFKQEYSQE
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Zhu, Xueliang
APPLICANT: Zhu, Xueliang
APPLICANT: Lee, Wen-Hwa
TITLE OF INVENTION: A No. 5710022el Nuclear Mitotic Phosphoprotein
NUMBER OF SEQUENCE: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: A370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2285;
                                                                                                                                                                                                      Sequence 2, Application US/09308375;
Sequence 2, Application US/09308375;
Patent NO. 630017
GENERAL INFORMATION:
APPLICANT: Genencor International, Inc.
ITLE OF INVENTION: Proteases From Gram-Positive Organisms
TILE REFERENCE: GC394-PCT
CURRENT APPLICATION NUMBER: US/09/308,375
CURRENT FILING DATE: 1999-05-14
EARLIER FILING DATE: 1999-05-14
SEALIER FILING DATE: 1997-09-15
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 3.0
SSEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.4%; Score 97.5; DB 3; Length 2
19.9%; Pred. No. 5.6;
Ltive 58; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1256 LEEKMLQPGGYSNSQIEAMQSVKSALESYISASE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 6, Application US/08328254 ; Patent No. 5710022
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                                                                                                                  1414 AYDKLEKTKNRLQQ 1427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Bacillius subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                          --KKMINTCNEYQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 65; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRY: USA
92122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52 QEYSQEASVLVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASA 111
                                                                                                                                                                                                                                                                                                1201 QLQDTQELLQEETRQK------LINVSTKLRQLEEERNSLQDQLDEEMEAKQN- 1246
                                                                                                                                                                                                                                                                                                                                                                               1247 ---LERHISTLNIQLSDSKKKLQDFASTVEALBEGK-----KRFQKEIENLTQQYBEKAA 1298
                                                                                                                                                                                                                 Sequence 1084, Application US/09538092
| Sequence 1084, Application US/09538092
| Patent No. 6753314
| GENERAL INFORMATION:
| APPLICANT: Giot, Loic
| APPLICANT: Mansfield, Traci A. TITLE OF INVENTION Protein-Protein Complexes and Method of Using Same TITLE OF INVENTION NUMBER: US/09/538,092
| CURRENT APPLICATION NUMBER: 00/00-03-29
| CURRENT FILING DATE: 1999-04-01
| PRIOR APPLICATION NUMBER: 60/127,352
| PRIOR APPLICATION NUMBER: 60/178,965
| PRIOR APPLICATION UNMER: 2000-02-01
| PRIOR PILING DATE: 2000-02-01
| NUMBER OF SEQ ID NOS: 1387
| SOFTWARE: CuraPatSeqFormatter Version 0.9
                                                222 FISLSATVKQANKDIDAAKLKL---ATBIAAIGEIKTETETTRFYVDYDDLMLSLLKGAA 278
                                                                                                     QEYSQEASVLVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEXNEKKASA 111
                                                                                                                                                                                                                                                                        165 YFÇSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIE---GKLIPELNNRLKTVONF 221
                        51
                                                                                                                                                                                      QYDILIRILDDGVK-----KLNEAQKSLLTSSQSFNNASGKLLALDSQLTNDFSEKSS
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Best Local Similarity. 21.0%; Pred. No. 4.4;
Matches 66; Conservative 51; Mismatches 108; Indels 89
                        EQTVEVVKSAIETADGA----LDLYNKYLDQVIPWKTFDETIKELSRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (0)...(0)
CTHER INFORMATION: Polypeptide Accession Number P35749
US-09-538-092-1084
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US-09-538-092-1084
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LENGTH: 1972
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2736 SGEKNRIAGELOLLIERIKSSKDOLKELTLENSELKKSLDCMHKDOVEKEGKVREELAEY 2795
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2676 QDTLEVLQSSYKNLENELELTKMDKMSFVEKVNKMTAKETELQREMHEMAQKTAELQEEL 2735
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08353700
Patent No. 5599919
GENERAL INFORMATION:
APPLICANT: YEN, TIMOTHY J.
APPLICANT: RATTURE, JEROME B.
TITLE OF INVENTION: NUCLEIC ACID ENCODING A
TITLE OF INVENTION: TRANSIENTLY-EXPRESSED KINETOCHORE PROTEIN,
TITLE OF INVENTION: ADD METHODS OF USE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                       Query Match 6.4%; Score 97.5; DB 4; Length 3210; Best Local Similarity 20.5%; Pred. No. 9.4; Matches 70; Conservative 70; Mismatches 126; Indels 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              261 RFYVD-YDDLMLSLLK-GAAKKMINT-----CNEYQQRHGK 294
                                                                                                                               , LOCATION: (0)...(0); OTHER INFORMATION: Polypeptide Accession Number P49454 US-09-538-092-1154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: DANN, DORFMAN, HERRELL AND SKILLMAN
STREET: 1601 MARKET STREET, SUITE 720
CITY: PHILADELPHIA
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09-DEC-1994
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NAME: REED, JANET E.
REGISTRATION NUMBER: 36,252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FELECOMMUNICATION INFORMATION
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COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
TYPE: Floppy disk
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TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 1
                                              TYPE: PRT
ORGANISM: Homo sapiens
PEATURE:
NAME/KEY: misc feature
LOCATION: (0)...(0)
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SEQ ID NO 1154
LENGTH: 3210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2008 SGEKNRLAGELQLLLEEIKSSKDQLKELTLENSELKKSLDCMHKDQVEKEGKVREEIAEY 2067
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Sequence 1154, Application US/09538092

Retent No. 6753314

GENERAL INFORMATION:

APPLICANT: Giot, Loic

APPLICANT: Mansfield, Traci A.

TITLE OF INVERTION: Protein-Protein Complexes and Method of Using Same

TILE OF INVERTION: Protein-Protein Complexes and Method of Using Same

TILE REPERENCE: 15966-542

CURRENT APPLICATION NUMBER: 00/127,352

FRIOR APPLICATION NUMBER: 60/127,352

FRIOR APPLICATION NUMBER: 60/177,352

FRIOR PILING DATE: 1999-04-01

FRIOR PILING DATE: 2000-02-01

FRIOR FILING DATE: 2000-02-01

SOFTWARE: CuraPatSeqFormatter Version 0.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SQEASVLVGDIKVLLMD---SQDKYFEAT-------OTVYEWCGVVTQLLSAY 97
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             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,254
FILING DATE: 24-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/141,239
FILING DATE: 22-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 9-CJ 1191
TELECOMMUNICATION NUMBER: 9-CJ 1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 6.4%; Score 97.5; DB 1; Best Local Similarity 20.5%; Pred. No. 6.3; Matches 70; Conservative 70; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (619) 535-9010
TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 2482 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: protein US-08-328-254-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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70 -MDSQDK--YFBATQTVYBWCGVVTQLLSAYILLFDBYNBKKAS------AQKDILIR 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2855 S----LKATTQILEELKKTKMDNLKYVNQLKKENER-----AQGKNKLLI------ 2895
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2736 SGEKNRLAGELQLLLEBIKSSKDQLKELTLENSELKKSLDCMHKDQVEKEGKVREEIAEY 2795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2796 OLRIHE-AEKKHQALLIDTINKQYEVEIQTYREKLISKEBCLSSQKLEIDLIKSSKEELINN 2854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2896 --KSCKQLEBEKEILQKELSQLQAAQEKQKTGTVMDTKVDELTTEIKELKETLEEKTKEA 2953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 BGKLIPELMNRLKTVONFFTSL-SATVKOANKDIDAAKL-KLATEIAAIGE-IKTETETT 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144 ASGKLLALDSQLTNDFSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVI 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98 ILLFDEYNEKKASA-----QKDILIRILDDGVKKLNEAQKS-----LLTSSQSFNN 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----QTVYEWCGVVTQLLSAY 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 EQTVEVVKSAIETADGALDLYN----KYLDQVIPW-----KTFDETIKELSRFKQEY
                                                                                                                                                                                                                                                                                                                                                                                         Length 3248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.4%; Score 97; DB 4; Length 961;
22.3%; Pred. No. 1.6;
Live 52; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          261 RFYVD-YDDLMLSLLK-GAAKKMINT----CNEYQQRHGK 294
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APPLICANT: Hyman, Paul
APPLICANT: Hyman, Paul
APPLICANT: Williams, Mark
TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
FILE REPRENCES: 841-010-999
CURRENT APPLICATION NUMBER: US/09/914,259
CURRENT FILING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 180
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 66
                                                                                                                                                                                                                                                                                                                                                                                   6.4%; Score 97.5; DB 5; 1
20.5%; Pred. No. 9.6;
Live 70; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55 SQEASVLVGDIKVLLMD---SQDKYFEAT----
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Patent No. 6495336
GENERAL INFORMATION:
                                                                                                                                                                              SS: not relevant not relevant
                   TELETAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
(215) 563-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 22.3$
Marches 67; Conservative
                                                                                                                 LENGTH: 3248 amino acids
TYPE: amino acid
STRANDEDNESS: not relevan
                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 20.5%
Matches 70; Conservative
                                                                                                                                                                                                                 TOPOLOGY: not releva:
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT CRGANISM: BOB taurus US-09-914-259-66
                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO
      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-914-259-66
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APPLICANT: Rathner, Jerome B.
APPLICANT: Rattner, Jerome B.
TITLE OF INVENTION: Nucleic Acid Encoding a Transiently
TITLE OF INVENTION: Expressed Kinetochore Protein, and Methods of Use
TITLE OF INVENTION: Expressed Kinetochore Protein, and Methods of Use
TITLE OF INVENTION: Expressed Kinetochore Protein, and Methods of Use
TITLE OF INVENTION: Expressed Kinetochore Protein, and Methods of Use
TITLE OF INVENTION:
ADDRESSED: Dann, Dorfman, Herrell and Skillman
STREE: 1601 Market Street Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----QTVYEWCGVVTQLLSAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 BQTVEVVKSALETADGALDLYN----KYLDQVIPW-----KTFDETIKELSRFKORY
                                                                                                                                                                                                                                                                                                                                                                                         Length 3248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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APPLICATION NUMBER: PCT/US95/16216
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 20.5%; Pred. No. 9.6;
Matches 70; Conservative 70; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SQEASVLVGDIKVLLMD---SQDKYFEAT----
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/353,700
APPLING DATE: 09-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application PC/TUS9516216 GENERAL INFORMATION:
                         SEQUENCE CHARACTERISTICS:
LENGTH: 3248 amino acids
TYPE: amino acid
                                                                                       TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                           ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCT-US95-16216-1
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Search completed: January 5, 2005, 10:59:00
Job time : 20.0526 secs
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Conservative
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Matches 73; Conserv
                                                                                                                                                                                                                                                                                               ORGANISM: lcaD;
                                                                                                                                                                                                                                                                                                                    US-08-924-629C-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141
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Patent No. 6610836
GENERAL INFORMATION
GENERAL INFORMATION
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: NUMBER: US/09/489,039A
CURRENT PILLING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 8352
LENGTH: 350
                      99 QKYVLIGNSYHEAEKERHAIEVLIRQRCSALIVHSKALSDDELSDFMQHIPGMVLINRIV 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           159 PGYAHRCVGLDNVSGALMA-TRMLLNHGHQRIGYLSSNHGIEDDDMRREGWSKALQEQGI 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :| :| | :| | ::|:
218 IAPDSWIGSGSPDMQCGEAAMVELLGRNIGLTAVFAYNDSMAAGALTTLKDNGIVVPQHL 277
119 ILDDGVKK--LNEAQKSLLTSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDRIRKE 176
                                                                          177 AYAGAAAGIVAGPFGLIISYSIAAGVIEGKL----IPELNNRLKTVQNFFTSLSATVK 230
                                                                                                                                                      231 QANKDIDAAKLKLATBIAAIGEIKTETETTRFYVDYDDLMLSILLKGAAKKMINTCNEYQQ 290
                                                                                                                                                                               95 SAYILLPDEYNE-KKASAQKDILIR-----ILDD------GVKKCNEAQ 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------LNNRLKTVQNFFTSLSATVKQANKDIDAAKLKLATEIAAIGEI-KTE 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      278 SLIGFDDIPISRYTDPQLTTVRYPVMSMA--------KLATELALLGAAGKLD 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39 TFDETIKELSRFKQEYSQEASVL---VGD-IKVLLMDSQDKYFEATQTVYEWCGVVTQLL 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KSLLTSSQSFNNASGKLLALDSQLTNDFSEKSSYFQS----QVDRIRKEAYAGA--AAGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93; Indels 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 6.4%; Score 96.5; DB 4; Length 350; Best Local Similarity 22.1%; Pred. No. 0.39; Matches 68; Conservative 46; Mismatches 93; Indels 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/08924629C;
Patent No. 6403082
GENERAL INFORMATION:
APPLICANT: Stiles, Michael E.
APPLICANT: Vederas, John C.
APPLICANT: Wan Belkum, Marius J.
APPLICANT: Worobo, Randy W.
APPLICANT: Worobo, Randy W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Klebgiella pneumoniae
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APPLICANT: Greer, G. Gordon
APPLICANT: McMullen, Lynn M.
APPLICANT: Leisner, Jorgen J.
APPLICANT: Leisner, Jorgen J.
APPLICANT: Poon, Alsion
APPLICANT: Poon, Alsion
APPLICANT: Franz, Charles M.A.P.
TITLE OF INVENTION: No. 6403082elBacteriocins, Transport and Vector System and Method
FILE REFERENCE: 660.005508
CURRENT APPLICATION NUMBER: US/08/924,629C
CURRENT PILING DATE: 1997-09-05
RRIOR APPLICATION NUMBER: US 60/026,257
RRIOR APPLICATION NUMBER: US 60/026,257
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.1 101 FD----EYNEKK-----ASAQKDILIRILDDGVKKLNEA---QKSLLTSSQS----- 140 150 VDTLISEFNQQSSDKQTADQQANHQIDVLKQGQSKNNQQLANYQAILTSINSNTKPTNNP 209 210 YQAIYDNYSAQLKS--AQTTDDKDQVKQTALSNVQQQIDQLQTTSSSYDSQIAGITKSGP 267 190 FGLIISYSIAAGVIEGKLI---PELNNRLKTVQNFFTSLSATVKQANKD------ 235 268 ISQSSTIDKIADIKQQQLASAQKEINDQ----QQSLDBLKAKQSSANEDYQDTVIKAPED 323 47 LSRFKQEYSQEASVLVGDIKVL-----LMDSQDKYFBATQTVYEWCGVVTQLLSAYILL 100 ----FNNASGKLLALDSQLTNDFSEKS----SYFQSQVDRIR--KEAYAGAAAGIV-AGP 189 3 SIFAEQTVEVVKSAIE-----TADGALD----LYNKYLDQVIPWKTFDETIKE 46 6.4%; Score 96.5; DB 4; Length 457; 11.6%; Pred. No. 0.59; (ve 63; Mismatches 113; Indels 89 ----IDAAKLKLATEIAAIGEIKTE-TETTRFYVDY 266 324 GILHLATÖKTKİKYFPKGTTİAQİYPKLİQKİALNVEY 361 This Page Blank (uspto)

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5.1.6
Compugen Ltd.
 GenCore version
Copyright (c) 1993 - 2005
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protein search, using sw model OM protein -

; Search time 17.5576 Seconds (without alignments)
1671.423 Million cell updates/sec 2005, 10:52:17 'n January Run on:

US-09-993-292B-2 1515 1 MTSIFAEQTVEVVKSAIETA......NEYQQRHGKKTLFEVPDVAS 305 Title: Perfect score:

Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 50 summaries

PIR 79:*
1: pir1:*
3: pir2:*
5: pir3:*
5: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

hypothetical prote bPS2 protein homol hypothetical prote hypothetical prote hypothetical prote hypothetical prote oRF MSV156 hypothe protein T22A3.8 [i hypothetical prote hypothetical prote hypothetical prote hemolysin A - Esch myosin heavy chain myosin heavy chain conserved hypothet hemolysin E - Esch hemolysin E [impor probable pore form hypothetical prote hypothetical prote myosin heavy chain protein J - Yersin phage lambda-relat hypothetical prote hypothetical prote naemolysin HlyE [i transmembrane prot Description SUMMARIES T28317 F87908 T723064 T43291 S30834 A64465 S10056 S110056 S21801 A90551 T724587 S75986 S75986 C64864 E90838 E85696 T05634 LEECA T22716 A90394 T12818 B59102 AC1814 AE0673 MWKW1 В Query Match Length 3305 1023 3305 1023 6223 31023 1023 1023 1023 1034 1034 1402 1387 1387 118 115.5 1115.5 1113.5 1113.5 1113.5 1113.5 1113.5 1113.5 1113.5 1113.5 1113.5 1113.5 1113.5 1113.5 1113.5 1110.5 110.5 110.5 110.5 110.5 110.5 110.5 110.5 110.5 110.5 110.5 1 Result Š

methyl-accepting c leukotoxin A - Pas	hypothetical prote	kinesin-related pr	hypothetical prote	hemolysin A toxin	myosin heavy chain	probable RAD50 DNA	myosin-like protei	methyl-accepting c	transmembrane prot	hypothetical prote	salivary agglutini	Tpr homolog - frui	hemolysin - Escher	gas-vesicle protei	hypothetical prote	hypothetical prote	kinesin-like prote	VSG expression sit	casp homolog - fis
H75001	B70232	A48669	T44825	T00227	T18296	D84727	S38173	F72288	AH1369	C90593	A35186	T13829	141078	T44967	AB1730	S54091	T48959	VMUT21	T41332
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7.2	2.2	7.2	7.1	7.1	7.1	7.1	7.1	7.0	7.0	7.0	7.0	7.0	7.0	7.0	6.9	6.9	6.9	6.9	6.9
109	109	108.5	108	108	108	107.5	107.5	106.5	106.5	106.5	106.5	106.5	106	105.5	105	104.5	104.5	104	104
30	35	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	20

AMONO AND THOSE [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain C'Species: Salmonella enterica subsp. enterica serovar Typhi
DiNote: this species has also been called Salmonella typhi
DiNote: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
S;Accession: ABG673
R;Parkhill, J; Dougan, G; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T; Comnerton, P; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov; A;Reference number: ABG502; MUID:21534947; PMID:11677608
A;Accession: ABG673
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-305 <PAR>A;Residues: 1-305 <PAR>A;Residues: 1-305 <PAR>A;Residues: 1-305 <PAR>A;Genetics: A;Genetics: A;Genetics: A;Gene: STY1498
C;Superfamily: Escherichia coli hemolysin E RESULT 1

ö Gaps .; 0 Query Match 99.2%; Score 1503; DB 2; Length 305; Best Local Similarity 99.7%; Pred. No. 4.2e-90; Matches 302; Conservative 0; Mismatches 1; Indels

1 MTSIFAEQTVEVVKSAIETADGALDLYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASV

9

63 LVGDIKVILMDSQDKYFEATQTVYEWGGVVTQLLSAYILLFDEYNEKKASAQKDILIRIL 122 LVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRIL 120 62 3 MTGIFAEQTVEVVKSAIETADGALDLYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASV 61 윤 ò 셤

181 AAAGIVAGPFGLIISYSIAAGVIEGKLIPELANRLKTVQNFFTSLSATVKQANKDIDAAK 240 242 Š g 8

DDGVKKLNEAQKSLLTSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDRIRKEAYAG 180

121

LKLATEIAAIGEIKTETETTRFYVDYDDLMLSLLKGAAKKMINTCNEYQQRHGKKTLFEV 300 241 243 셤 ò

hypothetical prote

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A, Cross-references: UNIPROT: Q9REB3; GB: AE005174; NID: g12514879; PIDN: AAG56033.1; GSPDB: GA
A, Experimental source: strain 0157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable pore forming hemolysin hlyE [imported] - Escherichia coli (strain 0157:H7, sube cises: Escherichia coli (strain 0157:H7, sube cisecies: Escherichia coli (strain 0157:H7, sube cipate: 16-Peb-2001 #sequence_revision 16-Peb-2001 #text_change 09-Jul-2004
[c]Accession: E85696
[R.Perna, N.T., Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, iller, L.; Grotheck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Pottamousis, K.; Apodaca, Nature 409, 529-533, 2001
[A.Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A;Accession: E90838
A;Status: preliminary
A;Status: preliminary
A;Molecule type: DMA
A;Molecule type: DMA
A;Residues: 1-305 cHAX>
A;Cross-references: UNIPROT:Q9REB3; GB:BA000007; PIDN:BAB35100.1; PID:g13361141; GSPDB:G1
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics: A;Genetics
A;Gene: ECa1677
C;Superfamily: Escherichia coli hemolysin E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DDGVKKLINEAQKSLLISSQSFNNASGKLLALDSQLINDFSEKSSYFQSQVDRIRKEAYAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243 LKLTTEIAAIGEIKTETETTRFYUDYDDLMLSLLKEAANKMINTCNEYQKRHGKKTLFEU
                                                                                                                                                                                                                                                                                                                                                                                              63 LVGNIKTLIAMDSQDKYFBATQTVYEWGGVATQLLAAYILLFDBYNEKKASAQKDILIKVL
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                                                                                                                                                                                                                                                       Query Match

91.6%; Score 1387; DB 2; Length 305;
Best Local Similarity 90.1%; Pred. No. 1.3e-82;
Matches 273; Conservative 18; Mismatches 12; Indels
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ilarity 90.1%; Pred. No. 1.3e-82;
Conservative 18; Mismatches 12;
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C,Superfamily: Escherichia coli hemolysin E
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A; Residues: 1-305 <STO>
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Matches 273;
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N.Alternate names: hemolysin-inducing protein
N.Alternate names: hemolysin-inducing protein
C.Species: Escherichia coli
C.Species: Bacherichia coli
C.Species: Bacherichia coli
C.Species: Bacherichia coli
C.Species: Escherichia coli
C.Species: Pacherichia coli
C.Species: L12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C.Accession: C64864
R.Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc
S.A.Rose, D.J.; Mau, B.; Shao, Y.
S.A.Rose, D.J.; Mau, B.; Shao, Y.
S.A.Rose, D.J.; Mau, B.; Shao, Y.
A.Title: The complete genome sequence of Escherichia coli K-12.
A.A.Cession: C64864
A.Status: nucleic acid sequence not shown; translation not shown
A.M.A.Cession: C64864
A.Status: nucleic acid sequence not shown; translation not shown
A.M.A.Cession: C64864
A.Status: nucleic acid sequence not shown; translation not shown
A.M.A.Cession: C64864
A.Status: nucleic acid sequence set shown
A.M.A.Cession: C64864
A.Status: nucleic acid sequence set shown
A.M.A.Cession: C64864
A.Status: nucleic acid sequence atrain K-12, substrain MG1655
C.Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DDGVKKINEAQKSILTSSQSFNNASGKILALDSQLTNDFSEKSSYFQSQVDRIRKEAYAG 180
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92.5%; Score 1402; DB 2;
Best Local Similarity 91.1%; Pred. No. 1.4e-83;
Matches 276; Conservative 16; Mismatches 11;
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PDV 305
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A, Description: attacks blood cell membranes and causes cell lysis
C; Superfamily: hemolysin A; hemolysin A homology
C; Superfamily: hemolysin A; hemolysin A homology
C; Keywords: calcium binding; cytolysis; exotoxin; hemolysis; lipoprotein; tandem repeat;
F; 246-791/Domain: hemolysin A homology <HLYA>.
F; 228-851/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIYF]-X)
F; 563, 689/Binding site: palmitate (Lys) (covalent) #status experimental
                                                                                                                                                                                                        required for the toxic activity
                                                  A;Molecule type: DNA
A;Residues: 1-1023 <FEL>
A;Cross-references: UNIPROT:P09983; GB:M10133; GB:M12863; NID:g146377; PIDN:AAA23975.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54 YSQEASVL-----VGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILL-FDEY 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 105 NEKKASAQKDILIRILDD---GVKKLNEAQKSLLTSSQSFNNASGKLLALDSQLTNDFSE 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    218 VQNFFTSLSATVKQANKDIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDLMLSLLKGA 277
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 TSIFAEQTVEVVK-----SAIETADGALDLYNKYLDQVIPWKTFDETIKELSRFKQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                             A; Experimental source: strain 196, O4 serotype
R; Stanley, P.; Packman, L.C.; Koronakis, V.; Hughes, C.
Science 266, 1992-1996, 1994
A;Title: Ratty acylation of two internal lyaine residues required for the A;Title: Ratty acylation of two internal lyaine residues required for the A;Reference number: A55387, MUID: 95099325; PMID: 7801126
A;Contents: annotation; lyaine palmitcylation
A;Note: lyaine modification is performed by the hlyC gene product
T; Refactlein, M; Schiesel, S; Wagner, W; Rdest, U; Kreft, J; Goebel, J; Cell Biol. 22, 87-97, 1983
A;Title: Transport of hemolysin by Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1,'T',3,'V',5,'T',7-44 <RES>
A;Cross-references: GB:M29173; NID:9146337; PIDN:AAA23957.1; PID:9146338
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98;
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7.7%; Score 116; DB 1; Length 1023;
Best Local Similarity 20.5%; Pred. No. 9.2;
Matches 69; Conservative 59; Mismatches 111; Indels 99
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A;Molecule type: DNA
A;Residues: 1-622 <WIL>
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R;Harris, B.
submitted to the EMBL Data Library, August 1996
A;Reference number: Z19604
A;Accession: T22716
                                                                                                                                                                                                                                                                                                                                                                                                              A, Accession: I41280
A, Status: translated from GB/EMBL/DDBJ
                          Accession: A24433
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C; Function:
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Database, February 1999
                                                                                                                                                                             | ||:||::| :: :: :::: ||::||:::|
153 IEAEKTVKGMKEMRGRDDVVVKMEEEKSQVEEKLKWKKEQFKHLEBEAYEKLKNLFKDSKK 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cispeciaes: Arabidopsis thaliana (mouse-ear cress)
Cispeciaes: Arabidopsis thaliana (mouse-ear cress)
Cispeciaes: Arabidopsis thaliana (mouse-ear cress)
Cispeciaes: Arabidopsis thaliana (mouse-ear cress)
Cispeciaes: Toosia degrana (a.g. M.; Wambutt, R.; Bancroft, I.; Mewes, H.W. submitted to the Protein Sequence Database, February 1999
A;Reference number: 215420
A;Reference number: 215420
A;Rocession: To5534
A;Molecule type: DNA
A;Rocession: 1-1496 <-BEV>
A;Rocession: 1-1496 <-BEV>
A;Coss-references: Unipre/Cispecial (a.g. Medicae)
A;Cross-references: Unipre/Cispecial (a.g. Medicae)
A;Experimental source: cultivar Columbia; BAC clone F20D10
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C;Species: Bscherichia coli
C;Decies: Bo-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 09-Jul-2004
C;Accesion: A24433; I, S. Welch, R.A.
R;Felmlee, T.; Pellett, S.; Welch, R.A.
J. Bacteriol. 163, 94-105, 1985
                                                                             AAAGIVAGPFGLIISYSIAAGVIEGKLIPELNNRLKTVQNFFTSLSATVKQANKDIDAAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein F20D10.190 - Arabidopsis thaliana
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A;Introns: 1042/2; 1212/2; 1232/1; 1263/3; 1349/3
A;Note: F20D10.190
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PEV 305
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A;Cross-references: GB:299115; GB:AL009126; NID:g2634478; PIDN:CAB14031.1; PID:e1183560, A;Experimental source: strain 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   316 RNWEEVVPEPIQSOL------NOKDEQIK---DLTKQVNQINKDKVGIEQOPNT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----LINDFSEKSSYFQSQVDRIRKEAYAGAAAGIVAG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFGLIISYSIAAGVIEGKLIPELNNRLKTVQNFFTSLSATVKQANKDIDAAKLKLATEIA 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   315
                                                                    235 KESKVSPDIKTQLEKEMEEINEKLKLKTNDRSELEIELKVLERVLEEVNESDRHHLDTCN 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84 YEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRILDDGVKKLNEAQKSLLTSSQSFNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 DLYNKY-LDQVIPWKTFDETIKELSRFKQEYSQEASVLVGDIKVLLMDSQDKYFEATCTV
182 RESSSNIVAK----TTYTIT--LTRQNKINBILNKIKVKKDELANLEFALKKIEBEIQN
                                               --LMLSLLKGAAKKM-----INTCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Residues: 1-478 <KUN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
7.6%; Score 114.5; Dest Local Similarity 22.6%; Pred. No. 4.3; Matches 57; Conservative 41; Mismatches
                                                      239 AKLKLATEIAAIGEIKTETETTRFYVDYDD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144 ASGKLLALDSQ-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Species: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: A90394
C;Accession: A90394
C;Accession: A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F. Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F. Submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cross-references: UNIPROT:Q97WH8; GB:AE006641; NID:g13815540; PIDN:AAK42408.1; GSPDB:q
        A, Cross-references: UNIPROT: Q20822; EMBL: Z78198; PIDN: CAB01573.1; GSPDB: GN00023; CESP: F5
A, Experimental source: clone F55C5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLL----TYFSPENR-----LVTQILSGDGNVEWFISTTSKINBIK--AKKEBLOKLLT 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DGVKKLINFAQKSLLTSSQSFNN---ASGKLLALDSQLTNDFSEKSSYFQSQVDRIRKEAY 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNNRLKTVQNFFTSLSATVKQANKDIDA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLMDSQDKYFEATQTVYEWCGVVTQLLSA-----YILLFDEYNEKKASAQKDILIRILD 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 VEVVKSAIETADGALDLYNKYLDQVIPWKTFDETI--KELSRFKQEYSQEASVLVGDIKV 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 AAAGIVAGPFGLIISYSIAAGVI-----EGKLIPELNNRLKTVQNFFTSLSATVK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                FRCFYMASSYSALHKYSEAAALFDRTVSRVQDABGKL----KKLKSSSFITNETQSSLN 472
                                                                                                                                                                                                                                                                                        : | | : : | | : : | | : : | 305 EKMALF----EKATADTRDAIDRISDIIRRKSSENADTTVLQSIKAYLEPLKMNGTASRY 360
                                                                                                                                                                                                                                                                                                                                    QVDRIRKEAYAG 180
                                                                                                                                                                                                                                                                                                                                                              LAI---IDNTKŚEKKŚKPQDLLRLYDSVIBIYKEVABIPGADHDKNLIQAFEVKVEYYRA 417
                                                                                                                                                                                                                              251 DKLISEM-RASATSAEVVTIEWGGAKSTVDDE-----KAKQVVQEWKQTEVELAQCQTPK 304
                                                                                                                                                                                                   97
                                                                                                                                                                                                                                                                   --ILLFDEYNEKKASAQKDILIRILDDGVKKLNE-AQKSLLTSSQSF-----NNASGKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QANKDIDAAK--LKLATEIAAIGEIKTETETTRFYVDYDDLMLSLLKGAAKKMINTCNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                 41 DETIKELSRFKQEYSQEASVLVGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAY---
                                                                                                                                                                     Gaps
                                                                                                                                                                     87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.6%; Score 115; DB 2; Length 587; 20.3%; Pred. No. 5.2; Live 66; Mismatches 103; Indels
                                                                                                                                                                     Indels
                                                                                                                                    ch
1 Similarity 21.2%; Pred. No. 5.2;
68; Conservative 56; Mismatches 109;
                                                           C;Genetics:
A;Gene: CSSP.F55C5.8
A;Mep position: 5
A;Introns: 24/3; 44/2; 147/3; 251/3; 561/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QQ----RHGKKTLFEVPDVAS 305
                                                                                                                                                                                                                                                                                                                                           LALDSQLTNDFSEKSSYFQS-
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Molecule type: DNA
Residues: 1-587 < KUR>
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Best Local S
Matches 61
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Best Local
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A,Residues: 1-1127 <AFO>
A,Cross-references: UNIPROT:Q9YVT6; EMBL:AF063866; NID:g4049647; PIDN:AAC97677.1; PID:g4
  15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               269 NSKINTLNENIKGVANLYTETKNKISNLQNEILNKDSTIKSLDEKQKLLDELDKNINNIT 328
                                                                                                                                                                                   253 INSRYONLEERITEASOK-----ALVSMRLAQSSRYKTLTSELOKTEQSLAKEQL-RYTD 306
                                                                                                                                                                                                                                                               84 YEWCGVVTQLLSAYILLFDEYNEKKASAQKDIL----IRILDDGVKKLNEAQKSLLTSS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               329 SLYNKSNIKITNIQQLESSLTDFNNANININELKSKIKLFPNDIQKLNND----- 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VAGPFGLIISYSIAAGVIEGKLIPELNNRLKTVQNFFTSLSATVKQANKDIDAAKLKLAT 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       246 BIAAIGBIKTET-----ETTRPY-----VDYDDLM-----LSLLKGAAKKMI 282
                                                                            IKVLLMDSQDKYFEATQTVYEWCGVVTQLL---SAYILLFDEYNEKKASAQKDILIRILD 121
                                                                                                                                                                                                                                       DG--VKKLNEAQKSLLT-SSQSFNNASG-----KLLALDSQLTNDF----- 159
                                                                                                                                                                                                                                                                                                                               ----SEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNNRL 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  214 DELNKLLDE--SKKEFIKKQEELNKTIDKKQEELIKKLNDKEINFNIDEKOKLLD---QI 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     367 GLIANEKS--LRESEQRIRSE-----LSKYPSLIAEYQ------RLLPEVETQR 407
                                                                                                                                                                                                                                                                                                                                                                                                                             KTVQNFF-TSLSATVKQANKDIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDL---- 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORP MSV156 hypothetical protein - Melanoplus sanguinipes entomopoxvirus C; Species: Melanoplus sanguinipes entomopoxvirus C; Species: Melanoplus sanguinipes entomopoxvirus C; Species: Melanoplus sanguinipes entomopoxvirus C; Accession: T28317
R; Afonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L. J. Virol. 73, 533-552, 1999
A; Title: The genome of Melanoplus sanguinipes entomopoxvirus.
A; Reference number: Z20484; MUID:99102612; PMID:9847359
A; Accession: T28317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DLYNKYLDQVI PWKTFDETIKELSRFKQEYSQEASVLVGDIKV-LLMDSQDKYFEATQTV
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                                              5 FAEQTVEVVKSAIETADGALDLYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVLVGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91; Gaps
  71;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : | : | : | : | : | : | 461 LGVVLALIWGMRHRIHSAQDLQKVSNLRLLGTVPKLA 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---MLSLLKGAAKKMINTCNEYQQRHGKKTLFEVPDVA 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 7.5%; Score 113.5; DB 2; Best Local Similarity 19.2%; Pred. No. 15; Matches 60; Conservative 56; Mismatches 106;
  Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
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58;
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  Conservative
  75;
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                                            hypothetical protein pXO1-90 - Bacillus anthracis virulence plasmid pXO1 C;Species: Bacillus anthracis C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 09-Jul-2004 C;Accession: B59102 R;Okinaka, R.T.; Cloud, K.; Hampton, O.; Hoffmaster, A.R.; Hill, K.K.; Keim, P.; Koehler A;Okinaka, R.T.; Cloud, K.; Hampton, O.; Hoffmaster, A.R.; Hill, K.K.; Keim, P.; Koehler A;Title: Sequence and organization of pXO1, the large Bacillus anthracis plasmid harbori A;Reference number: A59091; MUID:99445483; PMID:10515943
                                                                                                                                                                                                                               A;Accession: B59102
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Rolecule type: DNA
A;Rolecules: 1-652 < OKI>
A;Cross-references: UNIPROT:Q9X360; GB:AF065404; NID:g4894216; PIDN:AAD32394.1; PID:g489
A;Experimental source: strain Sterne
A;Rote: similar to hypothetical protein; PFB0765w (980 aa); Plasmodium falciparum (AE001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein all0059 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AC1814
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Cross-references: UNIPROT:Q8Z0N2, GB:BA000019; PIDN:BAB77583.1; PID:g17i35037; GSPDB:G
A,Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          294 INKKDSNRLELNSEIKKLNDRKAELLSLIMELIKQOSEPDKKIKNEKDELINR 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     171 DRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNNRLKTVQNFFTSLSATVK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATQ-----TVYEWCGVVTQLLSAYILLFDEYNE--KKASAQXDILIRILDDGVKK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LNEAQK-----SLLTSSQSFNNASGKLLALDSQLTNDFSEKSSYFQ---SQV 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    354 IAESKELAKKKAELNTKLVELFKVQEALNKKSGQYLYYINKLDNELRELADKYKNSDNKI 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QANKDIDAAKLKLAT-BIAAIGEIKTETETTRFYVDYDDL-----MLSLLKGAAKKMINT 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DLYNKYLDQVI PWKTFDETIKELSRPKQEYSQEASVL-----VGDIKVLLMDSQDKYFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.6%; Score 114.5; DB 2;
18.6%; Pred. No. 6.4;
ative 66; Mismatches 106;
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Pred. No. 8.6;
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Best Local Similarity 18.6
Matches 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CNEYQQRHGKK 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       496 AKEINKKLAEK 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: AC1814
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-727 < KUR>
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Best Local Similarity
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A;Gene: pXO1-90
A;Genome: plasmid
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Rizhu, X.; Kao, G.; Joh, K.; Hall, D.H.; Wadsworth, V.K.; Hutter, H.; Vogel, B.E.; Huans bubmitted to the EMBL Data Library, June 1998
A; Description: Expression, function and evolution of laminin alpha chains.
A; Reference number: 222397
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                                                                                                                                                                                                                                               A,Gener. CESP:T22A3.8
A;Map position: 1
A;Introns: 45/1; 282/2; 312/3; 416/2; 1255/3; 1329/3; 1418/3; 1776/2; 1988/2; 2760/2
A;Introns: 45/1; 282/2; 312/3; 416/2; 1255/3; 1329/3; 1418/3; 1776/2; 1988/2; 2760/2
C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --VKRLG 2136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1997 DEEYVQTAGRHAEKLEVQAQK-İVDRFYDTRTETENPLKASHAYENIVEALKNATEAVDS 2055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    194 ISYSIAAGVIE--GKLIPELMNRLKTVQNFFTSLSATVKQANKDIDAAKLKLATEIAALG 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134 LLISSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLI 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----DGVKKLNEAQKS 133
                                                                                                                                                               PIDN:CAB03385.1; GSPDB:GN00019; CESP:T22A3.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DLYNKYLDQVIPW-KTFDETIKELSRFKQEYSQEASVLVG------DIKVLLMDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           laminin alpha chain - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----YFEATQTV-----YEWCGVVTQLLSAYILLFDEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --DIKVLLMDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                     96; Indels 121; Gaps
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A;Cross-references: UNIPROT:045614; EMBL:AF074902; PIDN:AAC26793.1
                                                                                                                                                                                                                                                                                                                                                                                          Length 2823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2056 AAEASE----AVSKMLGSEGSESGDANEES--LRSQLEKLKNESSLSN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    252 BIKTETETTRFYVDYDDIMLSLLKGAAKKM-INTCNEYQQRHGKKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
submitted to the EMBL Data Library, October 1996
A;Reference number: Z19980
A;Accession: T28096
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residue: type: DNA
A;Residues: 1-2823 <WIZ>
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20.8%; Pred. No. 56;
ive 57; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 20.8%; Pred. No. 49;
Matches 72; Conservative 57; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105 NEK------KASAQKDILIRILD-
                                                                                                                                                                           A; Experimental source: clone T22A3
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Conservative
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Best Local Similarity
Matches 72; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73 ODK----
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A;Note: lama1/2
C;Superfamily: lam
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                                                                                                                                                      C;Species: Caenornabditis elegans
C;Species: Caenornabditis elegans
C;Date: 10-May-2001 #text_change 09-Jul-2004
C;Accession: 87908; E87908
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Title: Genome sequence of the nematode C. elegans; and www sanger.ac.uk/Projects/C ele
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www sanger.ac.uk/Projects/C ele
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: F87908
A;Accession: E87908
A;Residues: 1-2823 <STO>
A;Cross-references: UNIPROT:045614; GB:chr_I; PIDN:CAA15432.1; PID:g3924779; GSPDB:GN000
A;Accession: E87908
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A;Accession: E87908
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A;Accession: E87908
A;Accession: E87908
A;Accession: T22A3.8
A;Gene: T22A3.8
A;Gene: T22A3.8
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A;Gene: T22A3.8
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A;Gene: T
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Submitted to the EMBL Data Library, October 1997
A;Reference number: Z19669
A;Recession: T23064; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-2823 «WIL»
A;Residues: 1-2823 «WIL»
A;Residues: 1-2823 «WIL»
A;Residues: 1-2823 «WIL»
A;Residues: 1-2823 «WIL»
A;Residues: 1-2823 «WIL»
A;Residues: 1-2823 «WIL»
A;Reperimental source: clone H10E24
B;RcMurray, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1940 EDQIAYSRNSIEKARSEELMNMFEDKEKINMTLAELPDLVEQCQNITLL---YSQLIDEY 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2056 AAEASE----AVSKWLGSEGSESGDANEES--LRSQLEKLKNESSLSN----- 2097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 LLTSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLI 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISYSIAAGVIE--GKLIPELMNRLKTVQNFFTSLSATVKQANKDIDAAKLKLATEIAAIG 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----KASAQKDILIRILD-----DGVKKINBAQKS 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein T22A3.8 - Caenorhabditis elegans (fragment)
(5)Species: Caenorhabditis elegans
(5)Species: Caenorhabditis elegans
(5)Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
(5)Accession: T23064; T25096
R;Barlow, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 DLYNKYLDQVIPW-KTFDETIKELSRFKQEYSQEASVLVG------DIKVLLMDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----YFEATQTV-----YEWCGVVTQLLSAYILLFDEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 2823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BIKTETETTRFYVDYDDLMLSLLKGAAKKM-INTCNEYQQRHGKKT 296
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                                                                                                                   protein T22A3.8 [imported] - Caenorhabditis elegans
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C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: A64465
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-1024 <HES>
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A;Residues: 1-956 <DIB>
A;Cross-references: EMBL:U18779; NID:g603625; PIDN:AAB64999.1; PID:g603636; MIPS:YEL043w
                                                                                                                                                                                                                                                  EDQIAYSRNSIEKARSEELMNMFEDKEKINMTLAELPDLVEQCQNITLL---YSQLIDEY 1996
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                                                                             134 LLTSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDRIRKEAYAGAAAGIVAGFFGLI 193
                                                                                                                                194 ISYSIAAGVIE--GKLIPELMNRLKTVQNFFTSLSATVKQANKDIDAAKLKLATEIAAIG 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLS-----AYILLFDEYNEKKASAQKDI-----LIRILDDGVKKLNEAQKSLLTS---S 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    139 QSFNN----ASGKLLALDSQLTNDFS-EKSSYF------QSQVDRIRKEAYA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 GAAAGIVAGPFGLIISYSIAA-----V 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38 KTFDETIKELSRFKQEYSQEASVLVGDIKVLLMD-----SQDKYFEATQTVYEWCGVVTQ
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A. Description: The sequence of S. cerevisiae cosmids 8199, 8334, and 9871

A. Reference number: $50491

A. Accession: $50501
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                                                                                             252 EIKTETETTRFYVDYDDLMLSLLKGAAKKM-INTCNEYQQRHGKKT 296
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24.4%; Pred. No. 13;
ive 45; Mismatches
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Best Local Similarity 24.4%;
Matches 68; Conservative 4
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A;Map position: 5L
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A64465 hypothetical protein MJ1322 - Methanococcus jannaschii C;Species: Methanococcus jannaschii

RESULT 17

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Ribult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, i. Reich, C.I.; Overbeek, R.; Kirkness, B.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; rsnich, J.D.; Sadow; P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C. A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii A;Reference number: A64300; WUID:96337999; PMID:8688087
A;Reference number: A64465
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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K;Hess, J; Wels, W; Vogel, M; Goebel, W.
FEMS Microbiol. Lett. 34, 1-11, 1986
A;Title: Nucleotide sequence of a plasmid-encoded hemolysin determinant and its comparisc
A;Reference number: S07209
                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-1005 <BUL>
A;Cross-references: UNIPROT:Q58718; GB:U67572; GB:L77117; NID:g1591958; PIDN:AAB99331.1;
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711 TEKLEELKNIKDGLEEI------YNICNSKILAIDNIKRKYNKEDIEIYLNNK 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               209 PEL--NNR--LKTVQNFFTSLSATVKQANKDIDAAKLKLATEIAAIGEIKTETETTRFYV 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             505 DEILEDIKSQLNKFK---NFYNQYLSAVSYLNSVDEEGIRNRIKEIENIVSGWNKEKCRE 661
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C,Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 04-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 EQTVEVVKSAIETADGALDLYNKYLDQVIPWKTFDE----TIKELSRF-----KQEYSQ
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F;564,690/Binding site: palmitate (Lys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
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C, Keywords: lipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 7.5%; Score 113; DB Best Local Similarity 19.7%; Pred. No. 14; Matches 60; Conservative 55; Mismatches
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C,Superfamily: hypothetical protein MJ1322
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A, Modecule type: mRNA
A, Residues: 1-1999 < SUNN>
A, Residues: 1-1999 < SUNN>
A, Residues: 1-1999 < SUNN>
A, Residues: 1-1999 < SUNN>
A, Chantler. P.O.
R, Sun, W.; Chantler. P.O.
R, Sun, W.; Chantler. P.O.
Bjochem. Biophys. Res. Commun. 175, 244-249, 1991
Bjochem. Biophys. Res. Commun. 175, 244-249, 1991
Bjochem. Biophys. Res. Commun. 175, 244-249, 1991
A, Reference number: PN0013; WUID:91151356; PMID:1998509
A, Reference number: PN0013; WUID:91151356; PMID:1998509
A, Residues: 1914-1998, 'I' < SU2>
A, Residues: 1914-1998, 'I' < SU2>
A, Residues: actin binding; ATP; coiled coil: hydrolase; methylated amino acid; nucleotide: Status predicted
C, Keywords: actin binding; ATP; coiled coil: hydrolase; methylated amino acid; nucleotide-binding motif A (P-10op)
F; 84-763/Domain: myosin motor domain homology < WMOT>
F; 84-763/Domain: coiled-binding #status predicted
F; 551-575/Region: actin binding #status predicted
F; 815-1576/Region: actin binding #status predicted
F; 815-1576/Region: actin binding #status predicted
F; 815-1576/Region: actin binding #status predicted
F; 815-1576/Region: actin binding #status predicted
F; 815-1576/Region: actin binding #status predicted
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F; 815-1576/Region: actin binding #status predicted
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F; 815-1576/Region: actin bindi
                                                                                                                                                                      NyAlternate, names: wyosin II (NyAlternate names: myosin II (NyAlternate names: myosin II (NyAlternate names: myosin ArPase (EG 3.6.4.1) (Species: Rattus norvegicus (Norway rat) (Species: Rattus norvegicus (Norway rat) (Spaces 3.1-Dec-1993 #sequence revision 31-Dec-1993 #sequence revision 31-Dec-1993 #sequence revision 31-Dec-1993 #sequence revision 31-Dec-1993 #sext_change 09-Jul-2004 (Spaces sion: S21801; Mod 3) (Spaces sion: North Spaces S21801; Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sion: Mod 3) (Spaces sio
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A90551
conserved hypothetical protein MYPU_3130 [imported] - Mycoplasma pulmonis (strain UAB
C;Species: Mycoplasma pulmonis
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F;125/Modified site: N6,N6.trimethyllysine (Lys) #status predicted
F;180/Binding site: ATP (Lyg) #status predicted
F;637,703/Active site: Cys #status predicted
F;1916/Binding site: phosphate (Ser) (covalent) #status predicted
F;1916/Binding site: phosphate (Ser) (covalent) #status predicted
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myosin heavy chain - chicken)
C;Species: Gallus gallus (chicken)
C;Species: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 02-Feb-2001
C;Accession: S18199
R;Stewart, A.F.R.; Camoretti-Mercado, B.; Perlman, D.; Gupta, M.; Jakovcic, S.; Zak, R. R;Ewart, A.F.R.; Camoretti-Mercado, B.; Perlman, D.; Gupta, M.; Jakovcic, S.; Zak, R. A;Title: Erructural and phylogenetic analysis of the chicken ventricular myosin heavy a A;Reference number: S18199; MUID:92130260; PMID:1774788
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C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004 C;Accession: A90551 R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.; Nucleic Acids Res. 29, 2145-2153, 2001	65 IKVILMDSQDKYPEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIR
Ailtle: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm A;Reference number: A99512; MUD:21267165; PMID:11353084 A;Accession: A90551	Qy 119 ILDDGVKKLNRAQKSLLTSSQFPNQSFNLL 149 ::
A Molecule type: DNA A,Residues: 1-2819 «KUR» A,Cross-references: UNIPROT: 0980P8; GB:AL445566; PID:g14089727; PIDN:CAC13486.1; GSPDB:G	QY 150 ALDSQLTNDFSEKSSYFQSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIECKLIP 209
A;Genetics: Argustant Source: State Argustant Argustant Code: Argustant Code: SGC3	QY 210 ELNNRLKTVQNFFTSLSATVKQANKDIDAAKLKLATEIAAIGEIKT 255
Query Match Query Match Best Local Similarity 22.1%; Pred. No. 66; Matches 76; Conservative 54; Mismatches 104; Indels 110; Gaps 20;	Qy 256 ETETTR 261 : Db 974 STETSR 979
CY 25 DLYNKYLDQVIPWKIFDETIKELSRFKQEYSQEASVLVGDIKVLLMDSQDKYFEATQ 81	RESULT 23 S75986
OY 82 TVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRILDDGVKKLN 128	hypotherical protein - Synechocystis sp. (strain PCC 6803) C;Species: Synechocystis sp. A;Variety: PCC 6803 C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
OY 129 EAQKSLLISSQSFNNASGKLLALDSQLTNDFSEKSSYFOSQVDRIRKEAYAGAAAGIV 186 :	C; Accession: S75986 R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Res. 3, 109-136, 1996
Qy 187 AGPFGLIISYSIAAGVIEGKLIPELNNRLKTVQNFFTSLSATVKQANK 234	A;Title: Sequence analyBis of the genome of the unicellular cyanobacterium SynechocyBtis 8. A;Reference number: S74322; MUID:97061201; PMID:8905231
235 DIDAAKLKLATEIAAIGEIKTETETTRFYUDYDDLMLS 235 BISKDELSLVSNITSAIDALSTSNIVEKILEVFLAEVKONPOSKTNDLFASIOSIIKS	A:Status: preliminary A:Molecule type: DNA A:Residues: 1-584 «KAN» A:Grose-references: UND:ROT:055486; EMBL:D64006: GB:AB001339; NID:G1001291; PIDN:BAA10833
273LLKGAAKKWINTCNEYQQRHGKKTLFF 299	A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996 C;Superfamily: arginine-tRNA ligase
	Query Match 7.3%; Score 110.5; DB 2; Length 584; Best Local Similarity 23.4%; Pred. No. 10; Matches 73; Conservative 50; Mismatches 128; Indels 61; Gaps 15;
KESULT 22 T24587 Typothetical protein T06E4.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans	QY 11 EVVKSAIETADGALDLYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVLVGDIK 66
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C;Accession: T24587 R;Lloyd, C.	OY 67VLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKD 114
submitted to the EMBL Data Library, April 1996 A;Reference number: 219910	KAWQLLCEQSRREFQLIYDCLDITIEERGESFYNPFLPGVVELLQEKD
A;Accession: T24587 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA	QY 115 ILIRILDDGVKKLNEAQKSLLTSSQSFNNASGKLLALDSQLTNDFSEKSSYF 166
A;Cross-treferences: UNIPROT:022257; EMBL:270756; PIDN:CAA94789.1; GSPDB:GN00023; CESP:TC A;Experimental source: clone T06E4	167QSQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNNRLKTVQNFFTS
C;Genetics: A;Gene: CESP:T06E4.1 a.Mar nocition: 6	Db 341 TDAGQANHFAQFFQVAEKAGILTDPTQVVHVPFGLVKGEDGKKLKTRAGDTIRLKDL 397
A; nat postrons: 17/3; 218/2; 385/3; 481/3; 946/3; 1034/3; 1222/2	398 LTEAVTRARQDLETRLTABERSETEFKTEVAQRVGIGAVKYADLSQNRTSDYVFSFDKM
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Qy 6 AEQIVEVVKSAIETA-DGALDLYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVLAGD 64 : ::	SULT 24

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270
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            transmembrane protein (imported) - Disteria innocua (strain tilphilol)
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: Ad1739
C;Accession: Ad1739
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
D; Jones, L.M.; Karst, U.
Science 294, 484-985, 2001
A;Authors Kreft, J.; Kunn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AG1739
A;Roesidues: Draininary
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C;Genetics: A;Genetics:
A;Genetics: A;Genetics:
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A;Cross-references: UNIPROT:Q08581; EMBL:Z75103; NID:g1420464; PID:e252389; PID:g1420465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 QDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRILDDGVKKLNEAQK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLLTSSQSFNNASGKLLA----LDSQLTN-----DFSEKSSYFQSQVDRIRKEAYAGAA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              328 SLATGLNSLVDGŠNKLSAGLKELDGNLTNSQGKLAQLKQGMNDLQQGIDQLNQNVNGEDA 387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  277 VSTYTSGVDTL---SGGINQAYNGSTALSDGLNKWNGS-----VPALASGVTQLNDGGK 327
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N;Alternate names: hypothetical protein 04806
C;Species: Saccharomyces cerevisiae
C;Species: L2-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 09-Jul-2004
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transmembrane protein [imported] - Listeria innocua (strain Clip11262)
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R;Hughes, B.; Pohl, T.M.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S66685
A;Accession: S67087
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A,Cross-references: SGD:S0005721
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A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-376,'V', 378-390,'V', 392-576,'L',578-680,'I',682-1938 <DIB>
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A; Rikarn, J; Brenner, S.; Barnett, L.
B; Karn, J; Brenner, S.; Barnett, L.
A; Reference number: A: Barnett, L.
A; Reference number: A93958; MUID:83273600; PMID:6576334
A; Accession: A0293
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A; Residues: 24-93,'E',95-97,'R',99-376,'V',378-388,'GDV',392-407,'N',409-473,'G',475-576
C; Genetics:
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, Residues: 1-1938 <WIL>
, Cross-references: UNIPROT:P02567; EMBL:271261; PIDN:CAA95806.1; GSPDB:GN00019; CESP:R06.
, Experimental source: clone F21C3
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A;Title: Sequence analysis of the complete Caenorhabditis elegans myosin heavy chain gen. A;Reference number: S02771; MUID:89178677; PMID:2926820
A;Accession: S02772
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A;Cross-references: EMBL:Z71266; PIDN:CAA95848.1; GSPDB:GN00019; CESP:R06C7.10
A;Experimental source: clone R06C7
                                                    12;
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                                                                                                                                                                                                                                    -----IMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDIL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               myosin heavy chain D [similarity] - Caenorhabditis elegans
myosin heavy chain I
N;Alternate names: myosin heavy chain I
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C;Species: Caenorhabditis elegans
C;Date: 28-Feb-1986 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Accession: T21193; T23973; S02772; A02993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      177 AYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPBLAN.----RLKTVQNFFTSLSATVKQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----ETTRFYVDYDDL----
                                                                                                                                                         :: :: | :: | :: | :: | :: | 478 LKSKENELDNLKLSLKETLSISKDFNDSD-----LIGQINELISTKNN-LQQKMD----
                                                                                                               10 VEVVKSAIETADGALDLYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVLVGDIKVL-
                                                          Gaps
                                                          Indels 104;
Length 821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  233 NKDIDAAKL---KLATEIAA-----IGEIKTET----
                                                              52; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----MLSLLKGAAKKMINTCNEYOORHGKKTL 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;McMurray, A.
submitted to the EMBL Data Library, April 1996
A;Reference number: Z1938
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Reference number: Z19825
      7.3%; Score 110; 20.4%; Pred. No. 1
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A;Status: translated from GB/EMBL/DDBJ
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                                                                    68; Conservative
             Query Match
Best Local Similarity
Matches 68; Conserv
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- 1029

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C,Accession: T1996
R; Lindler, L.E.; Plano, G.V.; Burland, V.; Mayhew, G.F.; Blattner, F.R.
Infect. Immun. 66, 5731-5742, 1998
A;Title: Complete DNA sequence and detailed analysis of the Yersinia pestis KIMS plasmid
A;Reference number: Z18268; MUID:99043898; PMID:9826348
A;Accession: T14966
A;Accession: T14966
A;Accession: T14996
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-1545 <LIN>
A;Cross-references: UNIPROT:Q9ZH03; EMBL:AF074611; NID:g3883003; PID:g3883049; PIDN:AAC8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein PAB1294 - Pyrococcus abyssi (strain Orsay)
C;Dsecies Pyrococcus abyssi
C;Dstecies: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: F75008
C;Accession: F75008
C;Accession: Joseph Page 1999 #sequence to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Cross-references: UNIPROT:Q9UYA4; GB:AJ248288; GB:AL096836; NID:g5458960; PIDN:CAB5050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - 1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 LFDEYNEK----KASA-QKDILIRILDDGVKKLNEAQKSLLTSSQSFNNASGKLLAL--- 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----DSQLTND-----FSEKSSYFQSQVDRIRKEAYAGAAGIVAGPF 190
                                                                      ---DSQLTND-----FSEKSSYFQSQVDRIRKEAYAGAAGIVAGPF 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phage lambda-related host specificity protein J - Yersinia pestis plasmid pMT1
924 IAEEREARVEGDKANAKQIEAMKSSVDDSVAAVEEMKKTVAEVERASAEASTNIEALAKT 983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99 TINE 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Yersinia pestis
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 TSIFAEQTVEVVKSAIETADGALDLYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                              239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1545;
                                                                                                                                                                                                                                                          --IGEDIRASILE----ETTARVEADKTIATHISKLEAQLNDDISAA
                                                                                                                                                                                                              191 GLIISYSIAAGVIEGKLIPELNNRLKTVQNFFTSLSATVKQANKDIDAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLIISYSIAAGVIEGKLIPELNNRLKTVONFFTSLSATVKOANKDIDAA
                                                                                                                                984 NIDLALRQDEDQHKQMVNNAKIATTQKTFADDMSAMASKVEEIRAE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1025 NIDLALRODEDQHKOMVNNAKIATTOKTFADDMSAMASKVEEIRAE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19.7%; Pred. No. 41; tive 54; Mismatches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.2%; Score 109.5;
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A;Accession: F75008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 57; Conserv
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A;Molecule type: DNA
A;Residues: 1-595 <KAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Genome: plasmid pMT1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62
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C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Date: 20.5ep-1999 #sequence_revision 20.5ep-1999 #text_change 09-Jul-2004
C;Accession: T14652
R;Hu, P.; Elliott, J.; McCready, P.; Skowronski, E.; Garnes, J.; Kobayashi, A.; Carrano, submitted to the EMBL Data Library, March 1998
A;Referred to the EMBL Data Library, March 1998
A;Referrence number: Z18168
A;Accession: T14652
A;Accession: T14652
A;Accession: T14652
A;Accession: T14652
A;Accession: T14652
A;Accession: Jeeliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-1492 cHUP>
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C;Genetics:
A;Genome: plasmid pMT1
                                                                                                                                               muscle
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                         A;Map position: 1
A;Introns: 23/1; 229/1; 264/1; 320/1; 857/3; 1745/3; 1814/1; 1892/3;
A;Introns: 23/3; 114/3; 229/1; 264/1; 320/1; 857/3; 1745/3; 1814/1; 1892/3;
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Superfamily: myosin motor domain homology chWor>
F;87-773/Domain: myosin motor domain homology chWor>
F;87-773/Domain: myosin motor domain homology chWor>
F;87-773/Region: nucleotide-binding motif A (P-loop)
F;660-682/Region: actin binding #status predicted
F;764-778/Region: actin binding #status predicted
F;86-150/Region: 21.http://www.no.in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FSSÓLVEAKKAAEDELHERQEFHAACKNLEHELDQCHELLEEQINGK--DDIQRQLSRIN 1372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NEKKASAQKDILI------RILDDGVKKLNEAQKSLLTSSQSFNNASGKLLALD 152
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F;128/Modified site: N6,N6,N6-trimethyllysine (Lys) #status predicted
F;183/Binding site: ATP (Lys) #status predicted
F;700,710/Active site: Cys #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     208 IPELNNRLKTVQNFFTSLSATVKQANKDIDAAKLKLATEIAAIGEIKTETE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 1938;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.3%; Score 110; DB 1; Length 19:
8.9%; Pred. No. 51;
.ve 60; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.2%; Score 109.5; DB 2; Length 1
19.7%; Pred. No. 39;
cive 54; Mismatches 101; Indels
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Best Local Similarity 19.7%
Matches 57; Conservative
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Best Local Similarity 18.9
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Nichternten names: IktA protein
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Cispecies: Pasteurella haemolytica
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Cispecies: Pasteurella haemolytica
Cipacession: S37145, A35254; S34237; S34235
Cipacession: A.F.; Aitchison, K.; Donachie, W.
Submitted to the EMBL Data Library, September 1993
Airescription: DNA sequence of the leukotoxin A gene from P. haemolytica T10 serotype.
Airescription: DNA sequence of the leukotoxin A gene from P. haemolytica T10 serotype.
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A; Description: attacks cell memolysin A; hemolysin A homology
C; Keywords: calcium binding; cytolysis; exotoxin; hemolysis; lipoprotein; tandem repeat;
E;240-786/Domain: hemolysin A homology <HLYA>
F;240-786/Domain: hemolysin A homology <HLYA>
F;718-809/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIYF]-X)
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A/Molecule type: DNA
A/Molecule type: DNA
A/Rolecule type: DNA
A/Rolecule type: DNA
A/Ross-references: GB:M24197, GB:M34943; GB:M34944
A/Cross-references: GB:M24197, GB:M34943; GB:M34944
R/Lainson, A.F.; Altchison, K.D.; Donachie, W.
Submitted to the EMBL Data Library, June 1993
A/Rocession: DNA sequence of the carboxy terminal end of leukotoxin A from the T3 i
A/Rocession: S34235
A/Accession: S34237
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A; Residues: 745-955 <LA2>
A; Residues: 745-955 <LA2>
A; Residues: 745-955 <LA2>
A; Cross-references: EMBL: 222884; NID: 9311828; PIDN: CAA80498.1; PID: 9311829
A; Experimental source: serotype T3
A; Accession: S34235
A; Molecule type: DNA
A; Residues: 723-955 <LA3>
A; Cross-references: EMBL: Z22887; NID: 9311824; PIDN: CAA80501.1; PID: 9311825
A; Experimental source: serotype T10
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Similarity 18.3%; Pred. No. 24;
68; Conservative 63; Mismatches 139;
                                                                                                                                                                                             leukotoxin A - Pasteurella haemolytica (serotype T10)
                              SAIEQQTAAIEELRRAAQELKDMVGRMRQIVGK
262 FYVDYDDLMLSLLKGAAKKMINTCNEYQQRHGK
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F,792-800/Region:
F,801-809/Region:
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R; anonymous, Genoscope Benoscope Benoscocus abyssi genome sequence: insights into archaeal chromosome stru A; Reference number: A75001
A; Reference number: A75001
A; Retension: H75001
A; Statuus: perliminary
A; Molecule type: DNA
A; Residuas: 1-739 «KAMA»
A; Residuas: 1-739 «KAMA»
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                                             ; Score 109; DB 2; Length 59; Pred. No. 13; 55; Mismatches 109; Indels
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tive 71; Mismatches 138;
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                                                                                                               Conservative
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2139 <GUI>
A;Cross-references: UNIPROT:Q07569; EMBL:L03534; NID:g1850912; PID:g1850913; PIDN:AAB4806
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1012 LLEEEKDDLEQDRADVSATKDDIAKKLNKITIECEDAKDEIAKLEQELEDEENKNKDLTN 1071
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                                                                                                                                                                                                                                                                                                              267 GNVGKAVSQYILAQRWAQGLSTTAAĞAGLITSAVMLAISPLSPLAAADKFERAKQLESYS 326
                                                                                                                                                                                                                                                                                                                                                                                                                                         231 QANK-DIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDLMLSLLKGAAKKMINTCNEYQ 289
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                                                                                                                              ---LMDSQDKYFBATQTVYBWCGVVTQLLSAYILLF-----DEYNEKKASAQKDILIRIL 120
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myosin heavy chain - Entamoeba histolytica

C;Species: Entamoeba histolytica

C;Species: Entamoeba histolytica

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T18296

R;Guillen, N.

A;Reference number: Z18865

A;Reference number: Z18865
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                                                                                                                                                                                                                                                                121 DDGVKKLNE---AQK---SLLTSSQSFNNASGKLLALDSQLT----NDFSEKSSYFQSQV
                                                                                                                                                                                                                                                                                                                                                                                               DRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNNRLKTVQNFFTSLSATVK
                                          165 DIAKSSIELINQLVDTVSSINSTV---DSFSEQLNQLQGSFLSSKPRLSSV-GGKLQNLPD
                                                                                                                                                                        Gaps
EVVKSAIETADGALDLYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVLVGDIKVL--
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ilarity 19.6%; Pred. No. 78;
Conservative 48; Mismatches 124; Indels 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: mhcA
C;Superfamily: myosin heavy chain; myosin motor domain homology
F;91-780/Domain: myosin motor domain homology <MMO>
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les 75; Conserv
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A; Residues: 1-998 < MAKA
A; Residues: 1-998 < MAKA
A; Residues: 1-998 < MAKA
A; Croser-references: UNIPROT: Q46716; EMBL: AB011549; NID: g4589740; PIDN: BAA31774.1; PID: g3
A; Croser-references: UNIPROT: Q46716; EMBL: AB011549; NID: 950952
A; Experimental source: strain EHEC O157:H7, substrain RIMD 0509952
B; Burland, V.; Shao, Y.; Perna, N.T.; Plunkett, G.; Sofia, H.J.; Blattner, F.R.
B; Burland, V.; Shao, Y.; Perna, N.T.; Plunkett, G.; Sofia, H.J.; Blattner, F.R.
A; Furland, V.; Shao, Y.; Perna, N.T.; Plunkett, G.; Sofia, H.J.; Blattner, F.R.
A; Furland, V.; Shao, Y.; Perna, N.T.; Plunkett, G.; Sofia, H.J.; Blattner, F.R.
A; Furland, V.; Shao, Y.; Perna, N.T.; Plunkett, G.; Sofia, H.J.; Blattner, F.R.
A; Furland, V.; Shao, Y.; Perna, N.T.; Plunkett, G.; Sofia, H.J.; Blattner, F.R.
A; Furland, V.; Shao, Y.; Perna, N.T.; Plunkett, G.; Sofia, H.J.; Blattner, F.R.
A; Furland, V.; Shao, Y.; Perna, N.T.; Plunkett, G.; Sofia, H.J.; Blattner, F.R.
A; Furland, V.; Shao, Y.; Perna, N.T.; Plunkett, G.; Sofia, H.J.; Blattner, F.R.
A; Furland, V.; Shao, Y.; Perna, N.T.; Plunkett, G.; Sofia, H.J.; Blattner, F.R.
A; Furland, V.; Shao, Y.; Perna, N.T.; Plunkett, G.; Sofia, H.J.; Blattner, F.R.
A; Furland, V.; Shao, Y.; Perna, N.T.; Plunkett, G.; Sofia, H.J.; Blattner, F.R.
A; Furland, V.; Shao, Y.; Perna, N.T.; Plunkett, G.; Sofia, H.J.; Blattner, F.R.
A; Furland, V.; Shao, Y.; Perna, N.T.; Plunkett, G.; Sofia, H.J.; Blattner, F.R.
A; Furland, V.; Shao, Y.; Perna, N.T.; Plunkett, G.; Sofia, H.J.; Blattner, F.R.
A; Furland, V.; Shao, Y.; Perna, N.T.; Plunkett, G.; Sofia, H.J.; Plunkett, G.; Sofia, H.J.; Plunkett, G.; Sofia, H.J.; Plunkett, G.; Sofia, H.J.; Plunkett, G.; Sofia, H.J.; Plunkett, G.; Sofia, H.J.; Plunkett, G.; Sofia, H.J.; Plunkett, G.; Sofia, H.J.; Plunkett, G.; Sofia, H.J.; Plunkett, G.; Sofia, H.J.; Plunkett, G.; Sofia, H.J.; Plunkett, G.; Sofia, H.J.; Plunkett, G.; Sofia, H.J.; Plunkett, G.; Sofia, H.J.; Plunkett, G.; Sofia, H.J.; Plunkett, G.; Sofia, H.J.; Plunkett, G.; Sofia, H.J.; Pl
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DNA Res. 5, 1-9, 1998
A,Title: Complete nucleotide sequences of 93-kb and 3.3-kb plasmids of an enterohemorrha A,Reference number: Z14127; MUID:98290540; PMID:9628576
A,Accession: T00227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C.Species: Bscherichia coli
C.Species: Bscherichia coli
C.Joze: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
C.Jozession: T00227; T42148
R.Makino, K.; Ishii, K.; Yasunaga, T.; Hattori, M.; Yokoyama, K.; Yatsudo, H.C.; Kubota,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QKDILIRILDDGV----KKLNEAQKSLLTSSQSFNNASGKLLALDSQLTNDFSEKSSYFQ 167
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Superfamily: hemolysin A; hemolysin A homology

Superfamily: hemolysis; lipoprotein; toxin

$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\text{$\cite{A}$}$\tex
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                                                                                                                                                                                                                                                                    91; Indels 102;
                     A;Cross-references: UNIPROT:Q9RMD9; EMBL:AJ243431; PIDN:CAB57193.1
A;Experimental source: strain RAG-1
C;Genetics:
A;Gene: wzc
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                                                                                                                                                                                                    DB 2; Length 726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hemolysin A toxin protein - Escherichia coli plasmid p0157
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A;Experimental source: strain EDL933; serotype 0157:H7
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                                                                                                                                                                                                    7.1%; Score 108; DB
ilarity 21.7%; Pred. No. 19;
Conservative 49; Mismatches
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Best Local Similarity
Matches 66; Conserv
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                                                                                                                                                                                                                                                      Similarity
              A;Residues: 1-726 <NAK>
                                                                                                                                                                                                                                                                                     67;
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                                                                                                                                                                                                               Query Match
Best Local S
Matches 67
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Best Local Similarity
Matches 64; Conserv
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A; Residues: 1-539 <ARN>
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                                                                                                                                                                                                                                                                      A,Accession: S40647
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A,Gene: TM1146
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                                                                                                                                                                                                                                                                                             probable RAD50 DNA repair protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 0.2-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: D84727
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-1292 <STO>
A;Cross-references: UNIPROT:Q9SL02; GB:AE002093; NID:g4263721; PIDN:AAD15407.1; GSPDB:GN
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NyAlternate names: protein YKR05%; protein YKR415

NyAlternate names: protein YKR05%; protein YKR415

Sispeciae Saccharomyces cerevisiae

C;Speciae Saccharomyces cerevisiae

C;Accession: S38173; S40647; S31207

R;Baladrom, V; Ballesta, J.P.G.; Bou, G.; del Rey, F.; Esteban, P.F.; Garcia-Cantalejo, A;Reference number: S38158

A;Reference number: S38158

A;Reference number: B38173

A;Residues: 1-1875 - SAL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STLFKEQQRQYAALPEENED-----TIEELKEWKSKFEERLALLGTKIRKMEREMVD 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          447 KDEIKWGISKRIEEKEIERDSFEFEISTVDVKQTDEREKQVQVELERKTKQNSERGFESK 506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---TIKELSRFKQEYSQEASVL--VGDIKVLLMDSQDKYFEATQTVYEWCGVVTQLLSAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.1%; Score 107.5; DB 2; Length 1292; 17.2%; Pred. No. 44; ive 77; Mismatches 138; Indels 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 TSIFAEQTVEVVKSAIETADGALDLYNKYLDQVIPWKT-FDE-----
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SLLKGAAKKMINTCNEYQORHGK 294
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C,Superfamily: RAD50 protein
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A; Status: preliminary
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Best Local S
Matches 69
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A,Cross-references: UNIPROT:Q02455; EMBL:Z28320; NID:g486586; PID:g486587; MIPS:YKR095w A,Experimental source: strain S288C A,Experimental source: strain S288C C A,Fou, G.; Esteban, P.F.; Baladron, V.; Gonzalez, G.A.; Cantalejo, J.G.; Remacha, M.; Jin Yeast 9, 1349-1354, 1993 A,Title: The complete sequence of a 15 820 bp segment of Saccharomyces cerevisiae chromos A,Reference number: S40644; MUID:94205265; PMID:8154186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: F72288
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
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Ajītie: Evidence for lateral gene transfer between Archaea and Bacteria from genome seqn
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: F72288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: UNIPROT: Q9X0N0; GB: AE001772; GB: AE000512; NID: 94981693; PIDN: AAD3622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----PGLNNILITLRRERDILDT 1159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------QELQKHADVSKTİSELR 1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1062 EQLHTYKGOVKTLNLSRDQLENALKENEKSWSSQKESLLEQLDLSNSRIEDLSSQNKLLY 1121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96 EDKISLLKEOMFNLNNELDLOKKGMEK--EKADFKKRISILQNNNKEVEAVKSEYESKLS 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 -LIRILDDGVKKLN----EAQKSLLTSSQSFNNASGKLLA---LDSQLTNDFSEKSSYFQ 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         168 SQVDRIRKEAYAGAAAGIVAGPFGLIISYSIAAGVIEGKLIPELNNRLKTVQNFFTSLSA 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---FYVDYDDLM----LSLL 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            methyl-accepting chemotaxis protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-1875 <- ROU-
A; Residues: 1-1875 <- ROU-
A; Cross-references: EMBL:X73541; NID:9450550; PIDN:CAA51948.1; PID:9450554
A; Experimental source: strain 5288C
R; Koelling, R.; Nguyen, T.; Chen, E.Y.; Botstein, D.
Mol. Genet. 237, 359-359, 1993
A; Title: A new yeast gene with a myosin-like heptad repeat structure.
A; Reference number: $31207; MUID:93247549; PMID:8483450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 VLVGDIKVLLMDSQDKYFBATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-300,'A',302-1875 <KOB>
A;Cross-references: EMBL:L01992; NID:g171958; PIDN:AAA34783.1; PID:g1<sup>7</sup>1959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 EQTVEVVKSAIETADGALDLYNKYLDQVIPWKTFDETI-----KELSRFKQEYSQEAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1875;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 7.1%; Score 107.5; DB 2; 1 Similarity 19.9%; Pred. No. 71; 64; Conservative 49; Mismatches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 228 TVKQANKDIDAAKLKLATEIAAIGEIKTETETTR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: SGD:S0001803; MIPS:YKR095w A;Map position: 11R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1024 KIQND----LDQQTIYANTAQNNYE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1122 DQI----QIYTAADKEVNNSTNG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              275 KGAAKKMINTCNEYQQRHGKK 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: strain MSB8
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1272 <KUR>
A;Cross-references: UNIPROT:Q98PR8; GB:AL445566; PID:g14090066; PIDN:CAC13824.1; GSPDB:GN
A;Experimental source: strain UAB CTIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: C90593
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.; Nicleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmc A;Reference number: A99512; MUID:21267165; PMID:11353084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a Strep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein MYPU_6510 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C.Species: Mycoplasma pulmonis
C.Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        듕
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 DSQDKYFBATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRILDDGVKKLNEA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     489 DDKNKFSELS------LPQGYSISFKLASNSNNDEGTLDVKVIVQKQGKEVKTKELK 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 QKSLLISSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQV---DRIRKEAYAGAAAGIVA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Streptococcus sanguis
C;Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 09-Jul-2004
C;Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 09-Jul-2004
C;Accession: A35186
R;Demuth, D.R.; Golub, E.E.; Malamud, D.
J. Biol. Chem. 265, 7120-7126, 1990
A;Title: Streptococcal-host interactions: Structural and functional analysis of A;Recession: A35186
A;Recession: A35186
A;Recession: A35186
A;Residues: 1-1473 *OEM>
A;Residues: 1-1473 *OEM>
A;Cross-references: UNIPROT:P16952; GB:J05418
C;Superfamily: surface antigen spaP
                                                                                                                                              273
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                                                                     434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 KSAIETADGALDLYNKYLDQVIPWKTFDETIKELSRFKQEYS---QEASVLVGDIKVLLM
                                                                 388 A-----LAKQLAT---LQKSLSDLQNGLTFIKSNANFDAEAIKSKINATAGVSAE
---KTVONFFTSLSAT
                                                                                                                                              -- ETETTRFYVDYDDLMLSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1272;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       salivary agglutinin receptor precursor - Streptococcus sanguis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                        435 DKOKIIDAIQADLDKETOKSATOVATVEOLOSGLSGLDLAAIOTOVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.0%; Score 106.5; 23.1%; Pred. No. 50;
                                                                                                                                                      229 VKQ----ANKDIDAAKLKLATEIAAIGEIKT-
           183 AGIVAGPFGLIISYSIAAGVIEGKLIPELNNRL
                                                                                                                                                                                                                                                                                                         274 LKGAAKKMINTCNEYQORHG 293
                                                                                                                                                                                                                                                                                                                                                                                  484 QTGVAKISAG----YQAVHG 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.0%
Best Local Similarity 23.1%
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: MYPU 6510
A;Genetic code: SGC3
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Riglager, P. Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, P.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Domaiguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A.Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma A.Authors: Kreft, J.; Kuhn, M.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, O., C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Macference number: AB1077; MUID:21537279; PMID:11679669
A.; Reference number: AB1077; MUID:21537279; PMID:11679669
A.; Reference number: AB1077; MUID:21537279; PMID:11679669
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A.; Reference number: AB1077; MUID:21537279; PMID:11679669
A.; Reference number: AB1077; MUID:21537279; PMID:1167969
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                277 VSTYTSGVDŤL---AĞGINQAYTGSTALSDGLNKMNGS-----VPTLASĞITQLNNGQK 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLITSSQSFNNASGKLLA----LDSQLTN-----DFSEKSSYFQSQVDRIRKEAYAGAA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           328 ŚLATCLDŚLVDGŚNKLSAGLKELDGNLTDKQGKIAQLKQGMNDLQQGIDQLNQSVNGEDA 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   217 FKDGANTLEVGLKTYTDGVNTAAAGGDKLNAGVSTLAAGVGPLKDGVAALDGGATKLASG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRILDDGVKKLNEAQK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATVKQANKDIDAAKLKLATEIAAIGEIKTETETTRFYVDYDDLMLSLLKGAAKKMINTCN 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -DGVKKINEAQKSLLISSQSFNNASGKLLALDSQLT-----NDFSEKSSY--FQSQVDR 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173 IRKEAYAGAAAGIVAGPFGLIISYSIAA----GVIEGKLIPELNNRLKTVQNFFTSL--S 226
                                                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                             Species: Listeria monocytogenes
Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MTSIFAEQTVEVVKSAIETADG---ALDLYNKYLDQVIPW----KTFDETIKELSRFKQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---VLLMDS
                                                                                                                                                                                                            10 VEVVKSAIETADGAL---DLYNKYLDQVIPWKTFDETIKELSRFKQEYSQEASVLVGDIK
                                                                                                                                                                                                                                                                  206 IEKIRSKDEIGKAÅMAVEKLREILLDIITGINKASSEVSSSSEELSATSEELSANVNSIS
                                                                                                                                                                                                                                                                                                                                                               VLLMDSQDKYFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKASAQKDILIRILD-----
                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transmembrane protein [imported] - Listeria monocytogenes (strain EGD-e)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 127;
                                                                                                                                              35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 927;
                                                                 Length 539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----NEDIK-----
                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 7.0%; Score 106.5; DB 2; Best Local Similarity 20.5%; Pred. No. 33; Matches 78; Conservative 44; Mismatches 131;
                                                                     7.0%; Score 106.5; DB 2;
Local Similarity 19.4%; Pred. No. 17;
nes 59; Conservative 63; Mismatches 147;
C; Superfamily: methyl-accepting chemotaxis protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YSQEASVL----
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                                                                                    Query Match
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hypothetical protein YPR070w - yeast (Saccharomyces cerevisiae)

Nighternate names: hypothetical protein YP9499.25

Nighternate names: hypothetical protein YP9499.25

C;Species: Saccharomyces cerevisiae

C;Species: Saccharomyces cerevisiae

C;Date: 08-Jul-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004

C;Date: 08-Jul-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004

C;Date: 08-Jul-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004

C;Date: 08-Jul-1995 #sequence number: S54059

A;Accession: S54091

A;Accession: S54091

A;Accession: The sequence of S. cerevisiae cosmid 9513.

A;Bescription: The sequence of S. cerevisiae cosmid 9513.

A;Bescription: The sequence of S. cerevisiae cosmid 9513.

A;Bescription: The S69058

A;Accession: S69058

A;Residues: 1-566 cCOUP.
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(iSpecies: Arabidopsis thaliana (mouse-ear cress)
(cjspecies: Arabidopsis thaliana (mouse-ear cress)
(cjacession: 148959
(kj.dordan, N.; Bangert, S.; Wiedelmann, R.; Voss, H.; Unseld, M.; Mewes, H.W.; Rudd, S., I. submitted to the Protein Sequence Database, April 2000
A.Reference number: 225009
A.Accession: T48959
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A,Cross-references: UNIPROT.Q9LXV6, EMBL:AL163975; GSPDB:GN0061; ATSP:T15B3.190
A,Experimental source: cultivar Columbia; BAC clone T15B3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53 EYSQEASVLVGDIKVLLMDSQDK--YFEATQTVYEWCGVVTQLLSAYILLFDEYNEKKAS 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 AQKDILIRILDDGVKKLN-EAQKSLLTSSQSFNNASGKLJALDSQLTNDFSEKSSY---- 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 YLLDAYSHİBSDSTSHINIGSSDKSLDSSNASFINI-QCKL----DLFKYFTELSHYIRQC 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124
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C;Genetics:
                             47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 SAIETADGALDLYNKY-----LDQVIPWKTFDETI-KELSRFKQ--
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  251 GEIKTETETTRFYVD--YDDLMLSLLKGAAKKMINTCNEYQ-
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k; Pred. No. 24;
29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.9%;
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A;Map position: 16R
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Best Local Similarity 25.4'
Matches 57; Conservative
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A;Gene: ATSP:T15B3.190
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C; Accession: AB1730
R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
J; Donnes, L.M.; Karet, U.
Science 294, 849-852, 2001
Science 294, 849-852, 2001
A; Authors: Kreft, U.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
A; Authors: Kreft, U.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, O., C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A; Tierrez, M.; MulD:21537279; PMID:11679669
A; Accession: AB1730
A; Reference number: AB1077; MUID:21537279; PMID:11679669
A; Residues: 1-1601 GLA>
A; Residues: 1-1601 GLA>
A; Residues: 1-1601 GLA>
A; Residues: Linol GLA>
A; Conse-references: UNIRROT:092827; GB:AL592022; PIDN:CAC97610.1; PID:gl6414906; GSPDB:GCGenetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  +40 GIIAATGPVLTVGGKLVS-----MISGLIKGPAGLGKILGLGGKKLTS----LAAGFGAT 489
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                                                                                                                                                                                                                                                     155
                                                                                                                                                 107
                                                                                                                                                                                       134 FGEÄVDEFNAEVSDORIAFENTÄAAFEEYSDKFHREKVGALLAAVDELRARFANVTAAFD 193
                                                                                                                                                                                                                                                                                                                                                   --INDESEKSSYFQSQVDRIRKEAYAGAAAGIVAGPF------GLIIS---- 195
                                                                                                                                                                                                                                                                                                                                                                                   --YSIAAGVIEGKLIPELNNRLKTVQNFFTSLSATVKQANKDIDAAKLKLATEIAAIGEI 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62
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TTAV--EGTSLAAAGL-AGSFGALPAVIGLAGAALLGAGIYALDKHISKIEESKERVKTW
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                                                                                        SKEFVEVORAFTEYAASFADDVEQKQDTSSQVASIAAFREEMQQSSAVFESYSEEFDGDV
                                                                                                                                                    -- QTVYEWCGVVTQLLSAYIL---LFDEYNEK
                                                                                                                                                                                                                                                  108 KASAQKDILIRILDDGVKKLNEAQKSLLTSSQSFNNASGKLLALDSQL------
                                             6 AEQTVEVVKSAIETADGALDLYNKYLD---QVIPWKTFDETIKELSRFKQEYSQEASVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.9%; Score 105; DB 2; Length 1601;
20.3%; Pred. No. 84;
tive 60; Mismatches 134; Indels 88;
63;
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     143;
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     Mismatches
                                                                                                                                                            GDIKVLLMDSQDKYFEAT----
          44;
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          67; Conservative
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Best Local Similarity
Matches 72; Conserv
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A;Cross-references: UNIPROT:059795; EMBL:AL022243; PIDN:CAA18286.1; GSPDB:GN00067; SPDB:*A;Experimental source: strain 972h-; cosmid c364
C;Genetics:
A;Gene: SPDB:SPCC364.04c
    casp homolog - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                           C;Accession: T41332
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harris, Bubmitted to the EMBL Data Library, March 1998
A;Reference number: Z21988
A;Accession: T41332
A;Accession: T41332
A;Accession: T41332
A;Accession: T41332
A;Retere preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-633 <WOO>
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A; Introns: 18/1; 55/1
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C; Species: Trypanosoma brucei
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C; Species: Trypanosoma brucei
C; Species: Trypanosoma brucei
C; Stelly, D.F.; Ip, H.S.; Cross, G.A.M.
C; Ccession: A03395
A; Trylle: Coordinate transcription of variant surface glycoprotein genes and an expressic
A; Reference number: A90868; MUID:85254917; PMID:2861910
A; Reference number: A90868; MUID:85254917; PMID:2861910
A; Residues: Trype: mRNA
A; Residues: Trype: mRNA
A; Residues: Trype: MRNA
A; Residues: Trype: MRNA
A; Residues: Trype: MRNA
A; Residues: Trype: MRNA
C; Comment: The function of the ESAG proteins is not known but may be related to activati
C; Superfamily: VSG expression-site associated protein
C; Superfamily: VSG expression site-associated protein
F; 1-23/Pomain: signal sequence #status predicted content
F; 73, 294, 308/Binding site: carbohydrate (ABN) (covalent) #status predicted
A;Map position: 3
A;Introns: 95/3; 147/3; 175/3; 215/3; 253/3; 284/3; 314/3; 338/2; 363/2; 392/3; 412/2;
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                                                                                                                           13;
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                                                                            DB 2; Length 1229;
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6.9%; Score 104; DB 2; Length 63
23.3%; Pred. No. 29;
tive 50; Mismatches 127; Indels
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Streptoco Streptoco

Candida a

Mouse rec Mouse hya Protein e Drosophil Murine RH Mouse RHA Mouse rec

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The sequence represents the E. coli haemolysis regulator which may be used as an immunogen in a vaccine composition against tuberculosis (Wycobacterium tuberculosis). (Updated on 25-WAR-2003 to correct PN field.) (Updated on 25-WAR-2003 to correct PF field.) (Updated on 25-WAR-2003 to correct PA field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein expression vector; expression cassette; export protein; transformed host cell; bacterial cell; immune response; HJVE family; cytolysin A; ClyA; recombinant protein; bioreactor; bacterial growth; live vector immunogenic composition; animal feed; animal vaccination; food industry; nutritional supplement; biomediation; waste disposal;
                                                                       1 MTEIVADKTVEVVKNAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASV
                                                     MTEIVADKTVEVVKNAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASV
                           Gaps
                           ò
Length 309;
                           1; Indels
Score 1493; DB 2;
Pred. No. 5.3e-118;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Salmonella typhi cytolysin A (ClyA) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                             ABG73265 standard; protein; 305 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 5; Page 18; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        waste treatment; host bacterium
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  99.0%;
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               al Similarity 99.7
300; Conservative
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N-PSDB; ABX15174.
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  Query Match
Best Local S:
Matches 300,
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coding sequence genetically fused to a DNA sequence encoding the protein coding sequence genetically fused to a DNA sequence encoding the protein coding sequence genetically fused to a DNA sequence encoding the protein CC coding sequence state in a bacterial call transformed host call, where the expression cassette expression to the host call. The system is useful for which is exported out of the host call. The system is useful for expression described out of the host call. The system is useful for expression cassette, such that the export protein of interest gual that the export protein of interest is preferably an antigen and this method is useful computation of interest is preferably an antigen and this method is useful computed in sproduced and export protein of interest is preferably an antigen and this method is useful computed in useful for the production of recombinant protein. The system is useful for the production of recombinant protein. Computed an antigenic material against the fusion protein. Computed as a providing an animal antigenic material against which an immune response in a bioreactor, and various devices that facilitate the growth of bacterial against which an immune response in an enimal. The system is also the generation of an immune response in an animal. The system is also the generation of an immune response in an animal. The system is also to useful for preparing immunogenic compositions for vaccinating animals, so the generation of an immune response in an animal. The system is also to host bacterium can also be expressed. A population of recombinant host cells can be transformed with the expression, we ctor, and then the top copulation of bacterial host cells can be maintained in culture and used to produce proteins without having to harvest and lyse the host cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 91.1%; Pred. No. 2.7e-110;
Matches 276; Conservative 16; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABG73266 standard; protein; 749 AA.
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cytolysin A; ClyA; recombinant protein; bioreactor; bacterial growth; live vector immunogenic composition; animal feed; animal vaccination; food industry; nutritional supplement; biomediation; waste disposal; waste treatment; bact bacterium; sacB; mutant; mutein; lethal levansucrase.
                                                                                      23-NOV-2001; 2001US-00993292
                                                                                                  22-NOV-2000; 2000US-0252516P
                                                                                                                                    WPI; 2003-228013/22.
                                  Salmonella typhi.
Bacillus subtilis.
Synthetic.
                                                                                                             (GALE/) GALEN J E
                                                                                                                                          N-PSDB; ABX15191.
                                                               US2002146430-A1
                                                                           10-OCT-2002
                                                                                                                         Balen JE;
                                                     Chimeric
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cassette, where the expression cassette comprises an export protein cassette, where the expression cassette comprises an expression vector having an expression cassette, where the expression cassette comprises an export protein of interest, a host cell transformed host call, where the expression coding sequence encoding the protein of interest, a host cell transformed host call, where the expression cassette expresses the export protein-protein of interest fusion protein cassette expresses the export protein-protein of interest fusion protein of the host call. by providing an expression vector capression cassette, such that the export protein-protein of interest that produced had exported into the culture medium. The export protein of interest is predecad and exported into the culture medium. The export protein may be a member of the HIPS family such as cytolysin A correspond of interest is predecad and exported into the culture medium. The export protein may be a member of the HIPS family such as cytolysin A correspond of interest is predecad and exported into of recombinant proteins (CA). The system is useful for the production of recombinant proteins in the system is useful for the production of recombinant proteins in the system is useful for the production of recombinant proteins a large as a live vector immunogenic composition capable of facilitating mannal antigenic material adainst which an immune response for an animal antigenic material adainst which an immune response to be useful for preparing immunogenic compositions capable of facilitating confocial manual antigenic material adainst which an immune response in an animal. The system is also useful for preparing immunogenic compositions capable of facilitating confocial manual antigenic manual animal animal animal. The system is also to explain of parterial manual animal Novel system for expressing protein of interest, has expression vector with cassette having export protein coding sequence fused to protein coding sequence, host cell transformed with vector, and culturing present invention relates to a system for expressing a protein of 3xample 3; Page 25-28; 33pp; English.

Sequence 749

Gaps ö 93.0%; Score 1402; DB 6; Length 749; llarity 91.1%; Pred. No. 9.1e-110; Conservative 16; Mismatches 11; Indels (Query Match Best Local Similarity Matches 276; Conserv

180 300 120 180 AAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNKLKSVQNFFTTLSNTVKQANKDIDAAK 240 The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food 9 DDGITKLNEAQKSLLVSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDKIRKEAYAG LVGDIKTLLMDSQDKYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQKDILIKVL LKLTTEIAAIGBIKTETETTRFYVDYDDLMLSLLKEAAKKMINTCNEYQKRHGKKTLFEV New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder. Claim 20; SEQ ID NO 55580; 103pp; English. Novel human diagnostic protein #25212. ABG25221 standard, protein; 1035 AA. 30-MAR-2001; 2001WO-US008631. 31-MAR-2000; 2000US-00540217. 23-AUG-2000; 2000US-00649167. Tang YT; (first entry) Drmanac RT, Liu C, WPI; 2001-639362/73 (HYSE-) HYSEQ INC. 303 303 N-PSDB; AAS89408 WO200175067-A2. <u>..</u>5 biodiversity. PEV Homo sapiens 18-FEB-2002 11-OCT-2001 241 ABG25221; 61 61 121 121 181 181 241 301 301 셤 a 셤 යු 셤 쉽 8 ò ò 8 ઠે

Disclosure; Page; 175pp; English.

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of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymuclocitide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG303377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130 AQKSILVSSQSFNNASGKLIALDSQLTNDFSEKSSYFQSQVDKIRKEAYAGAAAGVVAGP 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fungicide; cytostatic; essential gene; Aspergillus fumigatus; infection; cancer; contamination; biofilm; antibody; immune response.
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100.0%; Pred. No. 8.4e-88;
iive 0; Mismatches 0;
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2001US-0295890P.
2001US-0303899P.
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05-JUU-2001; 2001US-0295890P
09-JUU-2001; 2001US-031899PP
31-AUG-2001; 2001US-0316362PP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 100.
1es 230; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1035 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       250
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The invention relates to novel purified or isolated nucleic acids of essential genes of Aspergillus funidatus. The isolated nucleic acids of the invention are used to treat or prevent infections by a pathogenic conganism such as A. funigatus, to treat a non-infectious disease in a conganism such as A. funigatus, to treat a non-infectious disease in a cubject (e.g. cancer), to prevent or inhibit formation on a surface of a by A. funigatus, or to prevent or inhibit formation on a surface of a biofilm comprising A. funigatus. The polynucleotides are useful for expressing recombinant protein for characterisation, screening or therapeutic use, as markers for host tissues in which the pathogenic corganisms invade or reside, for comparing with the DNA sequence of A. cumigatus to identify duplicated genes or paralogues having the same or funigatus to identify duplicated genes or paralogues having the same or cumiquatus biochemical activity and/or function, for comparing with DNA similar biochemical activity and/or function, for comparing with DNA sequences of other related or distant pathogenic organisms to identify esquences of other related or distant pathogenic organisms to identify and or expression patterns, for raising anti-protein antipodies, as an of expression patterns, for raising anti-protein another immune of expression patterns, for raising anti-protein another immune continement or the polypeptides may be used to raise antibodies or to interaction. The polypeptides may be used to raise antibodies or to elicit immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as a marker for factors. This sequence represents a protein of one of the essential genes correlative receptors or ligands in the case or virulence factors. This sequence represents a protein of one of the essential genes
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Pred. No. 0.2;
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WPI; 2003-895291/82.
N-PSDB; ADF03279.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   elicit immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fuluds, as a marker for host tissues in which pathogenic organism invade or reside, and to isolate correlative receptors or ligands in the case or virulence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of expression patterns, for raising anti-protein antibodies, as an antigen to raise anti-DNA antibodies or to elicit another immune response, and for identifying polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding
                                                                                                                                                                                                                                                                                                                                                                                                                                   purified or isolated nucleic acids of essential genes of Aspergillus higatus, useful for treating or preventing infections by A. fumigatus, for treating a non-infectious disease in a subject e.g. cancer.
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21.4%; Pred. No. 0.24;
ive 49; Mismatches
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                                                                                                                                                                      23-APR-2001; 2001US-0285697P.
27-APR-2001; 2001US-0287066P.
05-JUN-2001; 2001US-0295890P.
09-JUL-2001; 2001US-031899P.
31-AUG-2001; 2001US-0316362P.
                                                                                                                             23-APR-2002; 2002WO-US013142
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Aspergillus fumigatus.
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                                        WO200286090-A2.
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                                                                                                                              -----SLKSKFDSTEWQLKSVENDTQTLTERKS 472
                                                                             -LSNTVKQANKDIDAAKLK---LTTEIAAIGEIKTETETTRFYVDYDDLMLSLLKEA--- 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 8.2%; Score 124; DB 7; Length 1036; Local Similarity 21.5%; Pred. No. 0.27; Nismatches 127; Indels 116
                                                                                                                                                                                                                                       -- CNEYOKRHGK 294
                                                                                                                                                                                                                                                                                        = ::
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                                                                                                                                                                                                                                       -------AKKMINT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADF07451 standard; protein; 1036 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacterial polypeptide #3564.
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                                                                                                       -----KQANKDIDAAKLKITT-----BIAAIGEIKTETETTRFYVDYDDIM 270
                                                                                                                ----GITKLNEAOKSLLVSSOSFNNASGKLLALDSOL--T 156
                         TKHLNGVGN-KLQNLPNLDKLGTGLDTV---SGILSAISASFILSNADADTGTKAAAGVE 286
                                                                                    | | : | | : : | | : : | | PISALVGAITGIISGILEASKQSMFEHVAN---RMANTIAEWEKTHGKNFFENGYDARHS
                                                                                                                                                                                                                                                   Transport-associated protein; TRANP; nuclear pore; nuclear transport; vesicle trafficking; cancer; cystic fibrosis; multidrug resistance; hypercholesterolaemia; diagnosis; treatment.
                                             ----YAGAAAGVVAGPFGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "O-phosphorylated by casein kinase II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "O-phosphorylated by casein kinase II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "O-phosphorylated by casein kinase II"
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                                                                                                                                                                                                                                                                                                                                             "O-phosphorylated by casein kinase II"
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                                                                                                                                                                                                                                                                                                                                                           _note= "O-phosphorylated by tyrosine kinase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "O-phosphorylated by casein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                       "O-phosphorylated by casein kinase
                                                                           193 IISYSIAA--GVVEGKLIPELKNKLKSVQNFFTTLSNTV-----
                                                                                                                                                                                                                                       Human transport-associated protein-8 (TRANP-8).
                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                            "N-glycosylated"
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                                              NDFSEKSSYFQ-----SQVDKIRKEA-
                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                            AAY31646 standard; protein; 962 AA
                                                                                                                                        271 LSLLKEAAKKMINTCNEYOKR 291
                                                                                                                                                       ----YEEGKRLEKKPNEFÓKQ 535
                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= 785
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717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note=
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This sequence represents human transport-associated protein-8 (TRANP-8).

The DNA sequence was first identified in a human colon tissue cDNA concerns the full-length cDNA was derived from a series of overlapping and/or extended cDNA sequences and is a consensus. TRANP-1 to 9 (AAY31639 and/or extended cDNA sequences and is a consensus. TRANP-1 to 9 (AAY31639 and/or extended cDNA sequences and is a consensus. TRANP-1 to 9 (AAY31639 and/or extended cDNA sequences and is a consensus. TRANP-1 to 9 (AAY31639 and/or extended cDNA sequences and is molecular transport. Various disorders are involved in molecular transport. Various disorders are intracellularly or to the extracellular environment. Examples of such disorders include cystic fibrosis, multidrug resistance, concerns and creating forms of dispetes mellitus. Defective conclear transport may play a role in cancer. For example, the BRCA1 conclear transport may play a role in cancer. For example, the BRCA1 concerns of the nuclear win unclear pore complexes, but is aberrantly located in the cytoplasm in breast cancer cells. In other cancers, cells can secrete excessive amounts of darenaline and noradrenal medulla can excessive amounts of darenaline and noradrenaline, leading to secrete excessive amounts of adrenaline and noradrenaline, leading to result from either excessive or insufficient molecular transport disorders can antibodies and nucleic caids encoding TRANP can be used to treat or prevent a cancer associated with increased TRANP antisense concluded in the cancer called with increased TRANP antisense concluded transport of the cargetting mechanism for drugs. Alternatively, a a TRANP antisense concluded transport of the concluded transport of the concluded to treat a disorder caused by reduced transport of the concluded to treat a disorder caused by reduced transport of the concluded to treat a disorder caused by reduced transport of the concluded to treat a disorder caused by reduced transport of the concluded to treat a disorder caused by reduced transpo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human TRANP coding sequences, used to treat transport disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ë
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                                                                                                                                                                                                                                                          "O-phosphorylated by casein kinase II"
"O-phosphorylated by casein kinase II"
                                                                                                                           "O-phosphorylated by casein kinase II"
                                                                                                                                                                                        "O-phosphorylated by casein kinase II"
                                                                                                                                                                                                                                                                                                                                                                                        casein kinase II"
                                                                                                                                                                                                                                                                                                                                                                                                                                        902
/note= "O-phosphorylated by casein kinase II"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Guegler KJ, Corley NC,
                                                                    "O-phosphorylated by casein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.0%; Score 120.5; DB 2;
23.7%; Pred. No. 0.48;
vative 51; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                   "O-phosphorylated by
                                                                                                                                                                                                                                                                                                                                     "N-glycosylated"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lal P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                biologically active molecules
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Best Local Similarity 23.77
Matches 74; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hillman JL,
                                                                                                                                               /note=
780
/note=
                    /note=
754
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882
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                                                                                  note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-508646/42.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAZ11738
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Bandman O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           635
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This sequence represents human trancytosis-associated protein (TAP). This sequence may be used in the method of the invention for identifying an insulin response medulator. The method comprises contacting a composition comprising insulin-responsive aminopeptidase (TRAP), or its fragment, and TAP, or its fragment, and the test compound and determining the ability of the test compound to medulate binding of TRAP, or its fragment, to TAP, or its fragment. TAP interacts with IRAP in GLTM4 -containing vesicles. Binding of TAP to IRAP is competitively inhibited by a bioactive fragment comprising residues 1-109 of IRAP. TAP is thought to function as a tether which secures GLTM4 vesicles to an internal cellular component. The method of the invention is useful for identifying an insulin response
                                                                                                                                     162 KSSYPQSQVDKIRKEAYAGAAAGVVAGPFGLIISYSIAAGVVEGKL-----IPELKNKL 215
                                                                                                                                                                                                         KSVQNFFTTLSNTVKQANKDIDAAKLKLTTEIAAIGEIKTETETTRFYVDYDDLMLSLLK 275
                                                                                                                                                                                                                               695 QQHKDQYNLLKIQLGKDNQHQGSYSEGAQ----MNGIQPEEIGR---LREEIEELKRNQE 747
                                                                    -----AQKDILIKVLDDGITKLNEAQKSLLVS---SQSFNNASGKLLALDSQLTNDFSE 161
                                                                                                                                                                       864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying an insulin response modulator comprises contacting a composition comprising insulin-responsive aminopeptidase (IRAF) and trancytosis-associated protein (TAF) with test compound and determining modulation of IRAF:TAF binding.
                                                                                                                                                            748 LLQSQLTEKDSMIENMKSSQTSGTNEQSSAIVSARDSEQVAELKQELATLKSQL-NSQSV
K-----TLLM------DSQDKYFEATQTVYEWCGVATQLLAAYILLFDBYNEKKAS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enzyme; human; insulin-responsive aminopeptidase; IRAP; insulin response modulator; trancytosis-associated protein; TAP; GLUTY-containing vesicle; insulin; translocation; glucose clearance; blood glucose; sensitivity; resistance; diabetes; prediabetes; hyperglycemia; Type I diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 47-49; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                AAG79733 standard; protein; 962 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-MAY-2002; 2002WO-US014493
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                                                                                                                                                                                                                                                                                               DODOKILSLKNK 926
                                                                                                                                                                                                                                                                           EAAKKMINTCNE 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ADIP-) ADIPOGENIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human TAP
                                                                                                                                                                                                                                                                           576
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG79733;
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modulator, especially an IRAP:TAP modulator. The modulator is useful for modulating GLUT4 translocation, enhancing glucose clearance in an insulin resistant subject, and regulating blood glucose levels in a subject. Furthermore, The modulator is useful for treating a subject having an insulin response disorder, e.g. reduced insulin sensitivity or insulin resistance, or diabetes, for treating a subject having prediabetes or its symptoms, e.g. hyperglycemia and/or Type I diabetes
                                                                                                                                                                                                                                                                                                      161
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                                                                                                                                                                                                                                                                                                                                                                                                                                             914
                                                                                                                                                                                                                      694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .. .37
'note= "Escherichia coli beta-lactamase signal peptide
                                                                                                                                                                                                                                                                                                                                                              KSSYFQSQVDKIRKEAYAGAAAGVVAGPFGLIISYSIAAGVVEGKL-----IPELKNKL
                                                                                                                                                                                                                                                                                                                                                                                                                    KSVQNFFTTLSNTVKQANKDIDAAKLKLTTEIAAIGEIKTETETTRFYVDYDDLMLSLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                   K-----TLLM-----DSQDKYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKAS--
                                                                                                                                                                                                                                                                           QQHKDQYNLLKIQLGKDNQHQGSYSEGAQ----MNGIQPEEIGR---LREEIBELKRNQE
                                                                                                                                                                                                                                                                                                        ----AQKDILIKVLDDGITKLNEAQKSLLVS---SQSFNNASGKLLALDSQLTNDFSE
                                                                                                                                                                                                                                                                                                                                  148 LLQSQLTEKDSMİENMKSSQİSGTNEQSSAIVSARDSEQVAELKQELATLKSQL-NSQSV
                                                                                                                                                                                            7 DKTVEVVKNAIETADGALDLY-NKYLDQVIPWQTFDETIKELSRFKQEYSQAASVLVGDI
                                                                                                                                                                                                                                                                                                                                                                                        EITKLOTEKOELLOKTEAFAKSVEVOGETETIIATKTTD--VEGRLSALLOETKELKNEI
                                                                                                                                                               51;
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protein A (PspA)EF5668"
270. .627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Streptococcus pneumoniae pneumococcal protein A (PspA)Rx1" | 254. .625 | /note= "Encoded by bases GAATAATAGAAG"
                                                                                                                                     Length 962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunogenic composition; vaccine; Th2-type immune response;
pneumococcal surface protein A; PspA; beta-lactamase; bla;
                                                                                                                                                                 IndelB
                                                                                                                                       DB 6;
                                                                                                                                     ; Score 120.5; DB 6;
; Pred. No. 0.48;
51; Mismatches 136;
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                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DODOKILSLKNK 926
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pneumoniae.
Escherichia coli.
Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bla SS)"
                                                                                                                                                    Similarity
                                                                                                             Sequence 962 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
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                                                                                                              Ouery Match
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                                                                                                                                                                                                                                                                                                                                                                                          807
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259 ITRRYVDYDDLMLSLLKEAAKKMINTCNEYOKRHGK-KTLFE-----VPE 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 staged assembly; nanostructure; peptide nucleic acid; PNA; structural reinforcement; aerogel; paper; plastic; cement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    General vesicular transport factor p115 SEQ ID NO:155.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADB67135 standard; protein; 961 AA
                                                                                                                        Example 5; Fig 13; 94pp; English.
              16-APR-2002; 2002US-0372710P.
15-APR-2003; 2003US-00414532.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                       Local Similarity
les 79; Conserv
                                                  Curtiss R, Kang HY;
                                                                WPI; 2004-399655/37.
                             CURTISS R.
KANG H Y.
                                                                        N-PSDB; ADO52074
                                                                                                                                                                                                                    Sequence 627 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-DEC-2003
                                                                                                            bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                          441
                                                                                                                                                                                                                                                               11
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Matches
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The present invention describes a method (MI) for the staged assembly of a nanostructure using peptide nucleic acids (PNAs). MI comprises: (a) a nanostructure using peptide nucleic acids (PNAs). MI comprises: (a) contacting a nanostructure intermediate (NSI) having at least one unbound contacting a lement (JE) with an assembly unit (AU) that comprises several different JE where: (i) none of these JE can interact with itself or complementary. So that AU becomes non-covalently linked to NSI to produce complementary. So that AU becomes non-covalently linked to NSI to produce complementary JE in AU and a single unbound AU; and (c) a new NSI for us in subsequent cycles; (b) removing unbound AU; and (c) a new NSI for us in subsequent cycles; (b) removing unbound AU; and (c) a new NSI for us in subsequent cycles; (b) removing unbound AU; and (c) is that the complementary JE in at least one cycle are PNAs. Also cyclic respetition of (a) and (b) to form a nanostructure. The new feature of secribed are nanostructures formed from many AU, comprising different JE, where at least one AU includes PNA. MI is useful for producing consistent and inforcements (for aerogels, paper, plastics or cement, structural reinforcements (for aerogels, paper, plastics or cement, particularly as long fibres to improve tensile strength); identification construction of nanowires or nanocircules; size markers caffolds; for construction of nanowires or nanocircules; size markers or controlled; procedure memories; as artificial zeolite for absorbing ions from the transfer nanostructures, so will produce structures with predictable geometry computer memories; as artificial zeolite for absorbing ions and stoichiometry. The present sequence represents a protein containing colled coil dimerisation sequences that can be used for structural containing colled coil dimerisation sequences that can be used for structures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----AQXDILIKVLDDGITK--LNEAQKSLLVSSQSFNNASGKLLALDSQLTNDFSEK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  695 QOHKDOYNLLKVQLGKDSCHQGPYTDGAQ----MNGVQPEBISR---LREEIEELKSNRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --TLLMDSQDK--YFEATQTVYEWCGVATQLLAAYILLFDEYNEKKAS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 DKIVEVVKNALETADGALDLY-NKYLDQVIPWQTFDETIKELSRFKQEYSQAASVLVGDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staged assembly of nanostructures, useful e.g. in biosensors or as catalyst supports, using assembly units derived from peptide nucleic
tensile strength; identification marker; anti-counterfeiting m
ensyme support; catalyst support; assembly scaffold; nanowire;
nanocircuit; molecular sieve; molecular filter; biosensor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.8%; Score 118; DB 7; Length 961; 22.9%; Pred. No. 0.79; ive 54; Mismatches 138; Indels :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure, Page 58; 118pp; English.
                                                                                                                                                                                                                                                               21-FEB-2003; 2003WO-US005390.
                                                                                                                                                                                                                                                                                                          21-FEB-2002; 2002US-00080608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72; Conservative
                                                                                                                                                                                                                                                                                                                                                               (NANO-) NANOFRAMES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                     Goldberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-721788/68.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 961 AA;
                                                                                                                                                               WO2003072829-A1.
                                                                                                                                                                                                                     04-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acids.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to immunogenic compositions and vaccines comprising a live attenuated strain of pathogenic gram negative bacteria that secretes an antigen. The vaccine is useful in eliciting a Th2-type immune response in a vertebrate against pathogenis, e.g., helminths, fungi, viruses, protozoans or bacteria. The present sequence is Escherichia coli beta-lactamase signal peptide (bla SS)-Streptococcus pneumoniae pheumococcal surface protein A (PspA)ErSéG80-pspARxI chimeric protein. This sequence is used in the exemplification of the invention. Note: This sequence is stated to be similar to the sequence shown in the sequence listing, however these sequences differ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     382 RAMVVPEPEQLAETKKKSEEAKQKAPELTKKLEEAKAKL-EAAALEKAASEEMDKAVAA 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----SQLTNDFSEKSSY 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     322 EKAALEKAASEEMDKAVAAVQAYLAYQQATDKAAKDAADKMIDEAKKREEBAKTKFNTV 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DSQDKYFBATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQKDILIKVLDDGITKL--- 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       262 LKDAETLOSPVASOSKABKDYDAAKKDAKNAKKAVEDAQKALDDAKAAQKKYDEDQKKTE 321
                                                                                                                                                                                                                                                                                                                       New vaccine comprising a live attenuated strain of pathogenic gram-
negative bacteria, useful in eliciting a Th2-type immune response in a
vertebrate against pathogens, e.g., helminths, fungi, viruses, protozoans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166 FQSQVDKIRKEAYAGAAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNKLKSVQNFFTT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----LSNTVKQA------TE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EVVKNAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASVLVGDIKTLLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.8%; Score 118; DB 8; Length 627; 22.5%; Pred. No. 0.44; ive 50; Mismatches 128; Indels
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747

694

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Gaps

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cubound joining element with an assembly unit comprising at Least one unbound joining element with an assembly unit comprising at least one goining element with an assembly unit comprise to form a nanostructure, for the assembly unit in at least one cycle comprises a peptide nucleic where the assembly unit in at least one cycle comprises a peptide nucleic complementary joining element of the nanostructure intermediate are complementary joining elements, where the assembly unit is non-covalently complementary joining elements, where the assembly unit is non-covalently complementary joining element comprises; (i) capping the nanostructure with ct least one capping unit; and (ii) post-assembly conversion of specific on-covalent intermediate comprises if (i) capping the nanostructure with ct least one capping unit; and (ii) post-assembly conversion of specific non-covalent interactions of complementary joining elements to covalent intermediate comprises are stabilised. The nanostructure comprises as useface bound initiator assembly unit. A first assembly unit used in at least one cycle comprises at least one cycle comprises at least one cycle comprises at least one cycle comprises at least one cycle comprises at least one cycle comprises at least one cycle comprises at least one cycle comprises at least one cycle comprises at least one cycle comprises at least one cycle comprises at least one cycle comprises at least one cycle comprises at least one cycle comprises at least one cycle comprises one cycle comprise comprises of the first structural element to form a stable complex. The assembly unit the further comprising a peptide nucleic acid, or a first structural element comprising a peptide nucleic acid. The assembly unit the further comprising a peptide nucleic acid. The assembly unit the further comprising a peptide nucleic acid. The assembly unit the photonic nanoparticle, inorganic ion, carbon nanotube, lectin or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staged assembly of a nanostructure containing peptide nucleic acid assembly units comprises contacting a nanostructure intermediate with an assembly unit comprising different joining elements, and removing unbound
                                              865 ALSEERTAIKEQLDSSNS-----TIAILQNEKNKLEVDITDSKKEQDDLLV-LLAD 914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to staged assembly of a nanostructure comprising: (a) contacting a nanostructure intermediate comprising at least one
SSYFQSQVDKIRKEAYAGAAAGVVAGPFGLIISYSIAAGVVEGKL-----IPELKNKLK
                                                                                                                                                            SVQNFPTTLSNTVKQANKDIDAAKLKLTTEIAAIGEIKTETETTRFYVDYDDLMLSLLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide nucleic acid; PNA; nanostructure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 43-44; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADL99406 standard; protein; 961 AA.
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                                                                                                                                                                                                                                                                                                                         277 AAKKMINTCNEYQK 290
                                                                                                                                                                                                                                                                                                                                                                                                     915 QDQKIFSLKNKLKE 928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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GOLDBERG E B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hyman PL,
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chemiluminescent molecule. The assembly unit comprises sub-assembly units that bind to each other to form a complex. The present sequence represents a protein containing a coiled coil dimerisation sequence that can be used as a structural element in the method of the invention.
                                                                                                                                                                                        694
                                                                                                                                                                                                                                                                                                                                                                                               276
                                                                                                                                                                                                                                                                                                                                                                                                               865 ALSEBRIAIKEQLDSSNS-----TIAILQNEKWKLEVDITDSKKEQDDLLV-LLAD 914
                                                                                                                                                                                                                                                                             -----AQKDILIKVLDDGITK--LNEAQKSLLVSSQSFNNASGKLLALDSQLTNDFSEK 162
                                                                                                                                                                                                                                                                                                        806
                                                                                                                                                                                                                                                                                                                                     216
                                                                                                                                                                                                                                                                                                                                                       Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading
                                                                                                                                                                                                                                      217 SVQNFFTTLSNTVKQANKDIDAAKLKLTTEIAAIGEIKTETETTRFYVDYDDLMLSLLKE
                                                                                                                                                                                        DKKBEBVKKTLEQHDSIVTHYKNMIREQDLQLEELKQQISTLKCQNEQLQTAVTQQVSQI
                                                                                                                                                                                                                     K-----TLLMDSQDK--YFEATQTVYEWCGVATQLLAAYILLFDEYNEKKAS--
                                                                                                                                                                                                                                                                                                                                     163 SSYFQSQVDKIRKEAYAGAAAGVVAGPFGLIISYSIAAGVVEGKL-----IPELKNKLK
                                                                                                                                                             7 DKTVEVVKNAIETADGALDLY-NKYLDQVIPWQTFDETIKELSRFKQEYSQAASVLVGDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated nucleic acid encoding a Staphylococcus epidermis polypeptide, useful for diagnosing and treating bacterial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4820.
                                                                                                                       503
                                                                                                     8; Length 961;
                                                                                                  7.8%; Score 118; DB 8; Length 96 22.9%; Pred. No. 0.79; Ative 54; Mismatches 138; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 4820; 267pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABP39975 standard; protein; 1211 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-00134001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        277 AAKKMINTCNEYOK 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       915 QDQKIFSLKNKLKE 928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibacterial; gene therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus epidermidis.
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                                                                                                                                  Conservative
                                                                                               Query Match
Best Local Similarity
Matches 72; Conserv
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                                                                          Sequence 961 AA;
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WPI; 1993-351722/44.
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                                                                                                                                                                                                                                                                                                                                                                                                        381 KEVQELESLLYISDEQHDEKLEEIKNSYYTLMSEQSVVNNDIRFLEHTINENEAKKSRLD 440
frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABB35124 to ABB37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site
                                                                                                                                                                                                                                                                                         106 EKKASAQKDILIKVLDDGITKLNEAQKSLLVSSQSFNNASGKLLALDSQLTND----F 159
                                                                                                                                                                                                                                                                                                         SEKSSYFQSQVDKIRKEAYAGAAAGVVAGPFGLIISYSIAAGVVEGKLIPELKN----- 213
                                                                                                                                                                                                                                                                                                                                                        |: :||:|| BEELDNIESQIDSIKNEK------AQNEKLLADIKNKQKQLM 380
                                                                                                                                                                                                                                                                                                                                                                                      ------KLKSVQNFFTTLSNTVKQANKDI-------DAAKLKLT 244
                                                                                                                                                                                                                 59 S-----VLVGDIKTLLMDSQD-----KYFEATQTVYEWCGVATQLLAAYILLFDEYN 105
                                                                                                                                                                                                                                                         243 KEMEGSDVIVTVSDIDHYTEDNQRLDERLNHLKSQQAEKE--GQQAQINQ----LLQKYK 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TEIAAIGEIKTETETTRFYVDYDDLMLSLLKEAAKKMINTCNEYQKRHGKKTLFEVPE 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hyaluronan binding protein; HA; RHAMM; mediated motility; wound; healit diagnosis; treatment; cell locomotion; tumour invasion; birth defects; inflammatory disorder; Alzheimer's disease; dementia; Parkinson's diseases; Huntingfon's disease; AIDS; diabetes; auto; immune diseases; corneal dysplasia; hypertrophy; surgery; burns; stroke multiple sclerosis; depression; schizophrenia; CNJ; contraception; in vitro fertilisation; embryo development.
                                                                                                                                                                                             VADKTVEVVK-----NAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAA
                                                                                                                                                   7.8%; Score 118; DB 5; Length 1211;
19.3%; Pred. No. 1.1;
tive 53; Mismatches 112; Indels 124;
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(MANI-) MANITOBA CANCER TREATMENT & RES FOUND.
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                                                                                                                                                                 Local Similarity 19.3
tes 69; Conservative
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                                                                                                                                Sequence 1211 AA;
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09-JAN-2003
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The sequence is that encoded by a cDNA clone encoding the hyaluronan creeptor (HARC). The sequence was obtd. by screening a 3T3 library in lambda gtl1 with antibodies to HARC. A clone of 1.9 kb was obtained and lambda gtl1 with antibodies to HARC. A clone of 1.9 kb was obtained and lambda gtl1 with antibodies to HARC. A clone of 1.9 kb was obtained and cused to rescreen the library to obtain the full length, 2.9 kb clone. HA is dead to rescreen the library to obtain the full length, 2.9 kb clone. HA is dead to response to growth factors and in chemctaxis by white blood cells. HA may response to growth factors and in chemctaxis by white blood cells. HA may compose to growth factors and in chemctaxis forms of dementia, AlDS, inflammatory disorders, Alzheimer;s and other forms of dementia, AlDS, inflammatory disorders, Alzheimer;s and other forms of dementia, burns, surgical incisions and adhesions, strokes, multiple sclerosis, burns, surgical incisions and adhesions, strokes, multiple sclerosis, convoltang networking network sprouting; also in CNJ and spinal cord regeneration, contraception, in vitro fertilisation and embryo development. See also contraception, in vitro fertilisation and embryo development. See also correct PN field.) (Updated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 266 LTAESTNQ------EYA-----RMVQDLQNRSTLKEEBIKBITSSFLEKITDLK 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227 NTVKQANKDI------DAAKLKLTTEI---AAIGEIKTETETTRFYVD-YDD 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             206 ESVQEKYNDTAQSLRDVSAQLESYKSSTLKEIEDLKLENLTLQEKVAMAEKSVEDVQQQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 YAGAAAGVVAGPFGLIISYSIAAGVVEGKLIPELKUK-----LKSVQNFF----TTLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LDNLLREKEVELEKHIARQAQAILIAQEKYIDTA---QSLRVVTAQLESVQEKYNDTAQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MTEIVADKTVEVVKNAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LVGDIKTLLMDSQDKYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQKDILIKVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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DNA encoding hyaluronan receptor - used to produce proteins and antibodies for alteration of cell locomotion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 476;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match
Local Similarity 20.8%; Pred. No. 0.33;
les 69; Conservative 73; Mismatches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      369 EKQALLINEHGATQEQINKIRDSYAQLLGHQNL 400
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                                                                                                       Claim 7; Fig 23; 88pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present invention. Proteins encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and to biosynthesis and biodegradation, especially biosynthesis of Vitemain B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes-related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by L. monocytogenes and related organisms. Note: The sequence data for this monocytogenes and related organisms. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the preventive and in electronic format directly from WIPO at the printed specification, but was obtained in electronic format directly from WIPO at the printed specification and was obtained in the properties and related organisms.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GPFGLIISYSIAAGVVEGKLIPELKNKLKSVQNFFTTLSNTVKQANKDIDAAKLKLTTEI 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     222 NTLEVGLKTYTDGVNTAAAGGDKLNAGVSTLAAGVGPLKDGVAALDGGATKLASGVSTYT 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78 EATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQKDILIKVLDDGITKLNEAQKSLLVS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 EIVADKTIVEVVKNAIETADGALDLYNKYLDQVIPWQTFDETI----KELSRFKQEYSQAA 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----TLLMDSQDKYF 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and related
                                                                                                                                                                                                                                                                         Oucniseer C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P; Dussurget O, Checouani F, Nedjari H, Glaser P, Kunst F, Cossart P; Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA; Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A; Charkraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L; Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N; Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J; Rose M, Voss H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 6; SEQ ID NO 2425; 192pp; French.
                                                                                                                                              11-APR-2001; 2001WO-FR001118.
                                                                                                                                                                                               11-APR-2000; 2000FR-00004629.
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Listeria monocytogenes.
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                                           WO200177335-A2.
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ANH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (I) and have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the S. or epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts calls which express the colypeptides. The polypeptides (II) via the production of vectors containing the obypeptides may also be used to assay for other inhibitors of their creatment of S. epidermidis infections, e.g. endoarditis AAH53971 to AAH55090 represent oligonucleotide sequences from the present invention. AAH55091 to AAH55091 to AAH55090 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention. N.B. The present invention sequence listing of the present sequences given in the sequence listing of the present specification, however the sequences are given in the disclosure for SEQ ID NO:4465 to even though sequences are given the disclosure for SEQ ID NO:4465 to even though sequences are present in the disclosure for SEQ ID NO:4465 to even though sequences are present for SEQ ID NO:4465 to even though sequences are present colless are present and the colless are present and the colless are present and the colless are present and the colless are present and the colless are present and the colless are present and the colless are present and the colless are present and the colless are present and the colless are present and the colless are present and the colless are present and the colless are present and the colless are present and the colless are present and the colless are present and the colless are present and the colless and the colless are present and the colless are present and the colless are present and the colless are present and the colless are present and the colless are present and the colless are present and the colless are present and the colless are present and th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ETIKELSRFKQEYSQAAS-----VLVGDIKTLLMDSQD-----KYFEATQTVYEWCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92; Indels 118; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S. epidermidis open reading frame protein sequence SEQ ID NO:1660
                                                                                                       430 GVSAEDKOKI-----IDAIQADLDKETOKSATQVATVEOLOSG 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Length 885;
248 AAIGEIKTETETTRFYVDYDDLMLSLLKEAAKKMINTCNEYQKRHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 7.7%; Score 116; DB Best Local Similarity 20.0%; Pred. No. 1; Matches 63; Conservative 42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 18; Page 462; 2188pp; English.
                                                                                                                                                                                                                                                                                                                                                                               AAG82283 standard; protein; 885 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-NOV-2000; 2000WO-US030782.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus epidermidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GROUP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GLAX ) GLAXO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       endocarditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kimmerly WJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-SEP-2001
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Pred. No. 1.4;

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Best Local
Matches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to new Proteus mirabilis polypeptides and polymucleotides. The invention also relates to antibodies against the polypeptides, methods for producing the polypeptides, a method of generating vaccines for immunising an individual against P. mirabilis, a generating vaccines for immunising an individual against P. mirabilis polypeptide and a method for screening test compounds for ani-bacterial polypeptide and a method for screening test compounds for ani-bacterial exactivity. The polypeptides and polymucleotides are useful as molecular targets for diagnosing, preventing and treating pathological conditions resulting from bacterial infection, as reagents for diagnosis of bacterial diseases, as components of antibacterial vaccines, as targets for antibacterial diseases, as targets for antibacterial diseases, as targets squence represents a proteus mirabilis polypeptide of the invention.
                                                                                                                                                       239
                                                                                                 ------DAAKLKLTTEIAAIGEIKTETETTRFYVDYDDLMLSLLKEAAKKMINTCNE 287
  LALDSQLTND-----FSEKSSYFQSQVDKIRKEAYAGAAAGVVAGPFGLIISYSIAAGV 202
                                                             139
                                                              A----
                                                                                                                                                       -----AFNOLKDIQONITOTQKE
                                                                                    --KLKSVQNFFTTLSNTVKQANKDI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New Proteus mirabilis polypeptides and polynucleotides, useful as reagents for diagnosis of bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as
                                                                                                                                                                                                                                                                                                                                                       Proteus mirabilis infection; bacterial infection; antibacterial;
                                                        104 NVLEERKKANQSETNARYEEELDNLESQIDSIKNEK----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                 ADF07734 standard; protein; 1129
                                                                                                                                                           200 FLEHTINENEAKKSRLDSRLVE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                biocontrol agents for plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0128706P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-APR-2000; 2000US-00543681
                                                                                                                                                                                    YOKRHGKKTLFEVPE 302
                                                                                                                                                                                                         240 YOS--SKKSMEKVEQ 252
                                                                                                                                                                                                                                                                                                                                       Bacterial polypeptide #3847
                                                                                                                                                                                                                                                                                                                 12-FEB-2004 (first entry)
                                                                                        203 VEGKLIPELKN----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1129 AA;
                                                                                                                                                                                                                                                                                                                                                                                               Proteus mirabilis.
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                                                                                                                                                                                                                                                                                                                                                                          immunostimulant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             12-AUG-2003
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                                                                                                                                                                                                                                                                                           ADF07734;
                                                                                                                                                                                       288
                                                                                                                                        237
                                                                                                                                                                                                                                                RESULT 17
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useful for
infection
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     13;
                                                                             485
                                                                                                                                                                                    DDGITKLINEAQKS--LLVSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDKIRKEAY 178
                                                                                                                                                                                                                                                                                   601 AAADDIVNKIIGAPSGIVPSELIPDGLVKRAGFTKDRTLNIPDERIKDYLESDVNY--VM 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   an Moraxella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid encoding an Moraxella catarhalis polypeptide. The nucleic acid is useful for preparing a composition for diagnosing, preventing or treating infection caused by Moraxella catarrhalis. The present sequence represents the amino acid sequence of a M. catarrhalis protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --YSOA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                               63 GDIKTILIMDSQDKYFEATQTVYEWCGVATQL--LAAYILLFDEYNEKKASAQKDILIKVL
                                                                                                                                         486 SGKKSLLMDDINKY----QKIINEKSAVEVELNSLSNLAKLNKTQTRRQATLQRK--LQRI
                                                                                                                                                                                                             AGA---AAGVVAGPFGLIISYSIAAGVVEGK-----LIPE--LKNKLKSVQNFFTTL
                                        3 EIVADKTVEVVKNALETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid encoding a Moraxella catarrhalis polypeptide, preparing a composition for diagnosing, preventing or treating caused by Moraxella catarrhalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 718;
       46;
                                                                                                                                                                                                                                                                                                                                   226 SNIVKQANKDIDAAKLKLITEIAAI---GEIKTETETTRFYVDYDDLM 270
                                                                                                                                                                                                                                                                                                                                                          6 ADKTVEVVKNAIETADGALDLYNKYLDOVIPWOTFDETIKELSRFKOF
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         Indels
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21.0%; Pred. No. 0.86;
.ive 57; Mismatches 130;
         Mismatches 120;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADL05067 standard; protein; 718 AA
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               55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M. catarrhalis protein #833
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Best Local Similarity 21...
Best Local Similarity 70; Conservative
23.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Moraxella catarrhalis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Moraxella catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-178127/17.
N-PSDB; ADL03147.
Similarity
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                   67;
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Length 1129;

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Query Match

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RESULT 20
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ATEKLEVAKEATQ------DKVEKTQSLVEDIKDKAQSLQEDAADTVEALKQA 149
                        ASVLVGDIKTLLMDSQDKYFEATQTVYEWC-----GVATQLLAAYILLFDEYN--- 105
                                         206 TDQDQEKQTLKDKAVQAATAAKRKVEDVVDDVKHTTESFKNTASGKIDEIKQAAVDKTEE 265
                                                                                                                           LINDFSEKSSYFQSQVDKIRKEAYAGAAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNK 214
                                                                                                                                             LKSVQNFFTTLSNTVKQANKDIDAAKLKLTTEIAAIGEIKTETETTRFYVDYDDLMLSLL 274
                                                                                                                                                                                               ---EKKASAQKDILIKVLDDGITKLNEAQKSLLVSSQSF-NNASGKL----LALD--SQ 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 4824; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster polypeptide SEQ ID NO 4824
                                                                                                                                                                                                                                 KEAAKKMINTC-------297
                                                                                                                                                                                                                                                          KEEAQALQTNAQESLQAAKAAGEEYDATHEDKGL 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Myers EW;
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                                                                                                                                                                                                                                                                                                                        ABB59344 standard; protein; 2056
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11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  interactions.
                                                                                                                                                                                                                                                                                                                                                                           26-MAR-2002
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                        28
                                                                                                                                                                               215
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SELGEKCTKLOQEAENITNOLEEAELKASAAVKSASNMESÕLTEAQOLLEEETROKLGLS 1418
                                                                                                                                                                                                                                                                       1302 KTVLEKAKGTLEAENADLATELRSVNSSRQENDRRRKQAESQIAELOV---KLAEIERAR 1358
                                                                                                                                                                                                                                                                                                                                             1536 FDKILAEEKA------ISEQIAQERDTAEREAREKETKVLSVSRELDEAFDK 1581
                                16;
                                                                                                                                                                                                                                                                                                                                                                            264
                                                                                                                                                                                      -----KASAQKDI-LIKVLDDGIT 125
                                                                                                                                                                                                                                                                                                                207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antibacterial; fungicide; insecticide; polymorphism; genetic analysis; detection; food; gene expression; plant; animal; microorganism; toxin; antibiotic; biopesticide; virulence factor; disease model; plague;
                                                                                                                                                                                                                   SKLRQIESEKBALQEQLEEDDEAKRNYERKLABVTTQMQEIKKKABEDADLAKELEEGKK
                                                                                                                                                                                                                                                  126 KLN-----EAQ-KSLLVSSQSFNNASGKL-----LALDSQLTNDFS-EKSSYFQSQ
                                                                                                                                                                                                                                                                                                                                                                            208 IPELKNKLKSVQNFFTTLSNTVKQANK---DIDAAKLKLTTEIAAIGEIKTETETTRFYV
                                                             --- DQVIPWQTFDETIKELSRFK
                                                                                                                          QEYSQAASVLVGDIKTLLMDSQDKYFEATQTVYEWCGVATQLLAAYILLFDEYNEK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomic sequence of Photorhabdus luminescens and encoded polypeptides, useful e.g. as therapeutic antimicrobials and agricultural pesticides
                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Danchin A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to the isolation of genes and their encoded proteins from Photorhabdus luminescens. The isolated sequences are
                              Indels 140;
 Length 2056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Œ,
                                                                                                                                                                                                                                                                                                              170 VDKIRKEAYAGAAAGVVAGPFGLIISYSIA-----AGVVEGKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kunet
; Score 115; DB 4; Le; Pred. No. 4; 48; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Photorhabdus luminescens protein sequence #1200.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Frangeul L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; SEQ ID NO 1200; 1205pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ą.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; protein; 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (INSP ) INST PASTEUR.
(CNRS ) CNRS CENT NAT RECH SCI.
7.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --pbiQiT---EDAK 1645
                                                               KNAIETADGALDLYNKYL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-FEB-2002; 2002WO-IB003040.
                                                                                                                                                                                                                                                                                                                                                                                                                                          DYDDLMLSLLKEAAK 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-FEB-2001; 2001FR-00001659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Photorhabdus luminescens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Taourit S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-148459/14.
Query Match
Best Local Similarity
Matches 80; Conserv
                                                                                                                                                                                       WO200294867-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               whooping cough.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Duchaud E, T.
Buchrieser C;
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                                                                                                                                                        1359
                                                                                                                                                                                                                     1419
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                                                                                                                          22
                                                                                                                                                                                      108
                                                                                                                                                                                                                                                                                 1479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABM68103
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sources of probes and primers for detecting the genome of P. luminescens and related species; to study polymorphisms; for gene analysis and for detection/amplification of the genes. Antibodies (Ab) raised against the polymorphides (Ab) raised against the polymorphides explored to selection/identification of polymorphides expression of the density that correct are used for detection/identification of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that carry a gene-containing vector are used to select compounds that carry a gene-containing vector are used to select compounds that can animals or microorganisms other than P. luminescens and are able to alter response or sensitivity to toxins and antibiotics produced by P. crecombinant production of the proteins, particularly toxins and carried antibacterials useful as insecticides, bactericides and thugh that the proteins, particularly toxins and carried are sensitive to P. luminescens encoded toxins or antibiotics) and as care sensitive to P. luminescens encoded toxins or antibiotics) and as care sensitive to P. luminescens and the proteins are as virulence factors and for identifying targets of human diseases for which P. conditions of the genes and whooping cough). This sequence represents one of the isolated P. luminescens sproteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 6; Length 582;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.6%; Score 114.5; DB 6;
20.2%; Pred. No. 0.79;
ive 58; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 20.2%
nes 64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 582 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loc
Matches
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-----SQVDKIRKEAYAGAAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNKLKSVQN 220 221 FFTTLSNIVKQANK----DIDAAKLKLTTEIAAIGEIKTE--TETTRFYVDYDDLMLSL- 273 FEATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQKDILIKV------LDDGITK 126 193 YEYSEIKKESAHKIEKFQSAVEVIVDNTVDSPITLDNNDFİKIQNEIKNELYDLIDYQTR 252 127 LNEAQKSLLVSSQSFNNASGKLLALDS--QLTNDF----SEKSSYFQ----- 167 133 LETPPPAYYFLPFYIDQIKSWSSPWNSFENLGQYSNWKGPLIKYFTGYLKPEHFDIEENI 192 17 IETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASVLVGDIKTLLMDSQDKY 76 -----LKEAAKKMINT 284 ||: ||:::| 405 NSSIKELKKDQKKLLST 421 17 셤 g ઠ d 셤 à ò g ò 8 유 ò

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Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                               Protein encoded by Prokaryotic essential gene #28523.
       ABU42996 standard; protein; 1189 AA.
                                                                                                                                                                    21-MAR-2002; 2002WO-US009107.
                                                                                                                                                                                      21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
                                                                                                         Staphylococcus epidermidis.
                                              (first entry)
                                                                                                                              WO200277183-A2.
                                               19-JUN-2003
                                                                                                                                                  03-OCT-2002
                            ABU42996;
ABU42996
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The invention relates to an isolated nucleic acid comprising any one of the besula antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: cof the nucleic acid inhibits proliferation of a cell. Also included are: coll comprising a promoter operably linked to the nucleic acid; (2) a host cell containing the vector; (3) an isolated conclained by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibiting cellular continuous conclained by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation; (7) identifying a compound that influences the activity of proliferation, or that has an activity against a biological pathway in which a proliferation required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies compound's activity; (11) a culture comprising strains in which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the extent confouct is overexpressed or underexpressed; (12) determining the extent of compound's activity; (11) a culture compound that inhibits the strains; or (13) identifying the target of a compound that inhibits the strains; or (13) identifying the target of a compound that inhibits the compound that inhibits the strains; or (13) identifying the target of a compound that inhibits the compound that inhibits the strains; or (13) identifying the target of a compound that inhibits the compound that inhibits the strains; or (13) identifying the target of a compound that inhibits the compound that inhibits are useful for collieration of an organism. The antisense nucleic acids are useful for the collinar proliferation to the strains; or conditional a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                221 KEMEGSDVIVIVSDI-------DHYTEDNĢRLDERLMHLKSQQAEKEGQQAQINQLLQR 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     273 Y-------KGKRQON-----DYDIEKLN---YELVKATENYEQLSGKLNVLEERKK 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ND-----FSEKSSYFQSQVDKIRKEAYAGAAAGVVAGPFGLIISYSIAAGVVEGKLIPE 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of K. pneumoniae or P. seruginosa. Note: The, sequence data for this patent did not form part of the princed specification, but was obtained in electronic format directly from NIPO at
                                                                                                                                                                                                                                                                          New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 VADKTVEVVK-----NAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAA 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S-----VLVGDIKTLLMDSQDKYFEATQTVYEWC-------GVATQLLAA
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                                                                                                                                  Zyskind JW;
Xu HH;
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                                                                                                                                       Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 6;
                                                                                                                                       Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.6%; Score 114.5; D
20.1%; Pred. No. 2.1;
tve 45; Mismatches
                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 70920; 1766pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                            Malone C,
Carr GJ,
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
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                                                                                                  (ELIT-) ELITRA PHARM
                                                                                                                                            Zamudio C,
Trawick JD,
                                                                                                                                                                                                                     2003-029926/02
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                                                                                                                                                                                                                                                                                                                                                                                      Claim 25;
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96

---AONEKLLAD

314 NOSETNARYEEELDNLESQIDSIKNEK----

211 LKN-

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---KLKSVQNFFTTLSNTVKQANKDI------

SUVFLLYGHDYSKPLASVKAGTLK-LNVDDTGLHFBAELTDTTYSNDVYENISKGVVDSM 136

----RFKQEYSQ-AASVLVGDIKTLLMDSQDKYFEATQT-----VYEWC--GVATQL

ELTADSPKVEKENEKQPTDGKT1SGYALKFGQPSKDL-GGFVEVITP-----EALKEVDL

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77

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94 LAAYILLFDEYNEKKASAQKDILIKVLDDGITKLNEA------QKSLLVSSQSF--- 141
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an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid derived from Enterococcus faecium encoding a
Enterococcus faecium polypeptide useful for detection, prevention and
treatment of a pathological condition resulting from a bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vaccine, urinary tract infection, bacteraemia, endocarditis, wound, abdominal-pelvic infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.6%; Score 114; DB 7; Length 515;
13.3%; Pred. No. 0.74;
.ve 58; Mismatches 111; Indels 128;
                                                                                                                                      263
                                                                                                                                                                                    : | : | : | : | 412 | 442 | 442 | 442 | 442 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 443 | 44
                                                                                                                                 237 -DAAKLKLTTE-IAAIGEIK----TETETTRFY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              one if the disclosed E. faecium proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B. faecium protein sequence SEQ ID 5317.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                              ADC95690 standard; protein; 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-00107532,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97US-0051571P,
98US-0085598P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bush D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enterococcus faecium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Joucette-Stamm LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2003-799836/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ADC92036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 515 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JS6583275-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Si
Matches 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              infection
                                              350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADC95690;
                                                                                                                                                                                                                                                                                                                                                          RESULT 22
                                                                                                                                                                                                                                                                                                                                                                                               ADC95690

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243
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--NNASGKLLALDSQLTNDFSEKSSYFQSQVDKIRK------EAYAGAAAGVV 186
                                                                                                                             244 DG-----VTTVNAAAVVPEBVIGEVFDLKRSNYNLAQXATVKTVSNGQGKYPVATNQQ-- 296
                                                                                                                                                                                         The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an B-value greater by a factor of 3 than the B-value of most similar non-plant sequences are selected. The jobypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
                                                               187 AGPFGLIISYSIAAGVVEGKLIPELKNKLKSVQNF----FTTLSN-----TVKQAN
                                                                                                                                                                      -----DDLMLSLLKEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; SEQ ID NO 1241; 261pp + Sequence Listing; English.
                                                                                                                                                                     KDIDAAKLKLTTEIAAIGEIKTETETTRFYVDY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Herbicidally active polypeptide SEQ ID NO 1241.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Herbicidal; plant; agriculture; herbicide
                                                                                                                                                                                                                                      296
                                                                                                                                                                                                                                                        349 KDQLAKLVENTDNKHIMDLLKTFTKKT 375
                                                                                                                                                                                                                                      ---- AKKMINTCNEY ---- QKRHGKKT
                                                                                                                                                                                                                                                                                                                                                    Ä
                                                                                                                                                                                                                                                                                                                                                    ABB92030 standard; protein; 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-AUG-2001; 2001WO-EP009892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-AUG-2001; 2001WO-EP009892
                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-269010/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Weidler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 796 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200210210-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tietjen K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     herbicides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organisms
                                           142
                                                                                                                                                                                                      297
                                                                                                                                                                                                                                                                                                                                                                                    ABB92030;
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21;

Gaps

-----ALDLYNKYLDQVIPWQTFDETIKELS- 48

EIVADKTVEVVKNAIETADG-

m

23.3%;

Similarity 23.3 90; Conservative

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Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid derived from Enterococcus faecium polypeptide having Enterococcus faecium polypeptide having one of 10 fully defined sequences given in the (or comprising 40 equential nucleotides chosen from any of the nucleic acids, its complement or sequences hybridising to it). Also included are a recombinant vector comprising the nucleic acid operably linked to transcription regulatory element, a cell comprising the vector and a single-stranded probe comprising the nucleic acid. The nucleic acids are chosen from 3654 disclosed sequences encoding 3654 disclosed proteins.
                                 10;
                                                                                                                                                                   640
                                                                                                  DEYNEKKASAQKDILIKVLDDGITKLNEAQKSLLVSSQSFNNASGKLLAL-----DS 153
                                                                                                                                             204
                                                                                                                                                                                                            641 AEMAGVLKSMGLELDAVKONOKDTAEQIYAANENLOEKLEKLNOEITSKIEEVVRTPEIK 700
                                                        101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid derived from Enterococcus faecium encoding Enterococcus faecium polypeptide useful for detection, prevention and treatment of a pathological condition resulting from a bacterial
                                                                                                                                                                 BATSLKKEINKRFQEAVDRPEIREKVEAİKAEVASSGASSFDELPDALKEKVLKTKGEVE
                                                                                                                                                                                        GKLIPELKN----KLKSVQNFFTTLSNTVKQANKDIDAAKLKLTTBIAA-IGBIKTETETT
                                                       ETIKELSRFKQEYSQAASVLVGDIKTLLMDSQDKYFEATQTVYEWCGVATQLLAAYILLF
                                                                            EQILKAKETSTEAEPSSEVLNEMIEKLKSEIDDEYTEAAIAV----GLEERLTA----MR
                                                                                                                                            QLTNDFSEKSSYFQSQVDK-----IRKEAYAGAAAGVVAGPFGLIISYSIAAGVVE
                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  Vaccine; urinary tract infection; bacteraemia; endocarditis; wound; abdominal-pelvic infection.
                                    42;
              Length 796;
           7.6%; Score 114; DB 5; Length 790
24.9%; Pred. No. 1.3;
tive 44; Mismatches 119; Indels
                                                                                                                                                                                                                                     261 RFYVDYDDLMLSLLK-EAAK--KMINTCNEYOK 290
                                                                                                                                                                                                                                                          S------MVELLKVETAKASKTPGVTEAYOK 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; SEQ ID NO 3944; 243pp; English.
                                                                                                                                                                                                                                                                                                                                                                                 E. faecium protein sequence SEQ ID 3944
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THERAPEUTICS CORP
                                                                                                                                                                                                                                                                                                                   ADC94317 standard; protein; 1196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-0051571P.
98US-0085598P.
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                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bush
                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       Enterococcus faecium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-799836/75.
N-PSDB; ADC90663.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Doucette-Stamm LA,
                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENO-) GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-JUL-1997;
14-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               US6583275-B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                01-JAN-2004
                                       68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              infection
                 Query Match
Best Local S
Matches 68
                                                                                                                                                                                                                                                                                                                                          ADC94317;
                                                                                                        102
                                                                                                                             523
                                                                                                                                                   154
                                                                                                                                                                        581
                                                                                                                                                                                                                                                               701
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resulting from B. faecium bacterial infection (e.g. urinary tract infection, bacteraemia, endocarditis, wounds and abdominal-pelvic infection) and for screening drugs such as agonists and antagonists. The nucleic acid is useful for recombinant production of Candida albicans derived peptides or antisense polypeptides. Pharmaceutical compositions and vaccines containing the nucleic acid are useful for preventing or treating Enterococcus faecium infections. The present sequence represents
                                                                                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QA-----NKDIDAAKLKLTTEI--AAIGEIKTETE-----TTRFYVDYDDLMLSLLK 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 334 KVKHFEKLQESLMKAAAEKETEIQKAEANLİKTQQELEKYQKSTKELLAELRDQYVDLMQ 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptidoglycan-binding; peptidoglycan-associated site; outer-membrane; bacterial infection; vesicle-shedding; Bleb; filter sterilised; detergent; deoxycholate; homogeneity; antibacterial; vaccine; TolQ; TolA;
                                                                                                                                                                                                                                                                                                                                                                                                                                         52 QEYSQA-ASVLVGDIKTILLMDSQDKYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKAS 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQKDILIKVLDDGITKLNEAQKSLLVSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQV 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         230
                                                                                                                                                                                                                                                                                                                                                                                               222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified; Tol gene;
                                                                                                                                                                                                                                                                                                                                                                                 DKIRKEAYAGAAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNKLKSVQNFFTTLSNTVK
                                                                                                                                                                                                                                                                                                                                                  5 VADKTVBVVK------NAIETADG---ALDLYNKYLDQVIPWQTFDBTIKELSRFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107;
                                                                                                                                                                                                                                                                Length 1196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    n.,
                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thonnard
nucleic acids is useful for diagnosing pathological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hyperblebbing; Gram-negative bacterium; genetically
                                                                                                                                                                                                                                                                     DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EAAKKMINTCNEYQKRH-----GKKTLFEVPEV 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POA--AVGNELKYLERQYIQETAKSKOTLAKQSEV 426
                                                                                                                                                                                                                                                                                                             111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Poolman J,
                                                                                                                                                                                                                                                                     7.5%; Score 113.5; I
20.0%; Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                 50; Mismatches
                                                                                                                                                                                 one if the disclosed B. faecium proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Moraxella catarrhalis TolA protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DVLOERT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neyt CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABG80428 standard; protein; 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-FEB-2001; 2001GB-00003171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-FEB-2002; 2002WO-EP001361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OmpCD; xOmpA; PAL-1; PAL-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                               1 Similarity 20.0
67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Berthet FJ, Denoel P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Moraxella catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-657509/70.
N-PSDB; ABS66198.
                                                                                                                                                                                                                                Sequence 1196 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200262378-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        231
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                                                                                                                                                                                                                                                                            Query Match
Best Local 8
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The present invention relates to a new hyperblebbing Gram-negative bacterium genetically modified by one or more processes selected from down-regulating expression of one or more processes selected from peptidoglycan-binding activity by mutation of one or more gene(s) encoding a protein comprising a peptidoglycan-associated site. The invention is useful in a method of treatment of the human or animal body. The invention is also useful for protecting an individual against a bacterial infection. The invention has improved outer-membrane vesicle-bedding properties. Blebs are more easily made in higher yield from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention, and are more homogeneous in nature and can be more readily filter sterilised. The blebs can be made and harvested without the use of detergents such as deoxycholate, thus obviating chromatography purification and ultra centrifugation steps. Vesicles prepared from the purification have reduced particle size (allowing sterile filtration through 0.22 mum pores), increased batch homogeneity, and a superior yield. The present amino acid sequence represents a Moraxella catarrhalis protein,
                        Novel hyperblebbing Gram-negative bacterium that has been genetically modified by down-regulating expression of Tol genes, and/or attenuating peptidoglycan-binding activity useful for treating bacterial infection.
                                                                                                                                                Disclosure; Page 66; 71pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             described in the invention
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Sequence 458 AA;

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ASVLVGDIKTLLMDSQDKYFEATQTVYEWC-----GVATQLLAAYILLFDEYN--- 105
                                                                                                                                                                                                                           205 TDQDQEKQTLKDKAVQAATAAKRKVEDVVDDVKHTTESFKNTASEKIDEIKQAAVDKTEE 264
                                                                                                                                                                                                                                                                                              -----NOLFEQGKSALDEKVQELGEYGA-TEKINAVSEYVDLATQVI 365
                                                                                                                                                                     AS---DKVETTKAEAQSLKDDATQT-FESAKQAVEGKVEAIKEQVLDQVDSLKDDTDQDN 204
                                                                                                                                                                                                      ---EKKASAQKDILIKVLDDGITKLNEAQKSLLVSSQSFNNASG-----KLLALD--SQ 154
                                                                                                                                                                                                                                                                       LTNDFSEKSSYFQSQVDKIRKEAYAGAAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNK 214
                                                                                                                                                                                                                                                                                                                                          LKSVQNPFTTLSNTVKQANKDIDAAKLKLTTEIAAIGEIKTETETTRFYVDYDDLMLSLL 274
                                   78;
7.5%; Score 113; DB 5; Length 458; 20.4%; Pred. No. 0.76; tive 57; Mismatches 131; Indels
                                                                  6 ADKTVEVVKNAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQE-
                                                                                                                                                                                                                                                                                                                                                                                                                                      KERAQALQTNAQESLQAAKAAGEEYDATHEDKGL 399
                                                                                                                                                                                                                                                                                                                                                                                                           275 KEAAKKMINTC-----NBYOKRHGKKTL 297
                                   Conservative
               Local Similarity
nes 68; Conserv
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Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                    encoded by Prokaryotic essential gene #15619.
                 ABU30092 standard; protein; 1020 AA
                                                    (first entry)
                                                                                                        Enterococcus faecium
                                                                                                                         WO200277183-A2.
                                                    19-JUN-2003
                                  ABU30092;
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03-OCT-2002.

267

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311

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The invention relates to an isolated interest of the compression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid, (2) a host cell containing the vector; (3) an isolated containing the vector; (3) an isolated are:

(2) the polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid, (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid, (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular compliferation, or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for conjustion of the gene product or that has an activity against a biological pathway to which a proliferation, or that inhibits soliferation of an activity against a biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compunity of a culture comprising strains in which the gene or which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the culture or collection of strains; or (13) identifying the target of a compound that inhibits the captained collection of an organism. The antisense nucleic acids required for cellular proliferation of solate canning for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational
                                                                                                                                                                                                                                                                                                                                                                                                                  screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "74 DKYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQKDILIKVLDDGITKLNEAQKS 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLVSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVDKIRKEAYAGAAAGVVAGPFGLI 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ETADG---ALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQA-ASVLVGDIKTLLMDSQ
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Xu HH;
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                                                                                                                                                                                                                                                                                                                                                                                                               New antisense nucleic acids, useful for identifying proteins or so for homologous nucleic acids required for cellular proliferation isolate candidate molecules for rational drug discovery programs.
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                                                                                                                                                                                                                                                                  Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :| : | : | : | : | 268 ILAKQRKENAQADRLIEKNQVLIDLSEKLKQTEGQKDVLQERT--
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 25; SEQ ID NO 58016; 1766pp; English.
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                                                                                                                                                                                                                                                                  Malone C,
Carr GJ,
                                                                    2001US-00815242.
2001US-00948993.
2001US-0342923P.
2002US-00072851.
                      21-MAR-2002; 2002WO-US009107
                                                                                                                                                                    2002US-0362699P
                                                                                                                                                                                                                                                                    Malone
                                                                                                                                                                                                                  (ELIT-) ELITRA PHARM INC.
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Trawick JD,
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                                                                      21-MAR-2001;
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08-FEB-2002;
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335 ESVQEKYNDTAQSLRDVTAQLESYKSSTLKEIEDLKLENLTLQEKVAMAEKSVEDVQQQI 394
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               RHAWM 1 (AAR99673), or Receptor for Hyaluronic Acid Mediated Motility, is a hyaluronan receptor protein which is involved in cell locomotion or motility and cell proliferation and transformation. Its amino acid sequence was deduced from a CDNA clone (AAT34499) obtd. from murine 3T3 cells and a genomic sequence (AAT34500) from a mouse fibroblast genomic library. 2 Alternative mRNAs for RHAWM 1 were found, RHAWM 1A (see also AAT34523) and RHAWM 1B (AAT34524), that had identical translated proprisons increased expression of RHAWM 1 protein is indicative of a poor prognosis for breast cancer. The protein can be used to suppress or control a timour by modulating the interaction of cell-associated RHAMM
                                                                                                                                                                                                                                                                                                                                                                                                 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RHAMM 1-2a; receptor for hyaluronic acid mediated motility; hyaluronan receptor; cell locomotion; cell proliferation; breast cancer;
                                                                                                                                                                                                                                                                                                              1 MTEIVADKTVEVVKNALETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASV
                                                                                                                                                                                                                                                                  61 LVGDIKTLLAMDSQDKYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQKDILIKVL
                                                                                                                                                                                                                                                                                                                                               121 DDGITKLNEAQKSLL-VSSQSFNNASGKLLAL-DSQLTN-DFSEKSSYFQSQVDKIRKEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 606;
                                                                                                                                                                                              / Match 7.4%; Score 112; DB 2; Length 60. Local Similarity 20.5%; Pred. No. 1.4; length 60. conservative 63; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55. .79
/note= "exon 2A-encoded region"
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MANITOBA CANCER TREATMENT &
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Claim 2; Page 40-42; 117pp; English.
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                                                                                                                                                                              Sequence 606 AA;
                                                                                                                                                      with its ligand
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AAR99675
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                                                         --AAIGEIKTETE-----TTRFYVDYDDLMLSLLKEAAKKMINTCNEYQKRH----- 292
                                                                               354 QKAEANLİKTQQELBKYQKSİKBLLAELRÖQYUDLMQEQA--AVGNELKYLERQYIQETA 411
                                                                                                                                                                                                                                                                                                 RHAWM 1; receptor for hyaluronic acid mediated motility;
hyaluronan receptor; cell locomotion; cell proliferation; breast cancer;
                          ---NKDIDAAKLKLTTEI
                                                                                                                                                                                                                                                                             motility RHAMM 1.
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594. .596
/label= N-glycosylation_site
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label= Hyaluronan_binding_domain-I
           194 ISYSIAAGVVEGKLIPELKNKLKSVQNFFTTLSNTVKQA--
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(MANI-) MANITOBA CANCER TREATMENT & RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                           779. 281
/label= N-glycosylation_site
/label= N-glycosylation_site
/label= N-glycosylation_site
/label= N-glycosylation_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42. .344 Tabel= N-glycosylation_site 73. .375 Tabel= N-glycosylation_site
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|label= N-glycosylation_site
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/label= N-glycosylation_site
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| label= N-glycosylation_site
                                                                                                                                                                                                                                                                              Receptor for hyaluronic acid mediated
                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                      AAR99673 standard; protein; 606 AA.
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/label= Hy
                                                                                                                                                                                                                                                         (first entry)
                                                                                                                  293 -GKKTLFEVPEV 303
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KSKQTLAKQSEV 423
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                                                                                                                                             412
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                                           312
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Unidentified
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                                                                                                 RHAMM 1-2a (AAR99675) is an alternatively spliced variant of RHAMM 1 (AAR99673) (receptor for hyaluronic acid mediated motility), a protein involved in cell locomotion or motility and cell proliferation and transformation. It differs from RHAMM 1 by an insertion of 25 amino acids see also AAR99674) between amino acids 54 and 55 of RHAMM 1, resulting from an alternatively spliced exon 2A (AAR34502). RHAMM 1, 2a is the isoform that is overexpressed in tumours. Determination of the level of RHAMM 1-2a in a sample can be used to assess the prognosis of a tumour suppress or control a tumour. The RHAMM 1.2a protein can also be used to associated RHAMM with its ligand
                                                                                                                                                                                                                                                                                                                                               LVGDIKTLLMDSQDKYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQKDILIKVL 120
                                                                                                                                                                                                                                                                                                                                                                          DDGITKLNEAQKSLL-VSSQSFNNASGKLLAL-DSQLTN-DFSEKSSYFQSQVDKIRKEA 177
                                                                                                                                                                                                                                                                                                                                                                                                                  178 YAGAAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNK-----LKSVQNFF----TTLS 226
                                                                                                                                                                                                                                                                                                                                                                                                                                     LTAESTNQ-----EYA-----RMVQDLQNRSTLKEERIKEITSSFLEKITDLK 462
                                                                                                                                                                                                                                                                                         1 MTEIVADKTVEVVKNAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASV 60
                                       encoding
                               Receptor for hyaluronic acid-mediated motility protein, and DNA encodi
it - useful to treat or prevent diseases associated with the receptor,
e.g. breast cancer.
                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NTVKQANKDI ------DAAKLKLTTEIAAIGEIKTETETTRFYVDYDDL 269
                                                                                                                                                                                                                                                                      62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.4%; Score 112; DB 2; Length 631; 20.5%; Pred. No. 1.4; ive 63; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Multiprotein complex; eukaryote; drug target; diagnosis.
                                                                               Claim 8; Page 50-52; 117pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABR53560 standard; protein; 1875 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence #SEQ ID 1985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                          Similarity 20.5 60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae
        WPI; 1996-310997/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CELL-) CELLZOME AG.
                     N-PSDB; AAT34525
                                                                                                                                                                                                                             Sequence 631 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP1258494-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABR53560;
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Best Local 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              463
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The invention relates to multiprotein complexes from eukaryotes. Proteins of the invention and DNA sequences encoding them are given in records ABR52568-ABR53903 and ACC60610-ACC61944 respectively. The complexes are obtainable by using a protein as a bait and isolating the set of proteins which is attached thereto from cells. Such protein complexes may comprise up to 30 distinct proteins. Protein complexes of the invention are useful for diagnosing a disease or disorder, or as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder. Note: The sequence data for this pastent is not represented in the printed specification, but is based on sequence information supplied by the European Patent Office. The complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : |:|:: ::: | :: | 14 | | 15 | 16 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 174 | 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137 SSQSFNNASGKLLALDSQLTN----DFSEKSSYFQSQVDKIRKEAYAGAAAGVVAGPFGL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    193 IISYSIAAGVVEGKL-IPELKNKLKSVQNFFTTLSNTVKQANKDIDAAKLKLTTEIAAIG 251
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                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated protein complexes useful for diagnosing a disease or disorder, or as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of disease
       80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90,
       Kuester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 1985; 17pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.4%; Score 112; DB 6; Length 1875; 19.7%; Pred. No. 6.3; ative 66; Mismatches 122; Indels 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EIKTETETTRFYVDYDDLMLSLLKEAAKKMINTCNE--YOKRHGKK 295
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       Кгиве UD,
i P, Krause R, K
Superti-Furga GD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein complex; drug target; diagnosis.
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       Grandi P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
Bauer A, Gavin A, Grand.
Marzioch M, Schultz JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                              WPI; 2003-250078/25.
N-PSDB; ACC61602.
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les 68; Conserv
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804

Wed Jan

ADF04710 standard; protein; 808 AA.

ADF04710

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The invention relates to novel protein complexes comprising a first and a second protein, or its derivative, fragment, homologue or variant. The second proteins are selected from given protein complexes, which are not defined in the specification. The variants are encoded by nucleic acids that the specification. The variants are encoded by nucleic acids that the specification complexes are nesful as targets for an active conditions. The protein complexes are useful as targets for an active conditions. The protein complexes are particularly useful as drugs targets for the treatment or preventing of a disease or disorder. The complexes and methods above are useful in diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject. These are also useful in screening for a drug for treatment or prevention of a disease or disorder. The molecule that modulates the amount, activity or protein components of the complex is useful for the manufacture of a medicament or prevention of a disease or disorder. The sequence distance did not form part of the invention. (Note: the sequence data for this patent did not form part of the printed specification but was corrected the did not form part of the printed specification but was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            193 IISYSIAAGVVEGKL-IPELKNKLKSVQNFFTTLSNTVKQANKDIDAAKLKLTTEIAAIG 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         targets in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New proteins and protein complexes from eukaryotes, useful as targets drug screening, or in diagnosing or screening for the presence of a disease or disorder, or a predisposition for developing a disease or disorder in a subject.
                                                                                                                                                                                                                                                              Gavin A, Superti-Furga G, Kuester B, Schultz J; d, Grandi P, Krause R, Kruse U, Merino A, Bauch A; Leutwein C, Rick J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 2369; 13pp; English.
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                                                                 20-DEC-2002; 2002EP-00102902.
                                                                                                                               20-DEC-2001; 2001EP-00130253
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                                                                                                                                                                                                                                                                                Bauer A, Granu. ... Marzioch M, Granu. ... A. Leutwein C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
hes 68; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-638460/61.
                                                                                                                                                                                                       (CELL-) CELLZOME AG
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27-AUG-2003.
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ED----LLQKIDKHFNKES-----SLNILLSTIEK 342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238 AAKLKLITEIAAIGEIKTETETTRFYVDYDDLMLSLLKE---AAKKMINTCNEYQKRHCK 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GDIKTLLMDSQDKYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQKDILIKVLDD 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               257 IIESEAKKIVEKKIQTSETIQELINNAI--LASWV---RTGRELHKYKQEKCAFCGNILP 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to new Proteus mirabilis polypeptides and polymucleotides. The invention also relates to antibodies against the polypeptides, method of generating the polypeptides, method of generating vaccines for immunising an individual against P. mirabilis, a method for evaluating a compound for the ability to bind a P. mirabilis polypeptide and a method for screening test compounds for anti-bacterial activity. The polypeptides and polymucleotides are useful as molecular targets for diagnosing, preventing and treating pathological conditions resulting from bacterial infection, as reagents for diagnosis of bacterial diseases, as components of antibacterial vaccines, as targets for antibacterial diseases, as bio-control agents for plants; This sequence represents a Proteus mirabilis polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 IVADKIVEVVKNALETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQE-YSQAASVLV 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              343 ELLKIPNLLK-IKTIDFYSNFANDLNTLNDDLSKLSIDYSKSLSLIKEQIEKRKSDIFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNKLKSVQNFFTTLSNT--VKQANKDID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----PLEFHSSVSVEDSINELRYSYE---KIRSKSNDFTKSLNTEQVKARN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                         New Proteus mirabilis polypeptides and polynucleotides, useful as reagents for diagnosis of bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for plants.
                                                                                         Proteus mirabilis infection; bacterial infection; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 808;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.4%; Score 111.5; D
22.0%; Pred. No. 2.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 4995; 870pp; English.
                                                                                                                                                                                                                                                                                                               (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                              05-APR-2000; 2000US-00543681.
                                                                                                                                                                                                                                                                                99US-0128706P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22.0%;
                                                             Bacterial polypeptide #823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-895291/82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
hes 66; Conserv
                                                                                                                                              Proteus mirabilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 808 AA;
                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ADF00538
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                                                                                                                  immunostimulant.
                                                                                                                                                                                                                                                                                 09-APR-1999;
                                                                                                                                                                               JS6605709-B1.
                             12-FEB-2004
                                                                                                                                                                                                                                                                                                                                                  Breton GL;
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ADF04710;
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8 셤 8 용 ð EIKTETETTRFYVDYDDLMLSLLKEAAKKMINTCNE--YQKRHGKK 295 DEKTSLED-----KISLLKE---QMFNLNNBELDLQKKGMEK 992

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Sequence 435 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a polypeptide (I) which binds to hyaluronic acid (HA) and thereby inhibit the binding of HA to RHAMM teceptor hyaluronic acid mediated mctility), comprising an amino acid sequence of P16, P-16d, human P32, murine P32, murine S3, human S3, murine S7, human S7, murine V2 and human V2. Also described: (1) a pharmaceutical composition comprising (I); (2) an antibody which binds to (I) or to a polypeptide comprising murine V3 or human V3 amino acid sequence; (3) a vaccine composition for the treatment of multiple sclerosis, restenosis or diabetes mellitus, comprising an antigen for the antibody of (2); and (4) a method for treating multiple sclerosis, restenosis or diabetes mellitus, by administering (I), human or murine V3, or an antibody to these polypeptides. (I) has neuroprotective,
                                                                                                                                                                                                           RHAMM; receptor hyaluronic acid mediated motility; hyaluronic acid; HA, neuroprotective; vasotropic; antidiabetic; nootropic; antiarthritic; antiparkinsonian; antifilammatory; osteopathic; dermatological; vaccine; antiarteriosclerotic; cytostatic; vulnerary; hyaluronic acid antagonist; HA binding inhibitor; multiple sclerosis; restenosis; diabetes mellitus; neurological disease; Alzhaimer's disease; Parkinson's disease; cancer; arthinamatory joint disease; osteoporosis; atherosclerosis; inflammatory dermatosis; inflammatory bowel disease; metastesis; inflammatory disease; respiratory distress syndrome; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New P16, P-16d, human and murine P32, S3, S7, and V2 polypeptides, useful for treating e.g. multiple sclerosis, restenosis, diabetes mellitus, Alzheimer's disease, Parkinson's disease, arthritis, cancer and
--ELRLHEVYKFITDIK-----YVDERNTINKLLKEKEDLEKTSINIKONVDEKRKK 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vasotropic, antidiabetic nocropic, antiparkinsonian, antiaritritic, antiniflammatory, osteopathic, dermatological, antiarteriosclerotic, cytostatic and vulnerary activities, and can be used in vaccines and as an HA antagonist. The polypeptides and the antibodies to these polypeptides are useful for treating multiple sclerosis, restenosis or diabetes mellitus, as well as neurological diseases such as Alzheimer's disease, parkinson's disease, arthritis and other inflammatory joint diseases, osteoporosis, inflammatory dermatosis, inflammatory bowel's diseases, cancer and metastasis, and chronic and acute respiratory distress syndrome. The polypeptides may also be used to promote wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               distress syndrome. The polypeptides may also be used to promote healing. ABR56968 to ABR57022 and ACC79533 to ACC79537 represer sequences used in the exemplification of the present invention
                                                                                                                                                                              Mouse RHAMM V-3 region amino acid sequence SEQ ID NO:80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TRAN-) TRANSITION THERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Page 28-29; 215pp; English.
                                                                              ABR57002 standard; protein; 435 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-OCT-2002; 2002WO-CA001563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-OCT-2001; 2001US-00978309
                                                                                                                                                                                                                                                                                                                                                               RHAMM binding protein; RABP
                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                #O2003033535-A2
                                                                                                                                              05-AUG-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    metastasis.
                                                                                                             ABR57002;
445
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                                                                 ABR57002
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                                                                                                                                                               LDNLLREKEVELEKHIAAHAQAILIAQEKYNDTA---ÖSLRDVTAQLESVQEKYNDTAQS 155
                                                                                                                                                                                                                                                       206 ESVQEKYNDTAQSLRDVSAQLESYKSSTLKEIEDLKLENLTLQEKVAMAEKSVEDVQQQI 265
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                                                                                                                                                                                                                                                                                                                                  DDGITKLNEAQKSLL-VSSQSFNNASGKLLAL-DSQLTN-DFSEKSSYFQSQVDKIRKEA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 YAGAAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNK-----LKSVQNFF----TTLS 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     266 LTAESTNQ-----EYA-----RMVODLONRSTLKEEBIKBITSSFLEKITDLK 308
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                                                                                                                                                                                                                       LVGDIKTLLMDSQDKYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQKDILIKVL
                                                                                                           1 MTEIVADKTVEVVKNAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASV
                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            227 NIVKQANKDI------DAAKLKLITEIAAIGEIKTETETTRFYVDYDDL 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RHAMM-related peptide; V-3; RHAMM; murine; mouse; receptor; receptor for hyaluronic acid mediated motility; receptor; antiinflammatory composition; methyl donor compound; vitamin B12; synergistic action; Inflammatory disease; multiple sclerosis; MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Composition useful for treating e.g. viral diseases comprises a combination of a methyl donor compound, and an anti-viral, anti-proliferative, or anti-inflammatory compound.
                                                       62;
DB 6; Length 435;
7.4%; Score 111; DB 6; Length 43
20.5%; Pred. No. 1.1;
iive 63; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TRAN-) TRANSITION THERAPEUTICS INC.
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2002WO-CA000895.
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Query Match 7.4% Best Local Similarity 20.5% Matches 60; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
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cell surface target protein; AP-II; activating protein-1; response-to-injury; vaccine; inflammatory neurological disorder; diabetes mellitus; arthritis; inflammatory dermatosis; inflammatory bowel disease; cancer; kidney fibrosis; inflammatory lung disease; cancer; kidney fibrosis; inflammatory lung disease; obseity; lupus; cardiovascular disease; wound; multiple sclerosis; parkinson's disease; Alzheimer's disease; alpha helical peptide; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 DDGITKLNBAQKSJL-VSSQSFNNASGKLLAL-DSQLTN-DFSEKSSYFQSQVDKIRKEA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                206 ESVQEKYNDTAQSLRDVSAQLESYKSSTLKEIEDLKLENLTLQEKVAMAEKSVEDVQQQI 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178 YAGAAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNK-----LKSVQNFF----TTLS 226
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                                                                                                                                                                                                                                                                                                                                                                                                                               99 LDNLLREKEVELEKHIAAHAQAILIAQEKYNDTA---QSLRDVTAQLESVQEKYNDTAQS 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVGDIKTLLMDSQDKYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQKDILIKVL 120
antiproliferative or antinflammatory compound. The methyl donor compound acts synergistically with the antiviral, antiproliferative or antinflammatory compound to provide an enhanced therapeutic effect with minimal side effects. In the antinflammatory compositions of the invention, the amount and the frequency of administration is lower than that required for the antinflammatory compositions of the methyl donor compound. Compositions of the invention can be used in the treatment of viral disease, proliferative diseases (e.g., cancer), and inflammatory diseases such as multiple sclerosis. The present sequence represents a peptide fragment of murine RHAMM (receptor for hyaluronic acid mediated mediated mediated is specifically claimed as the antilifammatory compound in an antiinflammatory composition of the invention for the treatment of multiple sclerosis
                                                                                                                                                                                                                                                                                                                                                                                            1 MTEIVADKTVEVVKNAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            309 NQLRQQDEDFRKQLEBKGKRTAEKENVMTELT------MEINKWRLLYEEL 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NTVKQANKDI------DAAKLKLTTEIAAIGEIKTETETTRFYVDYDDL
                                                                                                                                                                                                                                                                                                                  7.4%; Score 111; DB 6; Length 435; 20.5%; Pred. No. 1.1; ive 63; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RHAMM; Receptor hyaluronic acid mediated motility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADC02471 standard; protein; 435 AA
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2000US-00541522.
2000US-00685010.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse RHAMM V3 protein.
                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                        Sequence 435 AA;
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The invention relates to a polypeptide comprising an amino acid sequence of plot, P32, murine S3, human S3, murine S7, c selected from the sequences of P16, P32, murine S3, human S3, murine S7, human S7, murine V2 and human V2, all derived from the protein RHAMM (Receptor hyaluronic acid mediated motility) a cell surface target (Receptor hyaluronic acid mediated motility) a cell surface target protein that is regionse to injury. Also included are an antibody that 1) pathway on response to injury. Also included are an antibody that compositions for treating an inflammatory neurological disorder or compositions for treating an inflammatory neurological disorder or cidabetes mellitus (comprising the above amino acid sequence or an antigen for the antibody cited above) and treating an inflammatory neurological disease, disbetes mellitus or wounds (comprising cancer, kidney fibrosis, inflammatory dermatosis, inflammatory lung disease, obesity, lupus, cardiovascular disease, diabetes mellitus or wounds (comprising administering to a patient the above polypeptide or antibody. In the above method, the inflammatory neurological disorder is multiple or sclerosis, Parkinson's disease or Alzheimer's disease. The present sequence is a mouse RHAMM active protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RHAMM; receptor hyaluronic acid mediated motility; hyaluronic acid; HA; neuroprotective; vasotropic; antidiabetic; nootropic; antiarthritic; antiparkinsonian; antiinflammatory; osteopathic; dermatological; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         266 LTAESTNQ------EYA-----RAVQDLONRSTLKEEBIKEITSSFLEKITDLK 308
                                                                                                                                                          S7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 DDGITKLINBAQKSLL-VSSQSFNNASGKLLAL-DSQLTN-DFSEKSSYFQSQVDKIRKEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ESVQEKYNDTAQSLRDVSAQLESYKSSTLKEIEDLKLENLTLQEKVAMAEKSVEDVQQQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178 YAGAAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNK-----LKSVQNFF----TTLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 LVGDIKTLLMDSQDKYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQKDILIKVL
                                                                                                                 New polypeptide for diagnosing, preventing or treating inflammatory neurological disorders, cancer, obesity, lupus or diabetes mellitus, comprises an amino acid sequence of P16, P32, or murine or human S3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   227 NTVKQANKDI-----DAAKLKLTTEIAAIGEIKTETETTRFYVDYDDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.4%; Score 111; DB 7; Length 435; 20.5%; Pred. No. 1.1; ive 63; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse RHAMM V-2 region amino acid sequence SEQ ID NO:77.
                                                                                                                                                                                                                     Disclosure; SEQ ID NO 80; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABR56999 standard; protein; 477
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                                                      Turley
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                         WPI; 2003-755209/71
                                                      Pastrak A,
PASTRAK A.
TURLEY E A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 435 AA;
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(PAST/)
(TURL/)
                                                      Cruz T,
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309 NOLROODEDFRKOLEEKGKRTAEKENVMTELT------MEINKWRLLYEEL 353

ABP97481 standard; peptide; 477 AA.

RESULT 36

ABP97481

227 NIVKQANKDI------DAAKLKLTTEIAAIGEIKTETETTRFYVDYDDL

178 YAGAAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNK-----LKSVQNFF----TTLS

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206 ESVQEKYNDTAQSLRDVSAQLESYKSSTLKEIEDLKLENLTLQEKVAMAEKSVEDVQQQI 265

us-09-993-292b-28.rag

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The present invention describes a polypeptide (I) which binds to hyaluronic acid (HA) and thereby inhibit the binding of HA to RHAMM (Irceptor hyaluronic acid mediated motility), comprising an amino acid sequence of P16. P-164, human P32, murine P32, murine S3, human S3, murine S7, human S7, murine V2 and human V2. Also described: (I) a pharmaccutical composition comprising murine V3 or human V3 amino acid sequence: (3) a vaccine composition for the treatment of multiple sclerosis, restenosis or diabetes mellitus, comprising an antigen for the antibody of (2); and (4) a method for treating multiple sclerosis, restenosis or diabetes mellitus, py administering (1), human or murine (V3) or an antibody to these polypeptides. (I) has neuroprotective, antiinflammatory, osteopathic, dermatological, antiarteriosclerotic, antiinflammatory, osteopathic, dermatological, antiarteriosclerotic, antiinflammatory, osteopathic, dermatological, antiarteriosclerotic, antiinflammatory, osteopathic, dermatological, antiarteriosclerotic, antianteriosclerotic, antianteriosclerotic, antianteriosclerotic, antianteriosclerotic, disease, parkinson's disease, arthritis and other inflammatory joint diseases, cancer and metasteasis, and chronic and acute respiratory diseases, cancer and metasteasis, and chronic and acute respiratory diseases, cancer and metasteasis, and chronic and acute respiratory diseases, cancer and metasteasis, and chronic and acute respiratory diseases, cancer and metasteasis, and chronic and acute respiratory diseases, cancer and metasteasis, and chronic and acute respiratory diseases, cancer and metasteasis, and chronic and acute respiratory diseases, cancer and metasteasis, and chronic and acute respiratory diseases, cancer and metasteasis, and chronic and acute respiratory diseases, cancer and metasteasis, and chronic and acute respiratory diseases, cancer and metasteasis, and chronic and acute respiratory wound chaling. ABRSF068 to ABRSF0292 and ACC79537 represent inventors
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antiarteriosclerotic; cytostatic; vulnerary; hyaluronic acid antagonist; the binding inhibitor; multiple sofaronist; restenosis; diabetes mellitus; neurological disease; Alzheimer's disease; Parkinson's disease; cancer; arthritis; inflammatory joint disease; osteoporosis; atherosclerosis; arthritis; inflammatory dermatosis; inflammatory bowel disease; metastasis; inflammatory disease; respiratory distress syndrome; wound healing; RHAMM binding protein; RABP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New P16, P-16d, human and murine P32, S3, S7, and V2 polypeptides, u for treating e.g. multiple sclerosis, restenosis, diabetes mellitus, Alzheimer's disease, Parkinson's disease, arthritis, cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TRAN-) TRANSITION THERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 27; 215pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Turley EA;
                                                                                                                                                                                                                                                                                                                                                                                     2002WO-CA001563.
                                                                                                                                                                                                                                                                                                                                                                                                                                           15-OCT-2001; 2001US-00978309.
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RHAMM-related peptide; V-2; RHAMM; murine; mouse; receptor for hyaluronic acid mediated mctlilty; receptor; antiinflammatory composition; methyl donor compound; vitamin B12; synergietic action; inflammatory disease; multiple sclerosis; MS;

antiinflammatory.

WO2003030929-A1.

Мив вр.

17-APR-2003

Murine RHAMM-related peptide, V-2.

26-SEP-2003 (first entry)

ABP97481;

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The invention relates to therapeutic compositions comprising at least one methyl donor compound (e.g., vitamin B12) and an antiviral, methyl donor compound (e.g., vitamin B12) and an antiviral, antiproliferative or antinflammatory compound; the methyl donor compound acts synergistically with the antiviral, antiproliferative or antinflammatory compound; or compound to provide an enhanced therapeutic effect with minmal side effects. In the antiinflammatory compound in so lower than that required for the antiinflammatory compound in the absence of the invention, the amount and the frequency of administration is lower than that required for the antiinflammatory compound in the absence of the creatment of viral disease, proliferative diseases (e.g., cancer), and inflammatory diseases such as multiple sclerosis. The present sequence represents a peptide fragment of murine RHAMM (receptor for hyaluronic cid mediated mediated mediated mediated mediated mediated mediated mediated mediated milinflammatory compound in an antiinflammatory composition of the invention for the treatment of multiple sclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Composition useful for treating e.g. viral diseases comprises a combination of a methyl donor compound, and an anti-viral, anti-proliferative, or anti-inflammatory compound.
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LVGDIKTLLMDSQDKYPEATQTVYEWCGVATQLLAAYILLFDBYNEKKASAQKDILIKVL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 DDGITKLNBAQKSLL-VSSQSFNNASGKLLAL-DSQLTN-DFSEKSSYFQSQVDKIRKBA 177
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62;

7.4%; Score 111; DB 6; Length 477; 20.5%; Pred. No. 1.2; ; Pred. No. 1.2; 63; Mismatches 108; Indels

Similarity 20.5 60; Conservative

Query Match Best Local S

Matches

ઠે 셤 δ 셤 ò

61

Sequence 477 AA;

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(TRAN-) TRANSITION THERAPEUTICS INC.

Cruz I, Pastrak A;

11-JUN-2002; 2002WO-CA000895.

2001US-0327700P.

05-OCT-2001; 25-MAR-2002; 11-JUN-2002; 11-JUN-2002;

03-DEC-2001;

2002US-0366539P 2002US-00167752 2002US-00167765

04-OCT-2002; 2002WO-CA001503

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cell surface target protein; AP-1; activating protein-1; response-to-injury; vaccine; inflammatory neurological disorder; diabetes mellitus; arthritis; inflammatory dermatosis; inflammatory bowel disease; cancer; kidney fibrosis; inflammatory lung disease; obesity; lupus; cardiovascular disease; wound; multiple sclerosis; Parkinson's disease; Alzheimer's disease; alpha helical peptide; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a polypeptide comprising an amino acid sequence selected from the sequences of P16, P32, murine S7,
                                                                                                                                                                           YAGAAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNK-----LKSVQNFF----TTLS 226
                                                                                                                                                                                                                            DDGITKLNEAQKSLL-VSSQSFNNASGKLLAL-DSQLIN-DFSEKSSYFQSQVDKIRKEA 177
                                                                                                     61 LVGDIKTLLMDSQDKYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQKDILIKVL 120
                                                                   S7
                                                 1 MTEIVADKTVEVVKNALETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASV 60
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                          Gaps
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                                                                                                                                                                                                                                                                                62;
 Length 477;
7.4%; Score 111; DB 6; Length 477
20.5%; Pred. No. 1.2;
tive 63; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RHAMM; Receptor hyaluronic acid mediated motility;
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                                                                                                                                                                                                                                                                                                                                                             ADC02468 standard; protein; 477 AA
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03-APR-2000; 2000US-00541522.
05-OCT-2000; 2000US-00685010.
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                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CRUZ/) CRUZ T.
(PAST/) PASTRAK A.
(TURL/) TURLEY E A.
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                  Local Similarity
nes 60; Conserv
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     Query Match
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Matches
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thuman S7, murine V2 and human V2, all derived from the protein RHAWM

CReceptor hyaluronic acid mediated motility) a cell surface target

Credity protein that is required for activation of the AP-1 (activating protein-

Credity protein that is required for activation of the AP-1 (activating protein-

Credity to the polypeptide cited above, a pharmaceutical or vaccine

Credity to the polypeptide cited above, a pharmaceutical or vaccine

Credity to the polypeptide cited above) and treating an inflammatory neurological

Credity the antibody cited above) and treating an inflammatory neurological

Credity fibrosis, inflammatory dermatosis, inflammatory bowel disease,

Cancer, arthritis, inflammatory dermatosis, inflammatory bowel disease,

Cardiovascular disease, diabetes mellitus or wounds (comprising

cardiovascular disease, diabetes mellitus or wounds (comprising

cardiovascular disease, diabetes mellitus or wounds (comprising

cardiovascular disease, diabetes mellitus or wounds (comprising

cardiovascular disease or Alzheimer's disease. The polypeptide or

sclerosis, Parkinson's disease or Alzheimer's disease. The polypeptide or

cardibody may also be used for diagnosing or preventing the above

cardiovascular sequence is a mouse RHAWM active protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tissue disorder; response-to-injury process; cell proliferating; RHAMM; hyaluronic acid; HA; receptor for hyalauronan-mediated motility; RHAMM; inflammatory neurological disorder; Parkinson's disease; Albateimer, disease; arthritis; multiple sclerosis; gastritis; nephritis; inflammatory dermatosis; psoriasis; inflammatory bowel disease; stenosis; restenosis; cancer; kidney fibrosis; inflammatory lung disease; stenosis; emphysema; asthma; cystic fibrosis; obesity; obesity related disease; lupus; cardiovascular disease; atherosclerosis; wound; scar; diabetes; tissue transplantation; stroke; inflammatory response; fibroit cresponse; mackical implant; Acquired immundeficiency syndrome; AlDS; hepatitis; myocardial fibrosis; hepatic fibrosis; chronic cystitis; acute mastitis; septic shock; thyroiditis; retinopathy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse receptor for hyalauronan-mediated motility (RHAMM).
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Matches 60;
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Mouse hyaluronic acid binding protein RHAMM.

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12-MAR-2002 (first entry)

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The invention describes a method of treating a tissue disorder associated with response-to-injury process or proliferating cells in a patient, comprising administering a polypeptide (1) which binds hyaluronic acid (HA), an antibody which binds one of domains D1-D5 of Receptor for hyalauronan-mediated motility (RHAMMMMM) a polypeptide fragment encoding any of D1-D5 of RHAMM, or a vector which expresses antisense RHAMM, and the propertied fragment encoding any of D1-D5 of RHAMM, or a vector which expresses antisense RHAMM, and inflammatory neurological disorder such as Parkinson's disease, Alzheimer's disease, arthritis including rheumatoid arthritis, osteoarthritis, multiple sclerosis, inflammatory dermatosis (psoriasis), inflammatory bowel disease, stenosis, cancer, kidney fibrosis, inflammatory lung disease (e.g. emphysema, asthma, cystic fibrosis, inflammatory lung disease (e.g. emphysema, asthma, cystic fibrosis, to prevent scar and also for treating or preventing diabetes mellitus. The method is also useful for treating tissue transplantation adhesions, to prevent scar and also for treating tissue transplantation catheters), inflammatory diseases such as AIDS, myocardial and hepatic fibrosis, chronic cystitis, acute maskitis, gastritis, neghtitis, neghtic shock, thyroiditis, and retinopathy. This sequence represents a receptor for hyalauronan-mediated motility protein used in the method of treating a tissue disorder described in the invention
                                                                                                                                                                                                                                      Treating tissue disorder associated with response-to-injury process or proliferating cells in mammals, e.g. fibrosis, inflammation, by administering a compound that alters activity of transition molecules within a cell.
                                                                                             (TRAN-) TRANSITION THERAPEUTICS & DIAGNOSTICS IN
                                                                                                                                                                                                                                                                                                                                                                       Disclosure, Fig 50; 215pp; English
05-OCT-2000; 2000WO-IB001534.
                                                 05-OCT-2000; 2000WO-IB001534
                                                                                                                                              Turley EA, Cruz TF;
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61 LVGDIKTLLMDSQDKYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQKDILIKVL 120
                                                                                                                                                                                               253 LDNLLREKEVELEKHIAAHAQAILIAQEKYNDTA---QSLRDVTAQLESVQEKYNDTAQS 309
                                                                                                                                                                                                                                                  121 DDGITKLNEAQKSLL-VSSQSFNNASGKLLAL-DSQLTN-DFSEKSSYFQSQVDKIRKEA 177
                                                                                                                                                                                                                                                                                                                       178 YAGAAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNK-----LKSVQNFF----TTLS 226
                                                                                                        1 MTEIVADKTVEVVKNAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASV 60
                                                                                                                                                                                                                                                                                                                                                                                                                227 NIVKQANKDI------DAAKLKLITEIAAIGEIKTETETTRFYVDYDDL 269
                                                                    62;
                               Length 631;
                               Query Match 7.4%; Score 111; DB 5; Length 63: Best Local Similarity 20.5%; Pred. No. 1.7; Matches 60; Conservative 63; Mismatches 108; Indels
Sequence 631 AA;
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AAU11437 standard; protein; 794 AA

RESULT 39 AAU11437 AAU11437;

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Mouse; hyaluronic acid binding protein; RHAMM; gene therapy;
receptor for HA mediated mobility; immunosuppressive;
cytostatic. conjugate; rheumatoid arthritis; scleroderma; liver fibrosis;
                                                                                                                                                                                                                                                                                                                                                  Protein conjugates that selectively target certain tissues and organs useful for treating and preventing various diseases, comprises glucoseaminoglycan-targeting domain conjugated to a therapeutic protein.
                                                                                                                                                                                                                                                                                                         Wiebe DJ;
                                                                                                                                                                    'note= "Encoded by CAC"
                                                                                                                  note= "Encoded by AAC"
                                                                                                                                  'note= "Encoded by ACG"
                                                                                                                                                   'note= "Encoded by CAA"
                                                                                                                                                                                    note= "Encoded by ACT"
                                                                                                                                                                                                      /note= "Encoded by GAT"
                                                                                                                                                                                                                                                                                                         Sereda TJ,
                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                       20-APR-2001; 2001WO-CA000533.
                                                                                                                                                                                                                                                                       20-APR-2000; 2000US-0198613P
                                                                                                                                                                                                                                                                                                        Voloski BMR, Williams AM,
                                                                                                                                                                                                                                                                                        (CANG-) CANGENE CORP.
                                                                                                                                                                                                                                                                                                                         WPI; 2002-075094/10.
N-PSDB; AAS17497.
                                                                                                                                                                             Misc-difference 540
                                                                                                                                                                                             Misc-difference 668
                                                                                                                                           Misc-difference 89
                                                                                                                                                            Misc-difference 91
                                                                                                                           Misc-difference
                                                                                                          Misc-difference
                                                                                                                                                                                                                       WO200180899-A2
                                                                                  Mus musculus.
                                                                   cancer
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The invention relates to a conjugate comprising an hyaluronic acid (HA) binding protein e.g. RHAMM (receptor of HA mediated mobility) or peptide
contiguous with, or coupled to a polypeptide conjugated to a therapeutic
agent, and the polynucleotides encoding them. Also included is a method
for preparation of the HA-binding protein by inserting a first nucleotide
sequence encoding a HA-binding protein by inserting a first nucleotide
sequence encoding a therapeutic protein into a suitable
nucleotide sequence encoding a therapeutic protein into a suitable
vector, expressing the vector in an acceptable host, purifying conjugate
altering in vivo the distribution of a therapeutic agent comprising
administering the composition to the animal where conjugate molecule
distribute primarily in tissues and organs containing high levels of
cistribute primarily in tissues and organs containing high levels of
cistribute primarily in tissues and organs containing high levels of
cistribute distribution to the animal level of HA e.g. rheumatoid arthritis,
scleroderma, liver fibrosis and cancer. Lower therapeutic dosages
crequired also translates into lower immunogenicity of the conjugates
improve patient compliance and reduce direct and indirect costs
associated with the drug substance and its administration. Conjugates allows for the use, where appropriate, of lower, safer, dosages as compared to the conventional dosage requirements for the unconjugated corresponding therapeutic agent. Conjugate molecules have an increased half-life and potency, resulting in prolonged circulation of the molecule, efficient distribution into the target tissues, and increased bloavailability. The present sequence represents a RHAMM protein

Claim 6; Page 116; 121pp; English.

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WO200171042-A2
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated
                                                                                                                                                                                 LVGDIKTLLMDSQDKYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQKDILIKVL 120
                                                                                                                                 DDGITKINEAQKSLL-VSSQSFNNASGKLLAL-DSQLTN-DFSEKSSYFQSQVDKIRKEA 177
                                                                                                                                              Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                        1 MTEIVADKTVEVVKNAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASV
                                                                                                        YAGAAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNK-----LKSVQNFF----TTLS
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K
                                        Gaps
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Xu HH;
                                                                                                                                                                                                           269
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                                                                                                                                                                                                          NTVKQANKDI-----DAAKLKLITTEIAAIGEIKTETETTRFYVDYDDL
                     DB 5; Length 794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ohlsen KL,
Forsyth RA,
                    ; Score 111; DB 5; Length 79;
; Pred. No. 2.4;
63; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                  Protein encoded by Prokaryotic essential gene #29209.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haselbeck R,
Yamamoto R,
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                                                                                                                                                                                                                                                                             ABU43682 standard; protein; 938
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Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P
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                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus haemolyticus.
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                       7.4%;
                                                                                                                                                                                                                                                                                                                   (first entry)
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                                1 Similarity 20.5 60; Conservative
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Trawick JD,
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N-PSDB; ACA47552
      Sequence 794 AA;
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08-FEB-2002;
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                       Query Match
Best Local
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polypeptide or its fragment whose expression is inhibited by the antisense mucleic acid; (4) an antibody capable of specifically binding consistence mucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) inhibiting cellular consistence in an operon required for proliferation or the activity of agene in an operon required for proliferation, or that has an activity against a biological pathway to required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological identifying a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibicitic; (10) profiling a compound's activity; (11) a culture comprising strains in which the extent compound is activity; (11) a culture comprising strains in which the extent compound is activity; (11) a culture comprising strains in which the conformation of compounds are compound that inhibits the compound of an organism. The antisense mucleic acids are useful for strains; or (13) identifying the target of a compound that inhibits the compound of an organism. The antisense mucleic acids are useful for dentifying proteins or screening for homologous nucleic acids required for proliferation to isolate candidate molecules for rational for cellular proliferation in cells other than S. aureus, S. typhimurium, cequired for proliferation in cells other than S. aureus, S. typhimurium, cequired for proliferation in cells other than S. aureus, S. typhimurium, cequired the prince essential genes. Note: The sequence data for this patent did not form part of the prince of the prince of the prince of the prince of the prince of the prince of the prince of the prince of the prince of the prince of the prince of the prince of the prince of the prince of the prince of the prince of the prince of the prince of the prince of the prince of the prince of the prince of the prince of the prince of the prince of the prince of the prince of the prince o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 --DILIKVLDDGITKLNBAQKSLLVSSQ---SFNNASGKLLALDSQLTNDFSEKSS--YF 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               189 TINKIKNAVYAAHDSLPQINKIADRI---FYLNDHQDDLDKYANQFR----ALGNYKGD 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GVDİASEGFDLANİRLINDAĞGYLTSAQÇRVGDYQEAAGRAQEVNNQANSALRQQŠTSGLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 ILDAQOKLNDVNAAI-----PSLNEKAKLİLALNEYMPNIEKLLDVASNDIPAQFPKINR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QSQVDKIRKEAYAGAAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNKLKSVQNFFTTLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 18.6%; Score 111; DB 6; Length 938; Similarity 18.6%; Pred. No. 3; Conservative 64; Mismatches 110; Indels
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The invention relates to constructing (M1) a strain of diploid fungal cells in which both alleles of a gene are modified, comprising modifying one allele by insertion or replacement by a casestet having an expressible selectable marker and modifying other allele by constructing other allele by the expression of the second allele is regulated by the promoter. (M1) is useful for constructing a strain of diploid fungal cells in which both alleles of a gene are modified. The diploid fungal cells in which both alleles modified are useful for identifying a gene that is essential to the survival or growth of a fungus, a gene that contributes to the virulence and/or pathogenicity of a fungus, a gene that contributes to the resistance of a diploid fungus to an antifungal agent that inhibits the growth of a diploid fungus and for identifying a therapeutic agent for treatment of a mammalian careivity of a gene product, preferably enzymatic activity, carbon compound catabolism, biosynthetic, transporter, transcriptional, carbon compound catabolism, biosynthetic, transporter, transcriptional, activity to inhibit growth or proliferation and cell division activity. The method is useful for identifying a compound having the antification by C. albicans. The present sequence is that of an essential Candida albicans protein used in the method of the invention.

Or sesential Candida albicans protein used in the method of the invention.

Or sesential candida albicans protein used in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |:|| : :|| | : : :::::||| KSKLINASENPIKTSTLKINHLQQQMBSDQMKLT-----KAKTENETLLSAIBLHRQFI 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  349 SNQTVFDNQENEYKQSNQELVQLKEEYANKQELLSTLSTGISSTGNVTSGY1--TQLNDV 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  specification but is based on sequence information supplied to Derwent by
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Constructing strains for identifying gene products as effective targets for therapeutic intervention, by inactivating in the strain one allele of a gene and placing other allele of the gene under conditional expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161 EKSSYFQSQVDKIR-----KEAYAGAAAGVVAGPFGLIISYSIAAGVVEGKLIPEL
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Pungus; yeast; tetracyclin; promoter; GRACB strain; biosynthesis;
signal transduction; DNA replication; cell division; growth;
proliferation; Candida albicans; fungicide; antifungal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 44; SEQ ID NO 7519; 167pp + Sequence Listing; English
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Local Similarity 18.3%; Pred. No. 4;
les 40; Conservative 53; Mismatches
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20-FEB-2001; 2001US-00792024.
22-AUG-2001; 2001US-0314050P.
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                                                                                                                                                                                                                                                                                                                     (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                         Roemer T, Jiang B,
                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-566694/60.
N-PSDB; ABZ32232.
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                                                                               Candida albicans
                                                                                                                    WO200253728-A2
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22-AUG-2001;
                                                                                                                                                           11-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QDLLDHKEQSSVSETDKGISSTDVQLLSEALKTL-----SSDKQLVVEKETIKELK 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EELADYKEDVEELRE-----VRQVVKEP----VRESRAAKLLYNR-VNKMISQLDNVLN 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  639 DLEARQHQIKQAESS-DYAASSPTVEPQQMVHIDELVATIRRMKEASDEERFKV-VGDLL 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KDIL-----IKVLDDGITK----LNEAQKSLLVSSQSFNNASGKLLALDSQLTNDFS 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           221 FFTTLSNTVKQANKDIDAAKLKLTTE------IAAIGEIKTETETTRFYVDYDDLM 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EYSQAASVLVGDIKTLLMDSQDKYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQ 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E------AEKLSGS 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             156 ITTDKLKETIRVLPDAVGAHTRHAIGESEGKVD--NK------TKIEIIKEEERKIR 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 IVADKTVEVV------KNAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQ 52
                                                                                                                                                                                                                                                                                              New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ٠,٠
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94;
                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 9159; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.4%; Score 111; DB 4; Length 1013; 21.6%; Pred. No. 3.3; ive 57; Mismatches 100; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 7519.
                                                                                                                                                                                                  Myers EW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Candida albicans essential protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         271 LSLLKEAAKKMINTCNEYQK 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABP73682 standard; protein; 1171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-MAR-2001; 2001WO-US009231.
                                                                                                23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                                  Adams M,
                                                                                                                                                                                                                                       2001-656860/75.
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nes 69; Conserv
                                                                                                                                                       (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1013 AA;
                                                                                                                                                                                                                                                           N-PSDB; ABL04892
                                                                                                                                                                                                                                                                                                                                         interactions
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                      27-SEP-2001
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ABP73682
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AC ABP7
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DT 30-J
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265

Gaps

168

---EGKLIPELKNK

GDIKTLIMDSQDKYFEATQTVYEWCGVATQLLAAYILLFDBYN-----EKKASAQKDIL

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57 GTLTPMLQG----MILFSETLSEKC---TELOTLYVSICGDEDLDSVVLESKLASDRASL 109
                                                                          117 IKVLDDGITKLN---EAQKSLLVSSQS-FNNASGKLLALDSQL--TNDFSEKSSYFQSQV 170
                                                                                                 171 DKIR---KEAYAGAAGV----VAGPFGLIISYSIAAGVV----
              63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein.
                                                                                                                                                                                                                                                         Streptococcus, GAS, GBS, group B streptococcus, Streptococcus agalactiae, group A streptococcus, Streptococcus pyogenes, antibacterial; antinflammatory, infection, vaccine, meningitis, gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fraser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Grandi G,
                   460 KTKQLEIDSKLGFEPTKIHQLRDQESELISQQNKFNQQ 497
-----YDDLMLSLLKEAAKKMINTCNEYQKR 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.3%; Score 110.5; DB 5;
21.6%; Pred. No. 0.71;
tive 57; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Margarit Y RosI,
                                                                                                                                                                                                                        Streptococcus polypeptide SEQ ID NO 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 3350; 4525pp; English.
                                                                                                                         ABP26411 standard; protein; 304 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-OCT-2000; 2000GB-00026333.
24-NOV-2000; 2000GB-00028727.
07-MAR-2001; 2001GB-00005640.
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                                                                                                                                                                                          (first entry)
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(GENO-) INST GENOMIC RES.
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                                                                                                                                                                                                                                                                                                                                 Streptococcus agalactiae.
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N-PSDB; ABN67042.
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                                                                                                                                                                                           02-JUL-2002
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Tettelin H;
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The invention relates to a novel immunogenic composition comprising a combination of 2-5 group B Streptococcus (GBS) polypeptides. Each polypeptide is encoded by a GBS polynucleotide sequence which is homologous to a polynucleotide sequence of group A Streptococcus (GAS), Streptococcus pneumoniae and/or least one other GBS serotype. The composition of the invention demonstrates antibacterial activity whilst the polypeptides and polynucleotides may be useful in assays to diagnose and identify streptococcal infections or for identifying, screening and developing vaccines and other treatments for streptococcal infections. The current sequence is that of a Streptococcus agalactiae ORF SAG protein of the invention.
                                 215 LKSVQNFFTTLSNTVKQANKDIDAAKL-KLTTEIAAIGEIKTETETTRFYVDYDDLM--- 270
                                                      228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunogenic composition useful as a vaccine for treating or preventing streptococcal infections, comprises group B Streptococcus polypeptides
169 SNAQSTVNQALAAVSTGFSGYNSKTGAFGKPTSGQMEWTKTVKKNWKEREDAKABELKSK
                                                                                                                                                                                                                                                                                                                                                         group B Streptococcus; GBS; antibacterial; vaccine; SAG.
                                                                                                                                                                                                                                                                                                                           Streptococcus agalactiae ORF SAG1030-related protein 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 10; SEQ ID NO 6104; 1194pp; English.
                                                                                                                                                                                                                           ADK99510 standard; protein; 304 AA.
                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus agalactiae 2603V/R.
                                                                                                                           :|||| || : :|
281 SNASAALLKEVAKSKLTDT 299
                                                                                                      ----LSLLKEAAK-KMINT 284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-AUG-2002; 2002US-0406676P.
28-AUG-2002; 2002US-0406757P.
                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Masignani V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GENO-) INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                                              immunogenic composition;
streptococcal infection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 304 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2004018646-A2.
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                                                                                                                                                                                                                                                                                              20-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34-MAR-2004
                                                                                                                                                                                                                                                               ADK99510;
                                                                                                          271
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16;

67; Gaps

Indels

69; Conservative

Best Local Similarity Matches 69; Conserv

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62

4 VSVSSVGTÇASTVAISMFSRV-----SALNDAITKLSSFAEAATLQGTAYSNAKSYAT 56 10 VEVVKNAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQ------EYSQAASVLV

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16;
                                                                                                                                                                                                         SNAQSTVNQALAAVSTGFSGYNSKTGAFGKPTSGQMEWTKTVKKNWKEREDAKAEELKSK 228
                                                                                                                                                                                                                                                                                                                                     GDIKTLLMDSQDKYPEATQTVYEWCGVATQLLAAYILLFDEYN-----EKKASAQKDIL 116
                                                                                                                                                       GTLTPMLQG----MILFSETLSEKC---TELQTLYVSICGDEDLDSVVLESKLASDRASL 109
                                                                                                                                                                                      117 IKVLDDGITKLN---EAQKSLLVSSQS-FNNASGKLLALDSQL--TNDFSEKSSYFQSQV 170
                                                                                                                                                                                                                                                    171 DKIR----KEAYAGAAAGV-----VAGPFGLIISYSIAAGVV------EGKLIPELKNK 214
                                                                                                                                                                                                                                                                                                                215 LKSVQNFFTTLSNTVKQANKDIDAAKL-KLTTEIAAIGEIKTETETTRFYVDYDDLM--- 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a novel immunogenic composition comprising a combination of 2-5 group B Streptococcus (GBS) polypeptides. Bach polypeptide is encoded by a GBS polynucleotide sequence which is homologous to a polynucleotide sequence of group A Streptococcus (GAS), Streptococcus pneumoniae and/or least one other GBS serotype. The composition of the invention demonstrates antibacterial activity whilst. the polypeptides and polynucleotides may be useful in assays to diagnose
                                                                                           VSVSSVGTQASTVAISMFSRV-----SALNDAITKLSSFABAATLQGTAYSNAKSYAT 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunogenic composition useful as a vaccine for treating or preventing streptococcal infections, comprises group B Streptococcus polypeptides
                                                             10 VEVVKNAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQ------EYSQAASVLV
                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        group B Streptococcus; GBS; antibacterial; vaccine; SAG.
                                67;
   Length 304;
7.3%; Score 110.5; DB 8; Length 21.6%; Pred. No. 0.71; ative 57; Mismatches 126; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus agalactiae ORF SAG1030-related protein 2.
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                                                                                                                                                                                                                                                                                                                                                                              ----LSLLKEAAK-KMINT 284
                                                                                                                                                                                                                                                                                                                                                                                                         281 SNASAALLKEVAKSKLTDT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADK99511 standard; protein; 278
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27-AUG-2002; 2002US-0406676P.
28-AUG-2002; 2002US-0406757P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunogenic composition;
streptococcal infection;
                                Conservative
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                Similarity
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                                69
Query Match
Best Local S
Matches 69
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94 LAAYILLFDEYN-----EKKASAQKDILIKVLDDGITKLN---EAQKSLLVSSQS-FNN 143
                                                                                                                                                                                                                                     144 ASGKLLALDSQL--TNDFSEKSSYFQSQVDKIR---KEAYAGAAAGV-----VAGPFGLI 193
                                                                                                                                                                                                                                                                                                       173
                                                                                                                                                                                                                                                                                                                                                      54
and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a novel immunogenic composition comprising a combination of 2-5 group B Streptococcus (GBS) polypeptides. Bach polypeptide is encoded by a GBS polymucleotide sequence which is homelogous to a polymucleotide sequence of group A Streptococcus (GAS),
and identify streptococcal infections or for identifying, screening and developing vaccines and other treatments for streptococcal infections. The current sequence is that of a Streptococcus agalactiae ORF SAG protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for treating or preventing
Streptococcus polypeptides
                                                                                                                                                                            :: | :| | | :
2 NDAITKLSSFAEAATLQGTAYSNAKSYATGTLTPMLQG----MILFSETLSEKC---TEL
                                                                                                                                                                                                                                                                                                      114 LKKRIKSNOKKLDNLNEFNAHSATVFADISNAOSTVNOALAAVSTGFSGYNSKTGAFGKP
                                                                                                                                                                                                                                                                                                                                    194 ISYSIAAGVV-----EGKLIPELKNKLKSVQNFFTTLSNTVKQANKDIDAAKL-KLT
                                                                                                                                                          41 DETIKELSRFKQ-----EYSQAASVLVGDIKTLIMDSQDKYPEATQTVYEWCGVATQL
                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunogenic composition; group B Streptococcus; GBS; antibacterial; streptococcal infection; vaccine; SAG.
                                                                                                                                90;
                                                                                                                                                                                                                                                                                                                                                                                                              234 NEAYKLGEIKKDT-----YESIISGLSNASAALLKEVAKSKLTDT 273
                                                                                                                                                                                                                                                                                                                                                                                              TEIAAIGEIKTETETTRFYVDYDDLM-----LSLLKEAAK-KMINT 284
                                                                                                    Length 278;
                                                                                                                               50; Mismatches 112; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus agalactiae ORF SAG1030-related protein 3.
                                                                                                    .,
9
                                                                                                  Score 110; DB & Pred. No. 0.69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunogenic composition useful as a vaccine streptococcal infections, comprises group B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 10; SEQ ID NO 6106; 1194pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADK99512 standard; protein; 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-AUG-2002; 2002US-0406237P.
27-AUG-2002; 2002US-0406676P.
28-AUG-2002; 2002US-0406757P.
                                                                                                    7.38;
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                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus agalactiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Masignani
                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-248071/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHIRON CORP
                                                                       Sequence 278 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2004018646-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-MAY-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rettelin H,
                                                                                                                                                                                                                                                                                                                                                                                              245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADK99512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CHIR )
(GENO-)
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SEQ ID NO 51864; 1766pp; English.

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New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                         94 LAAYILLFDEYN-----EKKASAQKDILIKVLDDGITKLN---EAQKSLLVSSQS-FNN 143
                                                                                                                                                                                                                                                                                                                144 ASGKLLALDSQL--TNDFSEKSSYFQSQVDKIR---KEAYAGAAAGV----VAGPFGLI 193
                                                                                                                                                                                                                                                                                                                                    LKKRIKSNQKKLDNLNEFNAHSATVFADISNAQSTVNQALAAVSTGFSGYNSKTGAFGKP 173
                                                                                                                                                                                                                                                                                                                                                                         194 ISYSIAAGVV-----BGKLIPELKNKLKSVQNFFTTLSNTVKQANKDIDAAKL-KLT 244
                                                                                                                                                                                                                                                                                                                                                                                                   174 TSGOMEWTKTVKKNWKEREDAKAEELKSKKAEESKKASKIENTTKKSNVSVDKKKLIKAA 233
                                                                                                                                                                                                                                                                                   54
       composition of the invention demonstrates antibacterial activity whilst the polypeptides and polynucleotides may be useful in assays to diagnose and identify streptococcal infections or for identifying, screening and developing vaccines and other treatments for streptococcal infections. The current sequence is that of a Streptococcus agalactiae ORF SAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zyskind JW;
Xu HH;
                                                                                                                                                                                                                            NDAITKLSSFAEAATLOGTAYSNAKSYATGTLTPMLOG----MILFSETLSEKC---TEL
                                                                                                                                                                                                 41 DETIKELSRFKQ-----EYSQAASVLVGDIKTLIMDSQDKYFEATQTVYEWCGVATQL
                                                                                                                                                                      90;
                                                                                                                                                                                                                                                                                                                                                                                                                                   TEIAAIGEIKTETETTRFYVDYDDLM----LSLLKEAAK-KMINT 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                      234 NEAYKIGEIKKDT-----YESIISGLSNASAALLKEVAKSKLTDT 273
one other GBS serotype.
                                                                                                                                           DB 8; Length 278;
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                                                                                                                                         7.3%; Score 110; DB 8; Length 27
22.9%; Pred. No. 0.69;
tive 50; Mismatches 112; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein encoded by Prokaryotic essential gene #9467.
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Yamamoto R,
pneumoniae and/or least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABU23940 standard; protein; 1163 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clostridium acetobutylicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ELIT-) ELITRA PHARM INC.
                                                                                     protein of the invention.
                                                                                                                                                                          66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-029926/02.
                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ACA27810.
                                                                                                                  Sequence 278 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200277183-A2
      Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-OCT-2002
                                                                                                                                              Query Match
Best Local S:
Matches 66
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The invention relates to an isolated nucleic acid comprising any one of the foll antisense sequences given in the specification where expression to the ancleic acid inhibits proliferation of a cell. Also included are: cof the nucleic acid inhibits proliferation of a cell. Also included are: cocding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated contisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) inhibiting cellular contisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (6) inhibiting cellular polyleration; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway continged for proliferation or that inhibits cellular proliferation; (8) inhibiting a centifying a gene required for cellular proliferation or the biological continged for proliferation. The antibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compount of an organism acts; (1) aculture compound that inhibits proliferation of an organism. The attrisense nucleic acids are useful for the decidentifying proteins or screening for homologous nucleic acids required for cellular proliferation of an organism. The antisense nucleic acids are useful for the decident confidence more and activity; (1) activity of the strains is present in a culture or collection of an organism. The antisense nucleic acids are useful for the decident decidence more and organism or for screening for homologous nucleic acids required for an organism. The arreason and promoted acids are useful for the decidence or the antisense and acids are useful for the provery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       165 YFQSQVDKIRKBAYAGAAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNKLKSVQNFFTT 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       332 IAKDNKEK------ALPKFMIKHHILDAIKEKDLEDNIKLEKKRLÖGKIEK 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DKYFBATQTVYBWCGVATQLLAAYILLFDBYN-------BKKASAQKDILIKV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --IDDGITKINEAQKSLLVSSQSFNNASGKLLALDSQLTN-------DFSEKSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IDLKEKRARLGESSSKVKPYIDNYENTLKQIDILKEQILSRENTMKAISLEKEDMEKKLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MTEIVADKTVEVVKNAIETADG-----ALDLYNKYLDQVIPWQTFDETIK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 6; Length 1163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----TTRFYVDYD-----DLMLSLLKEAAKKMINTCNEYQKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            y Match 7.3%; Score 110; DB 6; Length 11. Local Similarity 17.9%; Pred. No. 4.9; hes 73; Conservative 69; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LS-----NTVKQANKDIDAAKLKLTTEIAAIGEIKTETE----
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1935 KGPGSKIHAKELQ-----ELLKEKQQEVKQLQKDCIRYLGRISALEKTVKALEFVHTES 1988
                                                                                                                                                 1876 YYQDVTDAQIKNEQLESEMQNLKRCVSELEEEKQQLVKEKTKVESEIRKE-YMEKIQGAQ 1934
                                                                                                                                                                                                                                                                                         1989 QKDLDÄTKGNLAQAVEHHKKAQAELSSFKILLDDTQSEAARVLADNLKLKKELQSNKESI 2048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
                                                                           KDILIKVLDDGITKLN----EAQKSLLVSSQSFNNASGKLLALDSQLTNDFSEKS----S
                                                                                                                                                                                      187 AGPFGLIISYSIAAGVVEGKLIPELKNKLKSVQ-----NFFTTLSNTVK-----QA
                                                                                                                                                                                                                                                       233 NKDIDAAK-----LKLTTEIAAIGEIKTETETTRFYVDYDDLML------
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2049 KSQIKQKDEDLLRRLEQAEEKHRKE 2073
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----LKGRIABLEMEKQ-KDRELSQTL
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BAYER AG.
                                                                                                                     YFQSQVD-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus.
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                     1781
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(FARB )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a array. A method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially a compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the compound for identifying a compound or small molecule that regulates the activity of one or more of the cattivity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating complyablides or their antibodies. The polypurcleotide or the compound that modulates its activity is useful for preparing a medicament for treating colypeptides or their antibodies. The polynucleotide or the compound injury (CCI) and spared nerve injury (Numg), chronic constriction injury (CCI) and spared nerve injury (Numg) in an animal (e.g. spinal segmental nerve injury (Numg)) in an animal to the printed sequence data for this patent did not form part of the printed specification, but was obtained in alectronic form directly from WIPO at specification, but was obtained in alectronic form directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                     nerve injury;
                                                                                                  Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve i
chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
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20.8%; Pred. No. 19;
tive 65; Mismatches 114; Indels 126;
                                                                                                                                                                                                                                                                                                                                                                                                             Costigan M;
                                                                    Rat Protein BAA05026, SEQ ID NO 1870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page; 1017pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                             Befort K,
                                                                                                                                                                                                                                                                                     14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                       14-AUG-2002; 2002WO-US025765
                                    (first entry)
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Matches 80; Conservat
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                                                                                                                                                     Rattus norvegicus.
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                                                                                                                                                                                      WO2003016475-A2.
                                    29-JAN-2004
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The invention discloses a composition comprising two or more isolated rattor human polymuclectides or a polymuclectide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the nuvel polymuclectide, a host cell comprising the vector, a method for identifying a nuclectide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polymuclectide sequence
New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially
                                                                                                                                                                                              Claim 1; Page; 1017pp; English.
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18;

57 AASVLVGDIKTLLMDSQDKYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKA----SAQ 112

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1 MTEIVADKTVE---VVKNA-IETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQ 56

Conservative

Costigan M;

Befort K,

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9905 - 0138847P - 9905 - 0139119P - 9905 - 0139453P - 9905 - 0139453P - 9905 - 0139455P - 9905 - 0139458P - 9905 - 0139462P - 9905 - 0139462P - 9905 - 0139463P - 9905 - 0139463P - 9905 - 0139750P - 9905 - 0139750P - 9905 - 0139750P - 9905 - 0139750P - 9905 - 0139750P - 9905 - 0139750P - 9905 - 0139750P - 9905 - 0139750P - 9905 - 0139750P - 9905 - 0139750P - 9905 - 0139750P - 9905 - 0139750P - 9905 - 0139750P - 9905 - 0139750P - 9905 - 0139750P - 9905 - 0139750P - 9905 - 0139817P - 9905 - 0139817P - 9905 - 0139817P - 9905 - 0139817P - 9905 - 0139899P -
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  expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for producing a pharmaceutical composition, a cartivity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polymucleotide or the compound that polypeptides or their antibodies. The polymucleotide or the compound that polypeptides or their antibodies. The polymucleotide or the compound that collypeptides or their antibodies. The polymucleotide or the compound that paint (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from NIPO at (ftp. wipo.int/pub/published_pot_equences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1989 OKDEDATKGNEAQAVEHHKKAQAELSSFKILLDDTOSEAARVLADNEKEKKELQSNKESI 2048
                                                                                                                                                                                                                                                                                                                                   233 NKDIDAAK------LKLTTEIAAIGEIKTETETTRFYVDYDDLML------ 271
                                                                                                                                                                                                                                                                                                                                                                                                                             113 KDILIKVLDDGITKLN----EAQKSLLVSSQSFNNASGKLLALDSQLTNDFSEKS----S 164
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                                                                                                                                                                                                                                                                                                                                                                      57 AASVLVGDIKTLLMDSQDKYPEATQTVYEWCGVATQLLAAYILLFDEYNEKKA----SAQ 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein identification, signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                                                   1 MTEIVADKTVB----VVKNA-IETADGALDLYNKYLDQVIPWQTPDETIKELSRFKQEYSQ 56
                                                                                                                                                                                                                                                              Match 7.3%; Score 110; DB 7; Length 3187; Local Similarity 20.8%; Pred. No. 19; Local Similarity 65; Mismatches 114; Indels 126; Gaps
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RR 19-JUL-1999; 9908-0144332P.

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57 AASVLVGDIKTLLMDSQDKYFEATQTVYEWCGVATQLLAAYILLFDBYNEKKASAQKDI- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----LIKVLDDGITKLNEAQKSLLVSSQSFNNASGKLLAL-----DSQLTNDFSEK 162
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 5, 2005, 10:43:53; Search time 55.3174 Seconds
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3151.602 Million cell updates/sec
Title: US-09-993-292B-28
Perfect score: 1508
Sequence: 1 MTEIVADKTVEVVKNAIETA.....TCNEYQKRHGKKTLFEVPEV 303

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 1825181 segs, 575374646 residues

Total number of hits satisfying chosen parameters:

1825181

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 50 summaries

Database : UniProt_02:*
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 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Q6cxq4 kluyveromyc Q86tb8 homo sapien Q6buq9 debaryomyce Q9liw7 oryza sativ	Q7rel0 plasmodium Q7p7e4 fusobacteri Q895wl clostridium
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ALIGNMENTS

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MASS SPECTROMETRY, DISULFIDE BOND, AND MUTAGENESIS OF TYR-96; ASN-156; TYR-164 AND ARG-260.

TYR-164 AND ARG-260.

MEDLINER-205-56278; PubMed=11006277; DOI=10.1074/jbc.M005420200;

Atkins A., Wyborn N.R., Wallace A.J., Stillman T.J., Black L.K., Fielding A.B., Hisakado M., Artymiuk P.J., Green J.;

Fielding A.B., Hisakado M., Artymiuk P.J., Green J.;

Fielding A.B., The role of alpha G. ",

J. Blol. Chem. 275:41150-41155(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-17, AND MUTAGENESIS OF 87-GLY--VAL-89; 142-ASN-ALA-143; 182-ALA-GLY-183; 186-ALA-GLY-187; ASP-267 AND 292-GLY-LYS-293.
MEDLINE=99316011; PubMed=10383763;
Oscarsson J., Mizunoe Y., Li L., Lai X.-H., Wieslander A., Uhlin B.E.; "Molecular analysis of the cytolytic protein ClyA (SheA) from Escherichia coli.";
Mol. Microbiol. 32:1226-1238(1999).
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Sport A., Bosserhoff A., von Rhein C., Goebel W., Ludwig A.;
"Differential regulation of multiple proteins of Escherichia coli and
Salmonella enterica serovar Typhimurium by the transcriptional
                                                                                                                                 MEDILINE=97061202; PubMed=8905232;
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Yano M., Horiuchi T.;
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corresponding to the 12.7-28.0 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFIDE BOND FORMATION.
MEDLINE-22894281; Pubmed=14532000;
Wai S.N., Lindmark B., Soederblom T., Takade A., Westermark M., Oscarsson J., Jass J., Richter-Dahlfors A., Mizunoe Y., Uhlin B.E.; "Vesicle-mediated export and assembly of pore-forming oligomers of centerobacterial clyA cytotoxin.";
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Science 277:1453-1474(1997)
                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=CH9802;
Chang G.-N., Ho K.-C.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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STRAIN=KL2 / XLL1-BLUB;
King C.H., Shinnick T.M.;
Submitted (MRA-1996) to the EMBL/GenBank/DDBJ databases.
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J. Bacteriol. 184:3549-3559(2002)
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STRAIN-K12 / AB1157;
Woodgate R.;
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                                                                                            SEQUENCE FROM N.A.
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RADINE=20123445; PubMed=10660049;

RADINE=20123445; PubMed=10660049;

RADINE CA., Artymiuk P.J.,

REPLING CONTROL CARTON E (H1yE, ClyA, SheA): X-ray crystal structure of membrana do Sheavation of membrane pores by electron microscopy.";

REPLING CONTROL TOXIN, which has some hemolytic activity towards mammalian cells. Acts by forming a pore-like structure upon contact with mammalian cells.

CONTROL CONTROL CONTROL CARTON Secreted. Exported from an octamer. While in outer membrane vesicles, it oligomerizes to form a pore structure that is active. Probably forms an octamer.

CONTROL SUBCELULAR LOCATION: Secreted. Exported from the cell by outer membrane vesicles. Also found in the periplasmic space.

CONTROL CONTROL DATION Secreted. Exported from the cell by outer membrane vesicles. It is activated by SlyA, while it is silenced by H-CONTROL DATION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION SECRETION
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Pfam; PF06109; HlyE; 1.
3D-structure; Complete proteome; Cytolysis; Direct protein sequencing;
Hemolysis; Toxin; Transmembrane.
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MEDLINE=22829856; PubMed=12949101;
Wai S.N., Westermark M., Oscarsson J., Jass J., Maier E., Benz
Uhlin B.E.;
                                                                                                            dominantly negative mutant ClyA cytotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activity.
Y->C: Strongly reduces cytotoxic
activity.
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K -> R (in strain CH9802)

G -> A (in strain CH9802)
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EMBL; U13610; -; NOT ANNOTATED_CDS.
BDS; LQQY; X-ray, A=1-302.
ECHOBASE; EB3032; -.
ECOGENE; EG13243; hlyE.
                                                                                                                                 proteins in Bscherichia coli.";
J. Bacteriol. 185:5491-5499(2003).
[16]
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MEDLINE=20322319; PubMed=10865950; DOI=10.1016/S0923-2508(00)00143-1;
del Castillo F.J., Moreno F., del Castillo I.;
"Characterization of the genes encoding the SheA haemolysin in
BECharichia coli 0157:H7 and Shigella flexneri 2a.";
Res. Microbiol. 151:229-230(2000).
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MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfal G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7.";
Nature 409:529-533(2001).
Missing: In PMWK16; retained in cytoe
Loss of function.
AG->DD: Abolishes cytotoxic activity.
AG->DD: Abolishes cytotoxic activity.
R->K: Strongly reduces cytotoxic
activity.
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29-MAR-2004 (Rel. 43, Last sequence update)
29-MAR-2004 (Rel. 44, Last annotation update)
Hemolysin E (Cytotoxin clyA) (Silent hemolysin sheA).
Name=hlyE, Synonyms=clyA, sheA; OrderedLocusNames=z1944, ECs1677;
Escherichia coli 0157:H7.
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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STRAIN=0157:H7 / RIMD 0509952 / EHEC;
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Q9REB3;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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TEIVADKTVEVVKNAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGVVAGPFGLIISYSIAAGVVEGKLIPELKNKLKSVQNFFTTLSNTVKQANKDIDAAKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                           similarity).

PTM: In periplasm, it forms a disulfide bond, which prevents the oligomerization. In outer membrane vesicles, the redox status prevents formation of the disulfide bond, leading to oligomerization and pore formation (By similarity).

SIMILARITY: Belongs to the hemolysin E family.
                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Secreted. Exported from the cell by outer membrane vesicles. Also found in the periplasmic space (By
                                                                                                                                                                                   monomer, while in outer membrane vesicles, it oligomerizes to a pore structure that is active. Probably forms an octamer (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P77335; 1QOY.
InterPro; IPR010356; HlyE.
Pfam; PF06109; HlyE; HlyE.
Complete proteome; Cytolysis; Hemolysis; Toxin; Transmembrane.
INIT_MET 0 0 By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  By similarity.
Potential
In monomeric form (By similarity)
F261E29E1DE5FC87 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 302;
                                                                                                                                                                                                                                               membrane vesicles. Also found in the periplasmic space
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
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99.0%; Pred. No. 4.6e-86;
iive 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AJ238954; CAB64962.1; ALT_INIT.
EMBL; AE005335; AAG56033.1; ALT_INIT.
EMBL; AP002555; BAB35100.1; ALT_INIT.
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Best Local Similarity 99.0
Matches 299; Conservative
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PIR; E90838; E90838.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jacteriol. 185:2330-2337(2003).

J. Bacteriol. 185:2330-2337(2003).

J. Bacteriol. 185:2330-2337(2003).

J. Bacteriol. 1000: Which has some hemolytic activity towards mammalian cells. Acts by forming a pore-like structure upon contact with mammalian cells (By similarity).

J. SUBUNIT. Monomer and oligomer. In periplasm, it is present as a monomer, while in outer membrane vesicles, it oligomerizes to form a pore structure that is active. Probably forms an octamer (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CTI8;
MEDLINE=2153947; PubMed=11677608; DOI=10.1038/35101607;
MEDLINE=2153947; PubMed=11677608; DOI=10.1038/35101607;
MEDLINE=2153947; PubMed=11677608; Thomson N.R., Pickard D., Wain J., Churcher C.W., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G., William C., Milliple drug resistant Salmonella Complete genome sequence of a multiple drug resistant Salmonella
                                                                                                                                                                                                                                                                                                   STRAIN=TY21s, and SMI S2369/96;
MEDLINE=22215712; PubMed=12228306;
MEDLINE=22215712; PubMed=12228306;
MEDLINE=22215712; PubMed=12228306;
Mizunce Y., Wai S.N., Uhlin B.E.;
"Characterization of a pore-forming cytotoxin expressed by Salmonella enterica serovars typh; and paratyphi A.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTM: In periplasm, it forms a disulfide bond, which prevents the oligomerization. In outer membrane vesicles, the redox status prevents formation of the disulfide bond, leading to oligomerization and pore formation (By similarty). SIMILARITY: Belongs to the hemolysin E family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Secreted, Exported from the cell by outer membrane vesicles. Also found in the periplasmic space (By
                                                                                                 Q82727; Q934C4;
Q82727; Q934C4;
29-MAR-2004 (Rel. 43, Last sequence update)
29-MAR-2004 (Rel. 45, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
01-OCT-2004 (Rel. 45, Last annotation update)
Name-hlyE: Synonyms=clyA, sheA; OrderedlocusNames=STY1498, t1477;
Salmonella typhi
                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                               302 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=TY2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
                                                                                                                                                                                                                                               Enterobacteriaceae; Salmonella NCBI_TaxID=601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              enterica serovar Typhi CT
Nature 413:848-852(2001).
                                                                                 STANDARD;
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EMBL; AJ313032; CAC38360.1; -.

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121
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                                                                                                                                                                                                                  122 DGITKINEAQKSILIVSSQSFNNASGKILLALDSQLTNDFSEKSSYFQSQVDKIRKEAYAGA
                                                                                                                                                                                                                                                           182 AAGVVAGPFGLIISYSIAAGVVEGKLIPELKNKLKSVQNFFTTLSNTVKQANKDIDAAKL
                                                                                                                                                               2 TEIVADKTVEVVKNAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASVL
                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name-hlyE, Synonyms-clyA, sheA;
Salmonella paratyphi-a.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                            .;
0
                                                                                Potential.
In monomeric form (By similarity)
2BDFD835D044FDAE CRC64;
                             HSSP; P77335; 1QOY.
InterPro; IPR010356; H1yE.
Pfam; PF06109; H1yE; 1.
Complete proteome; Cytolysis; Hemolysis; Toxin; Transmembrane.
INIT MET 0 By similarity.
                                                                                                                     Score 1395; DB 1; Length 302; Pred. No. 3.4e-80;
                                                                                                                                           11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-MAR-2004 (Rel. 43, Created)
29-MAR-2004 (Rel. 43, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Hemolysin E (Cytotoxin clyA) (Silent hemolysin sheA)
                                                                                                                      92.5%; Score 1325.91.1%; Pred. No. 3.4e-80; tive 16; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                 302 AA
AJ313034; CAC38363.1; -.
AL627270; CAD01758.1; ALT_INIT.
AE016839; AAO69115.1; ALT_INIT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enterobacteriaceae; Salmonella
                                                                                            86 284 I
302 AA; 33658 MW;
                                                                                                                                  al Similarity 91.1
275; Conservative
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                                                                       198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=54388;
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Pfam; PF06109; HlyE; SEQUENCE 300 AA;
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                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                          VGDIKTLLMDSQDKYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQKDILIKVLD
                                                                                                                                                                                                                                                                                               TEIVADKTVEVVKNAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASVL
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                                                                                                                                                                                                                                                                                                                                                                                                                          AAGVVAGPFGLIISYSIAAGVVEGKLIPELKNKLKSVQNFFTTLSNTVKQANKDIDAAKL
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=964660;
MEDINE=99242013; PubMed=10227474;
Reingold J., Starr N., Maurer J., Lee M.D.;
"Identification of a new Escherichia coli She haemolysin homolog in
avian E. coli.";
PTM: In periplasm, it forms a disulfide bond, which prevents to oligomerization. In outer membrane vesicles, the redox status prevents formation of the disulfide bond, leading to oligomerization and pore formation (By similarity). SIMILARITY: Belongs to the hemolysin E family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
                                                                                                                                                                                                                                                                           ,
0
                                                                                                                                                                                                                        similarity).
                                                                                                                                                                                                                                                      Length 302;
                                                                                                                                                                                                                                                                           13; Indels
                                                                                                                                                                                                  By similarity.
Potential.
In monomeric form (By sim: , 22DB9112B763A061 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                     Query Match
91.2%; Score 1376; DB 1;
Best Local Similarity 89.7%; Pred. No. 5.4e-79;
Matches 271; Conservative 18; Mismatches 13;
                                                                                                                                       300 AA.
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DI 302
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66 KTLLMDSQDKYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQKDILIKVLDDGIT 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAINS-ATCC 12022 / Serotype 2b;
MRDLINE-201231445; PubMed=10660049;
WRDLINE-201231445; PubMed=10660049;
Wallace A.J., Stillman T.J., Atkins A., Jamieson S.J., Bullough P.A., Green J., Artymiuk P.J.;
Green J., Artymiuk P.J.;
T. coli hemolysin E (HlyE, ClyA, SheA): X-ray crystal structure of the toxin and observation of membrane pores by electron microscopy.";
Cell 100:265-276(2000).
                                                                                                                                                                                                                                                                                                                                                                                  4 ADQIVETYKTAIDTADKALDLYNKVLDQVIPWNTFNDTVKELSRFKEEYSQSASTLVGEI
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MEDLINE=20322319; PubMed=10865950; DOI=10.1016/S0923-2508(00)00143-1;
del Castillo F.J., Moreno F., del Castillo I.;
"Characterization of the genes encoding the SheA haemolysin in Escherichia coli 0157:H7 and Shigella flexneri 2a.";
Res. Microbiol. 151:229-230(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and 0157.";
                                                                                                                                                                                                                                                                                                                                                 6 ADKTVEVVKNAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASVLVGDI
                                                                                                                                                                                                                                                                                       Gaps
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MEDLINE=22272406; PubMed=12384590;
Jin O., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Jin O., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
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Enterobacteriaceae; Shigella.
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                                                                                                                                                                                                                      Length 300;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     246 EIAAIGEIKTETETTRFYVDYDDLMLSLLKEAAKKMINTCNEYQKRHGKK
                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                           33555 MW; 6580B66C44A7B4BC CRC64;
                                                                                                                                                                                                                   75.1%; Score 1133; DB 2;
76.9%; Pred. No. 1.2e-63;
tive 31; Mismatches 36;
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Vet. Microbiol. 66:125-134(1999).
BMBL; AF052225; AAD28079.1; -.
HSSP; P77335; 1QOY.
InterPro; IPR010356; HlyB.
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                                                                                                                                                                                               Query Match
Best Local Similarity 76.95
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pseudogene.
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Q55486;
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MEDLINE=22388214; PubMed=12471157; DOI=10.1073/pnas.252529799;
MEDLINE=22388214; PubMed=12471157; DOI=10.1073/pnas.252529799;
MEDLINE=22388214; PubMed=12471157; DOI=10.1079/pr. Readen P., Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D., Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T., Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence of uropathogenic Escherichia coll.";
Proc. Natl. Acad Sci. U.S.A. 99:177020-17024(2002).
I- SIMILARITY: Belongs to the hemolysin E family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MTEIVADKTVEVVKNAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASV
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Enterobacteriaceae; Escherichia.
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SEQUENCE 113 AA; 12879 MW; C328908D14C5C4EB CRC64;
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05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93 AA
 Nucleic Acids Res. 30:4432-4441 (2002)
                                                                                                                                                                                                                                                                                          EMBL; AF200955; AAF13995.1; -.
EMBL; AJ238955; CAB65415.1; ALT INIT.
EMBL; AE015143; -; NOT_ANNOTATED_CDS.
EMBL; AE016982; -; NOT_ANNOTATED_CDS.
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                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR010356; HlyE.
                                                                                                                                                                                                                                                                                                                                                                                                         Local Similario,
nes 111; Conservative
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Escherichia coli 06.
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Q8FIZ7:
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                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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01-NOV-1997 (Rel. 35, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Arginyl-ENNA synthetase (EC 6.1.1.19) (Arginine--tRNA ligase) (ArgRS).
Name=argS; OrderedLocusNames=sll0502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAUTION: Although it is strongly related to the hemolysin E toxin from E.coli K-12 strain, it lacks all the N-terminal part of the protein, and it is therefore probably not functional. May be a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              211 LKNKLKSVQNFFTTLSNTVKQANKDIDAAKLKLTTEIAAIGEIKTETETTRFYVDYDDLM
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Sugiura M., Tabata S.;
Sequence analysis of the genome of the unicellular cyanobacterium
Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
na Res. 2:153-166(1995).
-!-CATALYTIC ACTIVITY: AFP + L-arginine + tRNA(Arg) = AMP +
diphosphate + L-arginyl-tRNA(Arg).
-!-SUBUNIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
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Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
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Bacteria, Cyanobacteria, Chroococcales, Synechocystis.
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Pred. No. 2.5e-20;
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4; Mismatches
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HAMAP, MF_00123; -; 1
InterPro; IPR005148; ArgtRNAsynthet_N.
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Matches 86; Conserv
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Local Similarity 24.0%;
es 74; Conservative 4
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                                             Nature 430:35-44(2004)
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                                                                          SEQUENCE FROM N.A.
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Matches
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                                                                                                                                                                                                                                                                                                  ---LLMDSQDKYFEATQTVYEWCGVATQ-----LLAAYILLFDEYNEKKASAQKDI 115
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                                                                                                                                                                                                                                                                                                                                                                                                    LIK------VLDDGITKLNEAQKSLLV--SSQSFNNASGKLLALDSQLTNDFSEKSSYF- 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                            -OSQVDKIRKEAYAGAAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNKLKSVQNFFTTL 225
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                                                                                                                                                                                                                                                                                11 EVVKNAIBTADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASVL-VGDIKT-- 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S., Lafoncaine I., de Montigny J., Marck C., Neuveglise C., Talla E., Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V., Barnay S., Blanchin S., Beckerich J.M., Beyne B., Bleykasten C., Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A., Bespons L., Fabre B., Fairhead C., Ferry-Dumazet H., Groppi A., Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R., Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H., Nicolski M., Oztas S., Ozier-Kalogeropoulos O., Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O., Swennene D., Tekais F., Wasolowski-Louvel M., Westhof E., Wirth B., Zeniou-Meyer M., Zivanovic I., Bolotin-Pukuhara M., Thierry A.,
                                                                                                                                                                                                                                                     Gaps
InterPro; IPR001278; Arg_trNA-synt_ic.
InterPro; IPR008909; tRNA-synt_id_C.
InterPro; IPR001412; tRNA-synt_id_C.
InterPro; IPR001412; tRNA-synt_id_C.
InterPro; IPR001412; tRNA-synt_id_Dind.
Pfam; PF03485; Arg_trNA-synt_id_1.
Pfam; PF05746; tRNA-synt_id_1.
Pfam; PF05746; tRNA-synt_id_2.
PRINTS; PR01038; TRNASYNTHARG.
TIGRFAMS; TIGR00456; argS; 1.
PROSITE; PS00178; AA_TRNA_LIGASE I; 1.
Aminoacyl-tRNA synthetase; ATP-binding; Complete proteome; Ligase; Protein biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORFNames=YALIOF02387g;
Yarrowia lipolytica (Candida lipolytica).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.
                                                                                                                                                                                                                                                      65;
                                                                                                                                                                                                    B.9%; Score 133.5; DB 1; Length 584; Local Similarity 24.5%; Pred. No. 3; tes 77; Conservative 48; Mismarcher 17.
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01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to DEHAOCO96589 Debaryomyces hansenil IPF 1836.1.
                                                                                                                                                                             126 136 "HIGH" region.
584 AA; 65212 MW; 89602A1A5A3BD85B CRC64;
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456 KMLALQGNTAPYML 469
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1252 AMADNLTKDLAEK-----TKELVAAKSEL--ESSNTSSKEEVDVLTKKLSD 1295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     233 NKDIDAAKLKLTTEIAAIGEIKTETETTRFYVDYDDLMLSLLKEAAKK--MINT-CNEYQ 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 DKTVEVVKNAIETADGALDLYNKYL----DQVIPWQTFDETIKELSRFKQEYSQAASVLV.62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 AGVVAGPFGLIISYSIAAGVVE-----GKLIPELKNKLKSVQNF---FTTLSNTVKQA
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J., Wincker P., Souciet J.L.; "Genome evolution in yeasts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 GDIKTLIMDSQDKYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQKDILIKVLDD
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Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=2095;
                                                                                                                                                                                                                                                                                                                                                                                                         Length 1906;
                                                                                                                                                                                                                                     Genoscope;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR382132; CAG77705.1; -.
SEQUENCE 1906 AA; 210346 MW; F6ED7D1AF7B7562B CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                  8.6%; Score 129.5; DB 2;
24.0%; Pred. No. 22;
ive 46; Mismatches 119;
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GO; GO:0000166; F:nucleotide binding; IEA.
InterPro; IPR001359; AAA ATPase.
InterPro; IPR001270; Chaprnin_clpA/B.
PRINTS; PR00300; CLPPROTEASEA.
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PROSITE; PS00871; CLPAB_2; 1.
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67 ILLMDSQDKYFEATQ-----TVYEWCGVATQLLAAYILLFDEYNE--KKASAQKD 114
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                                                                                                               ----LKNHIGEYNKO 426
---SLLVSSQSFNNASGKLLALDSQLTNDFSE 161
                                    401
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                      162 KSSYFQSQVDKIRKEAYAGAAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNKLKSVQNF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=Sterne; PLASMID=virulence plasmid PX01;
MEDLINE=99445483; PubMed=10515943;
MEDLINE=99445483; PubMed=10515943;
MEDLINE=99445483; PubMed=10515943;
Medlines R.T., Cloud K., Hampton O., Hoffmaster A.R., Hill K.K.,
Keim P., Koehler T.M., Lamke G., Kumano S., Mahillon J., Manter D.,
Martinez Y., Ricke D., Svensson R., Jackson P.J.;
"Sequence and organization of pX01, the large Bacillus anthracis
plasmid harboring the anthrax toxin genes.";
J. Bacteriol. 181:6509-6515(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Ames / isolate 0581; PLASMID=DXO1;
Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Fer Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Bacillus anthracis comparative genomics.";
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AF065404; AAD23394.1; -.
EMBL; AF017336; AAT28865.2; -.
PIR; B59102; B59102.
TIGR; GBAA_DXO1_0124; -.
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PROSITE; PS01072; SLH DOMAIN; UNKNOWN_1.
Complete protecome; Plasmid.
SEQUENCE 652 AA; 76210 MW; 723F5FBE03516355 CRC64;
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Last annotation update)
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Plasmid virulence plasmid PX01, and Plasmid pX01
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                                                                                                                                                                                                                                                                       473 ---- DELGKRHKHRQELEASOKKALDEAKEI 499
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01-NOV-1999 (TrEMBLrel. 12, Last seq)
01-CCT-2004 (TrEMBLrel. 28, Last ann)
PXOJ-90 (6-layer protein,).
OrderedLocusNames=GBAA_pXOl_012;
  115 ILIKVLDDGITKLNEAQK-----
                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                   402 LADKYKNSDNKİSR------
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Best Local Similarity 20.5%
Matches 68; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                            203 VEGKLIPELKNKLKSVQNFFTTLSNTVKQANKDIDAAKLKLTTEIAAIGEIKTETETTRF 262
                                                                                                                                                                                                238 FGPTGVGKTEVARSLADILFNSPKKMIRLDMSEYMEKHSVAKLIGAPPGYVGYEGGRLT 297
                                                                                                                                                                                                                                                                 : : |:||| || || :||::|||| || 298 EAVRRNPYSIILFDEI-BKAHSDVFNILLQILDDGRLTDSLGKTIDFKNTIIVMTS--NI 354
                                                                                                                                                                                                                                                                                                                     ASGKLLALDSQLTNDFSE-KSSYFQSQVDKIRKEAYAGAAAGVVAGPFGLIISYSIAAGV 202
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                                                                                                                         237
                                                                                       --DETIKELSR 49
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MEDLINE-22061436; PubMed=12004073;
Read T.D., Salzberg S.L., Pop M., Shumway M., Umayam L., Jiang L.,
Holtzapple E., Busch J.D., Smith K.L., Schupp J.M., Solomon D.,
Keim P., Fraser C.M.;
Comparative denome Sequencing for Discovery of Novel Polymorphisms in
Bacillus anthracis.'
Science 296:2028-2033(2002).
Bacillus anthracis.'
InterPro; IPR001119; SLH.
InterPro; IPR001119; SLH.
InterPro; IPR010999; t-snare.
InterPro; IPR010999; t-snare.
InterPro; IPR010999; t-snare.
InterPro; IPR010999; t-snare.
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1 Similarity 20.5%; Pred. No. 10;
68; Conservative 57; Mismatches 108; Indels
              DB 2; Length 495;
                            ; Pred. No. 5.6;
47; Mismatches 119; Indels
                                                                                       2 TEIVADKTVEVVKNAIETADGALDLYNKYLDQVIPWQTF-----
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
S-layer protein, (PXOI-90).
Name=BXA0124;
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              Score 128;
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                                23.8%;
              Query Match
Best Local Similarity 23.8<sup>†</sup>
Matches 77; Conservative
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Best Local Similarity
Matches 68; Conserv
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1 MTEIVA-DKTVEVVKNAIETADGALDLYNKYLDQVIPW--QTFDETIKELSRFKQEYSQA
01-MAR-2001 (TrEMBLrel. 16, Last e
01-OCT-2004 (TrEMBLrel. 29, Last e
NORPEG-like protein (Ankycorbin).
                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                        SEQUENCE FROM N.A.
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-----LKNHIGEYNKQ 426
                     KSSYFQSQVDKIRKEAYAGAAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNKLKSVQNF 221
                                                      ----LKNHIGEYNKQ 426
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                                                                                                   FITLSNIVKOANKDIDAAKLKLITEIAAIGEIKTETETTRFYVDYDDLMLSLLKEAAKKM 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
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01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                             427 LEKIENELEECNKKIDNTKKOL-AEFDKSNKKOOELE
                                                                                                                                                                                      282 INTCNEYOKRH-----GKKTLFEVPEV 303
                                                                                                                                                                                                                             ----DELGKRHKHRQELEASQKKALDEAKEI 499
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NCBL_TaxID=261594;
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Bacillus anthracis str. Ames 0581.
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01-MAR-2001 (TrEMBLrel. 16,
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SEQUENCE 57BL/6; TISSUB=Brain;

MEDINRE-2598257; PubMed=12477932;

MISCHINE-2598257; PubMed=12477932;

MISCHINE-2598257; PubMed=12477932;

MISCHINE S.F., Zeeberg B. Buetow K.H., Schamen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hable F.,

MISCHINE R.F., Jordan H., Moore T., Max S.I., Wang J., Hable F.,

Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Wilalon D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Shevchenko Y., Bouffard G.G.,

Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakealey R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

M. Jones S.J., Marra M.A.,

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Kutty R.K., Kutty G., Samuel W., Duncan T., Bridges C.C.,
El-Sharbeeny A., Nagineni C.N., Smith S.B., Wiggert B.;
"Molecular characterization and developmental expression of NORPEG,
novel gene induced by retinoic acid.";
J. Biol. Chem. 276:2831-2840(2001).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                            979 AA; 108851 MW; B2E8C016D80237C4 CRC64;
annotation update)
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GO; GO:0005739; C:mitochondrion; IDA.
InterPro; IPR002110; ANK.
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PROSITE; PS50297; ANK REP REGION; 1.
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HSSP; P42773; 1IHB.
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Matches 78; Conservative 6
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PRINTS; PR01415; ANKYRIN.
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| ...| | ...| | ... | | | ... | ... | ... | ... | ... | ... | ...| | ...| | ...| | ...| | ...| | ...| | ...| | ...|
                                                              TISSUBERMDAYONIC tail;
Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
Okazaki N., Kikuno R., Ohara O., Koga H.;
Saga Y., Nagase T., Ohara O., Koga H.;
Faga Y., Nagase T., Ohara O., Koga H.;
III. The Complete Nucleotide Sequences of Mouse KIAA-homologous
III. The Complete Nucleotide Sequences of 500 Mouse KIAA-homologous
CONAS Identified by Screening of Terminal Sequences of cDNA Clones
Randomly Sampled from Size-fractionated Libraries.";
DNA Res. 10:167-180(2003).
ENEL; AKL2933; BAC98143.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    785 AEEKAAVSDAMVPKSS-----YEKLQASLESEVNALATKLKESVREREKAHS-----EV
                                         AQKDILIKVLDDGITKLNEAQKSLLV----SSQSFNNASGKLLALDSQLTNDFSEKSSY
                                                                                                166 P---OSQVDKIRK-EAYAGAAAGVVAGPPGLIISYSIAAGVVEGKLIPELKNKLKSVQN-
                                                                                                                                                      ------RFTTLSNTVKQ------ANKDIDAAKL--KL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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ilarity 21.5%; Pred. No. 17;
Conservative 64; Mismatches
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MKIAA1334.
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Matches 78; Conserv
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                                                                                                                                                                   166 F---OSQVDKIRK-EAYAGAAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNKLKSVON- 220
                                                                                                                                                                                    ---S 110
                                                                                 603
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                                                                                                                              1 MTEIVA-DKTVEVVKNAIETADGALDLYNKYLDQVIPW--QTFDETIKELSRFKQEYSQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S., Saga Y., Nagase T., Ohara O., Koga H.; Saga Y., Nagase T., Ohara O., Koga H.; Prediction of the cooding sequences of mouse homologues of KIAA gene: "II. the complete nucleotide sequences of 500 mouse KIAA-homologous conks identified by screening of terminal sequences of cDNA clones randomly sampled from size-fractionated libraries."; DNA Res. 10:167-180(2003).

GO: GO: 0005799; C:mitcchondrion; IDA.
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                                                                                                            AQKDILIKVLDDGITKLNEAQKSLLV----SSQSFNNASGKLLALDSQLTNDFSEKSSY
                                                                                                                                                                                                                           ------ANKDIDAAKL--KL
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                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                       ASVLVGDIKTLLMDSQDKYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKA----
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Last annotation update)
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Local Similarity 21.5%; Pred. No. 1'
les 78; Conservative 64; Mismatch
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PROSITE; PS50297; ANK REP REGION; 1.
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SMART; SM00248; ANK; 6.
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Pfam; PF00023; Ank; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Embryonic tail;
PubMed=14621295;
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821 AQV 823
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Matches
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Genome sequence and comparative analysis of the model rodent malaria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    parasite Plasmodium yoelii yoelii.";
Nature 419:515-519(2002)
-!- CAUTION: The sequence shown here is derived from an
--- EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                 Plasmodium yoelii yoelii.
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.3%; Score 125; DB 2; Length 27.
21.5%; Pred. No. 64;
tive 60; Mismatches 109; Indels
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                                  Last sequence update)
Last annotation update)
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InterPro; IPR003900; KID repeat.
InterPro; IPR004999; RetIculocyteBP.
Pfam; PF02524; KID; 6.
TIGRFAMS; TIGR01612; 235kDa-fam; 1.
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235 kDa rhoptry protein (Fragment)
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                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                      NCBI_TaxID=73239;
                                                                                                                                                                                                                                                                                                                                                                     PubMed=12368865;
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                                                                    TTBIAAIGEIKTETETTRFYVDYDDLMLSLLKEA---AKKMINTCNEYQKRHGKKTLFEV 300
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   LTQLKQLVDAHKENSVSITEHLQVITTLRTTAKEMEEKISALTGHLANKEAEVAKLEKQL 784
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Plasmodium yoelii yoelii.
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ489165; CAD32955.1; -.
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to the EMBL/GenBank/DDBJ databases
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Khan S.M., Jarra W.,
Submitted (DEC-2002)
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                                                                                                                                             3 EIVAD-----KTVE-VVKNAIETADGALDLY---NKYLDQVIPWQTFDETIKELSRF 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            657 TEN-AIKNLD---AKYNAQYKDFVAKSGDAFNGIQAKLNSVDTKVASANKAIDEHASEVT 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NRFNTEAEKLNEVINKRIKEA-ASEAALSVQGINDMILEVRNRLDETQEKVREKIEADAD 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----LIPELKNKLKSVQNFFTTLSNTVKQANKDIDAAKLKLTTELAAIGEIKTETETTRF 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   597 AELENTSKGMQEKLLSIREESEAKFETIKKDFETWKNRTDQQFTDARSFFDEKITNFAGL 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 KTVEVVKNA-IETADGALDLY----NKYLDQVIPWQTFDETIKELSRFKQEYSQAASVLV 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QKDILIKVLDDGITKLNEAQKSLLV-SSQSFNNASGKLLALD------SQLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
VCBI_TaxID=158;
                                                                                                                                                                                                      PubMed=15064399; DOI=10.1073/pnas.0307639101; Bisen J.A., Heidelberg J.F. Seshadri R., Myers G.S.A., Tettelin H., Elsen J.A., Heidelberg J.F. Dodson R.J., Davidsen T.M., Deboy R.T., Fouts D.E., Haft D.H., Selengut J., Ran Q., Elinkac L.M., Maduu R., Kolonay J.F., Durkin S.A., Daugherty S.C., Shetty J., Shvartsbeyn A., Gebregoorgis E., Ger K., Tsegaye G., Malek J.A., Ayodeji B., Shataman S., McLeod M.P., Smajs D., Howell J.K., Pal S., Amin A., Vahisth P., McNeill T.Z., Xiang Q., Sodergren E., Baca E., Weinstock G.M., Norris S.J., Fraser C.M., Paulsen I.T.; "Comparison of the genome of the oral pathogen Treponema denticola with other spirochete genomes"; J. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. School P. Sc
               Treponema denticola.
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
NCBI_TaxID=158;
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InterPro; IPR009057; Homeodomain like.
InterPro; IPR010992; IHF like_DNA_bnd.
InterPro; IPR002017; Spectrin.
Complete proceemes; Hypothetical protein.
SEQUENCE 1081 AA; 123105 MW; 6490D3EA8068C18A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.6%; Pred. No. 40, rive 46; Mismatches 133;
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4.6%; Pred. No. 23;
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InterPro; IPR009074; Apolipo_A_E_C3.
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STRAIN=ATCC 35405 / DSM 14222;
                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=ATCC 35405 / DSM 14222;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A
EMBL; AE017253; AAS12812.1;
      OrderedLocusNames=TDE2293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 GDIKTLLMDSQDKY-----FEATQTVYB-WCGVATQLLAAYILLFDEYNEKKASA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seshadri R., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.F., Dodson R.J., Davidsen T.M., DeBoy R.T., Fouts D.E., Haft D.H., Selengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J., Durkin S.A., Daugherty S.C., Shetty J., Shvattsbeyn A., Gebregeorgis E., Geer K., Tsegaye G., Malek J.A., Ayodeji B., Shatsman S., McLeod M.P., Smajs D., Howell J.K., Pal S., Amin A., Vashisth P., McNeill T.Z., Xiang O., Sodergren E., Baca E., Weinstock G.M., Norris S.J., "Comparison of the genome of the oral pathogen Treponema denticola with other spirochete genomes.";

Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651(2004).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NDFSEKSSYFQSQVDKIRKEAYAGAAAGVVAGPFGLIISYSIAAGVVEGK-----
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EMBL; AE017269; AAS40708.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112 QKDILIKVLDDGITKLNEAQKSLLV-SSQSFNNASGKLLALD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                             1 protein.
1081 AA; 123105 MW; 6490D3EA8068C18A CRC64;
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Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263 YV---DYDDLMLS-----LLKEAAKKMINTCNE 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 124.5;
Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 24.6*
watches 82; Conservative
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TGILVDRLISSEKEKLINLEDLLKKYVKGODOAIKAVTSAIMRSRSGIKNPDKPIGSFLF 455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----NDFSEKSSYFQSQVDKIRKEAYAGAAAGVVAGPFGLIISYSIA--AGVVEGKL--I 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     516 EAVRRNPYSIVLFDEI-EKAHTDVFNILLQILDDGRLTDSLGKTIDFKNTIIVMTS--NI 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144 ASGKILALDSQLTNDFSEKSSYFQSQVDKIRKEAYAGAAAGVVAGPFGLIISYSIAAGVV 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 573 ASQYLLTSDELVQVD----DQKIQEELNKVFRPEFINRIDNIVY--FNALSVQTI--GEI 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  204 EGKLIPELKNKLKSVQNFFTTLSNTVKQANKDID------AAKLK-----LTTE 246
                                                                                                                                               209 PELKNKLKSVQNFFTTLSNTVKQANKDIDAAKLKLTTEIAAIGEI------KTETETTRF
                                                                                                                                                                             DGYEKKLITITKTKEAEYTAAKEQSTKSTAAADLVTKYETAKSNALGNDIAKEYLEAKTAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----KQEYSQA-ASVLVGDIKTLLMDSQDKYFEATQTV-----YEWCGVAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Westberg J., Persson A., Holmberg A., Goesmann A., Lundeberg J.,
Johansson K.-E., Pettersson B., Uhlen M.;
"The genome sequence of Mycoplasma mycoides subsp. mycoides SC type
strain PGIT, the causative agent of contagious bovine pleuropneumonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 TEIVADKTVEVVKNAIETADGALDLYNKYLDQVIPWQT-----FDETIKELSRF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=cîpB; OrderedLocusNames=MSC 0613;
Mycoplasma mycoides (subsp. mycoīdes SC).
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
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SEQUENCE 713 AA; 80782 MW; 1B5D204A9E29BE50 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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22.3%; Pred. No. 16;
tive 52; Mismatches 131;
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                                                                                                                                                                                                                                                                                                                                                                                                            713
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                                                                                                                                                                                                                                                                                          -----KILNEAGISMLSQANQ 455
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05-JUL-2004 (TrEMBLrel. 27, Last ann
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Genome Res. 14:221-227(2004).
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Best Local Similarity
Local 73; Conserva
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                                                                                                                                                                                                                                                62 VGDIKTILIMDSQDKYFBATQTVYEWCGVATQLLAAYILLFDBYNEKKASAQKDILIKVLD 121
                                                                                                                                                                                                                                                                                                                                                                                                            DG-----ITKINEAQKSLLVSSQSFNNASGKLL-----ALDSQLT----- 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                        267 DGYEKKLITIKIKEAEYIAAKEQSIKSIAAADLVIKYETAKSNALGNDIAKEYLEAKTAY 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TEIVADKTVEVVKNAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASVL 61
                                                                                                                                                                                                                                                                                                                                                             235 A----TL------KPTDAT-----YAAKAAELDAATTALNON-------KVLV
                                                                                                                                                                                                                  2 TEIVADKTVEVVKNAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASVL
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                                                                                                                         DB 2; Length 465;
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
PRINTS; PR00207; FLAGELLIN.
ProDom; PD000316; Flagellin C; 1.
Complete protecome; Flagellinm.
SEQUENCE 465 AA; 49855 MW; E4C307E7717381D5 CRC64;
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Last annotation update)
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                                                                                                                      8.2%; Score 123.5;
23.1%; Pred. No. 10;
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tes 75; Conserv
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inter, 500.7. IPR004089, Chmtaxis_transd.
InterPro; IPR003660, HANP.
InterPro; IPR004090, Me_chemotaxis.
InterPro; IPR005829, Sug_transporter.
InterPro; IPR005889, t-snare.
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HYLB OR GSU1374.
                                                                                                                                                   EMBL; AE017180; AAR34750.1; -.
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                                                                                                                                        Science 302:1967-1969(2003).
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STRAIN=PCA / ATCC 51573;
PubMed=14671304;
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                                                                                                                                                                 GSU1374; -
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AAR34750;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      -----KQEYSQA-ASVLVGDIKTLLMDSQDKYFEATQTV-----YEWCGVAT 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Westberg J., Persson A., Holmberg A., Goesmann A., Lundeberg J., Johansson K.-E., Pettersson B., Uhlen M.; "The genome sequence of Mycoplasma mycoides subsp. mycoides SC type strain PGIT, the causative agent of contagious bovine pleuropneumonia (CBPP).";
                                                                                                                                                                                                                                                                                                                                                                       Gaps
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Methyl-accepting chemotaxis protein.
Name=hylB; ORFNames=GSU1374;
Geobacter aulfurreducens.
Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
Geobacteraceae; Geobacter.
NCBI_TaxID=35554;
                                                                                                                                                                                                                                                                                                                                                                     71;
                                                                                                                                                     Mycoplasma mycoides (subsp. mycoides SC).
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxIb=44101;
                                                                                                                                                                                                                                                                                                                                                  Length 713;
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                                                                                                      02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
13-APR-2004 (TrEMBLrel. 27, Last annotation update)
ATP dependant protease ClpB.
CLPB OR MSC_0613.
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              PRT;
247 IAAIGEIKTETETTRFYVDYDDLMLSL
                                                                                                    Created)
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Genome Res. 14:221-227(2004)
EMBL; BX842644; CAE77235.1;
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                                                                              PRELIMINARY;
                                                                                                                                                                                                      SEQUENCE FROM N.A.
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PubMed=14762060;
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                                                                              CAE77235
CAE77235;
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Q74DE2;
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SEQUENCE FROM N.A.

STRAIN=PCA / ATCC 51573;

STRAIN=PCA / ATCC 51573;

PubMed-14671304; DOI-10.1126/science.1088727;

Methe B.A., Nelson K.B., Elsen J.A., Paulsen I.T., Nelson W.C.,

Heidelberg J.F., Wu D., Wu M., Ward N.L., Beanam M.J., Doddon R.J.,

Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,

Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,

Davidsen T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,

Weidman J.F., Khouri H.M., Feldblyum T.V., Utterback T.R.,

Wan Aken S.E., Lovley D.R., Fraser C.M.,

"Genome of Geobacter sulfurreducens: metal reduction in subsurface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 NAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASVLVGDIKTLLMDSQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75 KYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQKDILIKVLDDGITKLNEAQKSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79 TWTEGRKSVEBAKKTIAEKLOAYLATNLAEEEKKHLEEAKPLIKVAD------ATLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           135 LVSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVD---KIRKEAY------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32 NTARTANNGLD--TVYRDRVLP-----LKDLKIIADMY----AVNIVDVSHKVRNGNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211 LKUKLKSVQNFFT---TLSNTVKQANKDIDAAKLKLTT---EIAA-IGEIKTETE 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Geobacter sulfurreducens.
Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 541;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PP00615; MAMP; 1.
Pfam; PP00015; MCPsignal; 1.
PRINTS; PR0026; CHEMTRANSDUCR.
SMART; SM00304; HAMP; 1.
SNART; SM00304; HAMP; 1.
PROSITE; PS50011; CHEMOAXIS_TRANSDUC_2; 1.
PROSITE; PS00216; HAMP; 1.
PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
SEQUENCE 541 AA; 57093 MW; 3C9BEDAEAF7C3812 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 8.2%; Score 123; DB 2; Lu
Local Similarity 22.7%; Pred. No. 13;
hes 67; Conservative 44; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --AGAAAGV-VAGPFGLIISYSIAAGVVE-----
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63 GDIKTLLMDSQDKYFEATQTVYEWCGVATQLLAAYILLFDEYNEK------KA 109
                                                 180 LETKTVALSKVEEAKKVSKVHSE----KIELLRKEIAAVNESVEOTKLACSQARKEQSEI 235
                                                                               110 SAQKDILIKVLDDGITKLNEAQKSLLVSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQ 169
                                                                                                                                                                                                                                            340 KMEHDEVEAKEAEIESVAGDLHLKLSRSKSELEQCVTEESKAKAALEDMMLTINQISSET 399
                                                                                                                                               170 VDKIRKEAYAGAAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNKLKSVQNFFTTLSNTV
                                                                                                                                                                                                                KQANKDIDAAKLKLTTEIA----AIGEIKTE----TETTRFYVDYDDLMLSLLK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J., Qin Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z., Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.; "Genome-based analysis of virulence genes in a non-biofilm-forming Staphylococcus epidermidis strain (ATCC 12228)."; Mol. Microbiol. 49:1577-1593(2003).
                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus epidermidis.
Bacteria, Firmicutes, Bacillales, Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                              Ş
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interpro; IPR003439; ABC_transporter.
Interpro; IPR005289; GTP-binding.
Interpro; IPR003405; SMC_C.
Interpro; IPR010935; SMC_hinge.
Interpro; IPR003395; SMC_N.
                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 23, Created)
(TrEMBLrel. 23, Last seq
(TrEMBLrel. 26, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chromosome segregation SMC protein. OrderedLocusNames=SE0909;
                                                                                                                                                                                                                                                                              EAAKK----MINTCNEYOK 290
                                                                                                                                                                                                                                                                                                             400 EAARREAEGMRNKAKELMK 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1189 AA; 137542 MW;
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Pfam; PP06470; SMC_hinge; 1.
Pfam; PP02463; SMC_N; 1.
TIGRFAMS; TIGR00650; MG442; 1.
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                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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Best Local Similarity
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STRAIN=ATCC 12228;
PubMed=12950922;
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                                                                                                                                                                                                                                                                                                                                                                                                                              LVSSQSFNNASGKLLALDSQLTNDFSEKSSYFQSQVD---KIRKEAY------ 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LASILSAEDAEALTAFTVSELYPAIDPVSAKFSSLVDDQLKIAKQEYDHSSGLYRASRTI 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --AGAAAGV-VAGPFGLIISYSIAAGVVE--------GKLIPE 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 ADKTVEVVKNAIETA-DGALDLYNKYLDQVIPWOTFDETIKELSRFKQEYSQAASVL--V 62
                                                                                                                                                                                                                                                                                                                            NTARTANNGLD--TVYRDRVLP-----LKDLKIIADMY----AVNIVDVSHKVRNGNI 78
                                                                                                                                                                                                                                                                                                                                                              KYPEATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQKDILIKVLDDGITKLNEAQKSL
                                                                                                                                                                                                                                                                                             NAIETADGALDLYNKYLDQVI PWQTPDETIKELSRFKQEYSQAASVLVGDIKTLLMDSQD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LKNKLKSVQNPFT---TLSNTVKQANKDIDAAKLKLTT---EIAA-IGEIKTETE 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 core eudicots; rosids;
Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C., Heidelberg J.F., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J., Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S., Gwinn M.L., Kolonay J.E., Sullivan S.A., Haft D.H., Selengut J., Davidsen T.M., Zafar N., White O., Tran B., Romero C., Forberger H.P. Weidman J., Khouri H.M., Peldblyum T.V., Utterback T.R., Van Aken S.B., Lovley D.R., Fraser C.M.; "Genome of Geobacter sulfurreducens: metal reduction in subsurface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Myosin heavy Chain-like.

Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosidi
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=20181125; PubMed=10718197;
Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Structural analysis of Arabidopsis thaliana chromosome 5. X. Se features of the regions of 3,076,755 bp covered by sixty Pl and
                                                                                                                                                                                                                                                               72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54;
                                                                                                                                                                                                                             Length 541;
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                                                                                                                                                                                                                                                               44; Mismatches 112; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Res. 7:31-63(2000).
EMBL; AB018120; BAA97285.1; -.
INTECTOR: INFRO08545; DUF827.
Pfam; PF05701; DUF827; 1.
SEQUENCE 649 AA; 72430 MW; B7D51EFB295D55BB CRC64;
                                                                                                                                                                                               541 AA; 57093 MW; 3C9BEDAEAF7C3812 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             649 AA.
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Best Local Similarity 22.7%; Pred. No. 13;
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                                                                                                                                                                EMBL; AE017211; AAR34750.1; -
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                                                                                                                                               Science 302:1967-1969(2003).
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                                                                                                                                                                                                                                                                 67; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=3702;
                                                                                                                                  environments.'
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                                                                                                                                                                                               SEQUENCE
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Q9LVQ4
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     Sarararragas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 VADKTVEVVK-----NAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAA 58
GO; GO:0016020; C:membrane; IEA.

GO; GO:0005534; C:nucleus; IEA.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0005525; F:ATP-binding; Cassette (ABC) transporter acti. . .; IEA.

GO; GO:0005525; F:GTP binding; IEA.

GO; GO:00070559; P:Chromosome agergation; IEA.

GO; GO:0006810; P:transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.2%; Score 123; DB 2; Length 1189;
19.6%; Pred. No. 32;
tive 52; Mismatches 112; Indels 124; Gaps
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1395 TIDDNYISKCIKDIADLKTYILSEB-----NNINTYLK 1427
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(TrEMBLrel. 27, Last sequence update)
                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                  05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 21.7*
Conservative 75; Conservative
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                                                                                                                                                                               PRELIMINARY,
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SEQUENCE 927 AA:
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AAT05096;
10-MAY-2004 (
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AAT05096
ID AAT0
AC AAT0
DT 10-M
DT 10-M
                                                                                                                        RESULT 30
Q71X69
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                                                                                                                                                                                        셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELK-NKLKSVQNFFTTLSNTVKQANKDID-----AAKLKLTTEIAAIGEIKTETET 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111 AQKDILIKVLDDGITKLNEAQKSLLVSSQSFNNASGK-----LLLALDSQLTNDFS 160
                                                                                                                                                                                                                                                                                     | : | | : | | : | | EEELDNIESQIDSIKNEK-------AQNEKLLAELKNKQKQLN 358
                                                                                                                                                                                                                                                                                                                                                                                                  359 KEVQELESLLYISDEQHDEKLEEIKNSYYILMSEQSDVNNDIRFLEHTINENEAKKSRLD 418
               S-----VLVGDIKTLLMDSQD-----KYFEATQTVYEWCGVATQLLAAYILLFDEYN 105
                                                   221 KEMEQSDVIVTVSDIDHYTEDNQRLDERLNHLKSQQAEKE--GQQAQINQ----LLQKXK 274
                                                                                                                              EKKASAQKDILIKVLDDGITKLNEAQKSLLVSSQSFNNASGKLLALDSQLTND-----F 159
                                                                                                                                                                      160 SEKSSYFQSQVDKIRKEAYAGAAAGVVAGPFGLIISYSIAAGVVEGKLIPELKN----- 213
                                                                                                                                                                                                                                                                                                                                                              -----KLKSVQNFFTTLSNTVKQANKDI-------DAAKLKLT 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           245 TEIAAIGEIKTETETTRFYVDYDDLMLSLLKEAAKKMINTCNEYOKRHGKKTLFEVPE 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 BIVAD-----KTVE-VVKNALETADGALDLY---NKYLDQVIPWQTFDETIKELSRF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=21273138; PubMed=11378199;
Khan S.M., Jarra W., Bayele H., Preiser P.R.;
Khan S.M., Jarra W., Bayele H., Preiser P.R.;
"Distribution and characterisation of the 235 kDa rhoptry multigene family within the genomes of virulent and avirulent lines of Plasmodium yoelii.";
Mol. Blochem. Parasitol. 114:197-208(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 21.3%; Pred. No. 86;
Matches 72; Conservative 58; Mismatches 108; Indels 100;
Matches 72; Conservative 58; Mismatches 108; Indels 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.2%; Score 123; DB 2; Length 2752; 11.3%; Pred. No. 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         plasmodium yoelli yoelli.
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium
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2752 AA; 322608 MW; E834E3753168AF76 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
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EMBL, AF923442; AAK15625.1; -.
InterPro; IPR006499; ReticulocyteBP.
TIGRPAMS; TIGR01612; 235kDa-fam; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             235 kDa rhoptry protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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01-JUN-2001
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PubMed=15115801; DOI=10.1093/nar/gkh562;

PubMed=15115801; DOI=10.1093/nar/gkh562;

PubMed=15115801; DOI=10.1093/nar/gkh562;

PubMed=15115801; DOI=10.1093/nar/gkh562;

A Nelson X.E., Fouts D.E., Mongodin E.F., Gill S.R., Paulsen I.T.,

Rolonay J.F., Rasko D.A., Angiuoli S.V., Gill S.R., Paulsen I.T.,

Rolonay J.F., Masko D.A., Angiuoli S.V., Gill S.R., Madupu R.,

Brinkac L.M., Daugherty S.C., Dodson R.J., Durkin A.S., Madupu R.,

Haft D.H., Selengut J., Van Aken S.E., Khouri H.M., Fedorova N.,

Rorberger H.A., Tran B., Kathariou S., Wonderling L.D., Uhlich G.A.,

Bayles D.O., Luchansky J.B., Fraser C.M.;

"Whole genome comparisons of serotype 4b and 1/2a strains of the food-
porne pathogen Listeria monocytogenes reveal new insights into the

Nucleic Acids Res. 32:2386-2395(2004).

Romal, ABOTIS30; AANTOS096; Chmtaxis transd.

Richerp. IPRO01809; Outrsurface.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        389 -----LAKQLAA-----LOKSLGDLONGLTFIKS---NANFDAEAIKSKINATA 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 BATQTVYEWCGVATQLLAAYILLEDEYNEKKASAQKDILIKVLDDGITKLNEAQKSLLVS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138 SOSFNNASGKILA----LDSQLTN-----DFSEKSSYFQSQVDKIRKEAYAGAAAGVVA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ...VGDIK-----TLLMDSQDKYF 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               222 NTLEVGLKTYTDGVNTAAAGGDKLNDGVSTLAAGVGPLKDGVAALDGGATKLASGVSTYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     282 SGVDTL---AGGINQAYTGSTALSDGLNKWNGS-----VPTLASGITQLNNGQKSLATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 EIVADKTVEVVKNAIETADGALDLYNKYLDQVIPWQTFDETI----KELSRFKQEYSQAA
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                                                                                                                                                                      OrderedLocusNames=LMOCING-2330;
Listeria monoytogenes (serotype 4b / strain F2365).
Bacteria, Firmicutes; Bacillales; Listeriaceae; Listeria.
NCBI_TaxID=265669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         927 AA; 97232 MW; 9AE73C67B14685CA CRC64;
                                                               Created)
Last sequence update)
Last annotation update)
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21.7%; Pred. No. 26;
927
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12;

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01-WAR.2003 (TrEMBLrel. 23, 01-WAR.2003 (TrEMBLrel. 23, 01-WAR.2003 (TrEMBLrel. 23, Rhoptry protein (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
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Submitted (DEC-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4007 AA;
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nes 73; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78 BATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQKDILIKVLDDGITKLNEAQKSLLVS 137
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Nelson K.E., Foute D.A., Angiuoli S.V., Gill S.R., Faulsen I.T.,
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Haft D.H., Selengut J., Van Aken S., Khouri H., Fedorova N.,
Forbegger H., Tan B., Kathariou S., Wonderling L.D., Uhlich G.A.,
Bayles D.O., Luchansky J.B., Fraser C.M.;
"Whole genome comparisons of serotype 4b and 1/2a strains of the food-
borne pathogen Listeria monocytogenes reveal new insights into the
core genome components of this species.";
Nucleic Acids Res. 32:2386-2395(2004).
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Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 927;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             248 AAIGEIKTETETTRFYVDYDDLMLSLLKEAAKKMINTCNEYOKRHG 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.1%; Score 122.5; DB 2; Length 9
21.7%; Pred. No. 26;
tive 35; Mismatches 137; Indels
                                                                 Listeria monocytogenes str. 4b F2365.
Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GVSAEDKOKI -----IDAIQADLDKETQKSATQVATVEQLQSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE017330; AAT05096.1; -.
SEQUENCE 927 AA; 97232 MW; 9AE73C67B14685CA CRC64;
  Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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10-MAY-2004 (TrEMBLrel. 27,
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01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
                        Membrane protein, putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                  Listeria monocytogenes
NCBI_TaxID=265669;
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Name=NCU00658.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neurospora crassa.
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                                                                                                                                                                                      SEOUENCE FROM N.A.
                                                                                                                                                                                                                 STRAIN=4b F2365;
                                                                                                                                                                                                                                     PubMed=15115801;
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11D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D DDT 10D D
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RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Poley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamyysselis M., Maucell E., Bielke C., Rudd S., Frishman D.,
RA Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Noelker R.,
Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
Randson I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
I'The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1332 ODEIKKLTAGHNEKIRNLEHRINDLKAELKODRA------EFDKKKALLEGEVA 1379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1380 TLQGKVDDKSSKLSSKEAEFNELKKLNEAQIAELRKDVADKSNSLQDKLEELSDLKGQQK 1439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----SQLTNDFSEKSSYFQSQVDKIRKEAYAGAAAGVVAGPFGLIISYSIAAGVVEGKL- 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EKKOLAVOHKTEMESLIDRYHEKEK-----LATOYOERVOALSAELADKKTALAEYKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 AASVLVGDIKTLLMDSQDKYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --SAQKDILIKVLDDGITKLNEAQKSL----LVSSQSFNNAS-----GKLLALD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 EVVKNAIETADGAL-----DLYNKYLDQVIPWQTFDETIK-----ELSRFKQEYSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -I- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

EMBL/AABXO1000001, EAA35562.1; -.

InterPro; IPR003909; KID repeat.

InterPro; IPR001638; SEZI.

InterPro; IPR001638; SEZI.

Pfam; PF06818; FEZI, SP_Dac_3.

Pfam; PF05524; KID; 5.

PROSTER: P801039; SBP_BACTERIAL_3; UNKNOWN_1.
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Bukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
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to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.1%; Score 122.5; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
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PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=73239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=12368865;
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01-MAR-2004
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                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                               51 KQEYSQAASVLVGDIKTLLMDSQDKYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKAS 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQKDILIKVLDDGITKLNEAQKSLLVSSQSFNNASGKLLALDSQL-TNDFSEKSSYF--- 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --- OSQVDKIRKEAYAGAAAGVVAGPFGLIISYSIAAGVVEG-KLIPELKNKLKSVQNFF 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      198 NILKLNKIKKIIDKVKEYTDEIKKNNKSINDELINSGKIITKIKENSSLTECQSKIESTI 257
                                                                                                                                                                                                                                                                                                                                                                       1 EKVÁDINTYNEDPKEIEKKIENVVKKIDKKKNIÝKEINKLLNEISEIEKDKTSLEELKNI 60
                                                                                                                                                                                                                                                                                                                            3 EIVAD-----KTVE-VVKNAIETADGALDLY---NKYLDQVIPWQTFDETIKELSRF
                                                                                                                                                                                                                                                                                      Gaps
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Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein P2010.190 (Hypothetical protein AT4g38070).
Name=F20D10.190; Synonyme=AT4g38070;
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Etreptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                    96;
                                                                                                                                                                                                                                       Length 852;
                                                                                                                                                                                                                                       %; Score 122; DB 2; Length 852
%; Pred. No. 25;
61; Mismatches 108; Indels
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL035538; CAB37547.1; -.
Green J.L., Holder A.A.;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EU Arabidopsis sequencing project;
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                              026995B7A6E658B1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         258 DDNYISKCIKDIADLKTYILSEE----NNINTYLK 288
                                                                                     Bayele H.K.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ
EMBL; AJ489163; CAD32953.1; -.
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21.1%;
                                                                                                                                                                                                                                                                                    71; Conservative
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                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  317 KYENGKLEQENRELLGSLK------ELQEATIQGSGNSALSKLKNKFRNLEN 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EYSQAASVIVGDIKTL--IMDSQDKYFEATQTVYEWC-GVATQLLAAYILLFDEYNEKKA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----SQVDKIRKEAYAGAAAGVVAGPFGLIISYSIAAGVVEG----KLIPELKNKLKSVQN 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 363 IHKNCSANLRSKEAEWSSQVEKMVEBINDYKLQLQSKEAALKEVELELENCRSSTAKMRL 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   213 EWEEEKSKLLDEIYSLOTKLDSVTRISEDLOKKLOMCNGALTO------EETRRKHL 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---SNTVKQANKDIDAAKLKLTTEIAAIGEIKTETE-----TTRFYV 264
                                                                                                                                                                                                                                                                                                                                                                                                                          22
                                                                                                                                                                                                                                                                                                                                                                                                                       4 IVADKTVEVVKNAIETADGALDLYNK--YLDQVIPWQT-----FDETIKELSRF----KQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 SAQKDILIKVLDDGITKLNEAQKSLLVSSQSFNNASGKLLALDSQLTNDFSEKSSYFQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence and comparative analysis of the model rodent malaria
                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                          78;
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Nature 419:512-519(2002).
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                                                                                                                                                       Length 1496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium yoelii yoelii.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                          Match 8.1%; Score 122; DB 2; Length 14 Local Similarity 18.9%; Pred. No. 49; es 64; Conservative 72; Mismatches 124; Indels
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                                                                                                                                                                                                                          03BBB75DCD2B03FE CRC64;
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NON TER 1 1
SEQUENCE 1081 AA; 126062 MW;
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EMBL; AL161592; CAB80472.1; -. PIR; T05634; T05634. InterPro; IPR001092; HLH_basic.
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SMART; SM00353; HLH; 1.
PROSITE; PS50888; HLH; 1.
Hypothetical protein.
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REDLINE=22388257; PubMed=12477932;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Ehat N.K.,

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A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Pahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

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A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

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T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                         KTLLMDS--QDK---YPBATQTVYEWCGVATQLLAAYILLFDBYNEKKASAQKDI--LIK 118
                                                                                                                                                                                                          119 VLDDGIT------KLNEAQKSLLVSSQSFNNASGKLLALDSQLTN------ 157
                                                                                                                                                                                                                                                      574 KYSDEVAEKKYIEELKLKLKLKETIKDIYKKKBYIK----KAIDLKKEIENKNKYIDELGKK 629
                                              DKTVEVVKNA I ETADGALDLYNKYLDQVI P-WQTFDETI KELSRFKQEYSQAASVLVGDI
                                                                                                                                                                                                                                                                                                       158 -----DFSEKSSYFQSQVDKIRKEAYAGAAAGVVAGPFGLIISYSIAAGVVEGKLIPEL
                                                                                                                                                                                                                                                                                                                                                630 TPPQIBBYVKKKDTIYSTIKTELSEIYKG------NIİBLYNELSSVVQENTİDPI
                                                                                                                                                                                                                                                                                                                                                                                                 KNK-----LKS-VQNFFTTLSN----TVKQANKDIDAAKLKLTTEIAAI-----GEIKTE
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             257 TETTRFYVDYDDLMLSLLKEAAKKMINTCNEYQKRHGKKTLFE 299
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Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases
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GO:0005737; C:cytoplasm; IEA.
GO:0016020; C:membrane; IEA.
GO:00016555; F:protein transporter activity; IEA.
GO:0006886; P:intracellular protein transport; IEA.
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(TrEMBLrel. 22, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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TISSUE=Uterus;
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                                                                                                                                                                                                                                                                                                                               701 ILKKKNMDYEYDSKKILEYSNNFISKENIILKDIER-ISKISNEVKTSLPKYDNEVKKIY 759
                                                                                                                                                                                                                                                                                                                                                                                                 NNASGKLLALDSQL------TNDFSEKSSYFQSQVDKIRKEAYAGAAA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                             760 PNSNGEYLQVKKLIEQIKEYTSEEYLNKYRNKVNDIKTTVSDETKÖIQTTNKRMDNYKVL 819
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                                                                                                                4 IVADKTVEVVKNAIETAD-----GALDLYNKYLDQVIPWQTFDETIKELSRFKQEY
                                                                                                                                                                                                          SQAASVLVGDIKTL----LMDSQDKYFEATQTVYEWCGVATQLLAAYILLFD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GVVAGPFGLIISYSIAAGVVEGK--LIPELKNKLKSVQNFFTTLSNTVKQA-----NKDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DAAKLKLTTEIAAIGEIKTETETTRFY-------VDYDDLMLSL------
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Nature 419:512-519(2002).
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                                                                    Gaps
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                   8.1%; Score 121.5; DB 2; Length 1081;
19.1%; Pred. No. 36;
tive 72; Mismatches 129; Indels 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plasmodium yoelii yoelii.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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21.0%; Pred. No. 40;
[ve 57; Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1116 1116
1116 AA; 131905 MW; 3B264B3B5701B222 CRC64;
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WEDLINE=98148093; PubMed=9478999,
Sohda M., Misumi Y., Yano A., Takami N., Ikehara Y.;
Sohda M., Misumi Y., Yano A., Takami N., Ikehara Y.;
Sohda M., Misumi Y., Yano A., Takami N., Ikehara Y.;
Thosphorylation of the vesicle docking protein pl15 regulates its
association with the Golgi membrane.";
T. Biol. Chem. 273:5385-5388(1998).
T. Biol. Chem. 273:5385-5388(1998).
The ranscytotic fusion and/or subsequent binding of the vesicles to the target membrane. May well act as a vesicular anchor by interacting with the target membrane and holding the vesicular and target membranes in proximity (By similarity).

T. SUBCELLULAR LOCATION: Peripheral membrane protein which recycles between the Gytosol and the Golgi apparatus during interphase.

T. SUBCELLULAR LOCATION: Peripheral membrane grotein which recycles coil) and a highly acidic C-terminal domain.

T. PPM: Phosphorylated in a cell cycle-specific membrane;
Phosphorylated in interphase but not in mitotic cells.
Debtosphorylated protein associates with the Golgi membrane;
Phosphorylated protein associates with the Golgi membrane;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               216 KSVQNFFTTLSNTVKQANKDIDAAKLKLTTEIAAIGEIKTETETTRFYVDYDDIMLSLLK 275
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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05-JUL-2004 (Rel. 44, Last annotation update)
General vesicular transport factor pl15 (Transcytosis associated protein) (TAP) (Vesicle docking protein).
                                                                                                                                                                                                                                                                                                                                                                               51;
                                                                                                                                                                                                                                                                                                               Length 961;
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                                                                InterPro; IPR006955; Usol pl15_C.
InterPro; IPR006953; Usol pl15_head.
Pfam; PF048971; Usol pl15_C; 1.
Pfam; PF0486971; Usol pl15_head; 1.
Prositte; PS50176; ARM REPEAT; 1.
SEQUENCE 961 AA; 107765 MW; DCFC4888F4B8C02A CRC64;
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23.7%; Pred. No. 36;
ive 51; Mismatches
                                   Armadillo.
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914 DQDQKILSLKNK 925
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tes 74; Conserv
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060763;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           748 ILLOSQITEKDSMİENMKSSOTSGINEQSSAİVSARDSEQVAELKQELATLKSÖL-NSOSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                695 QQHKDQYNLLKIQLGKDNQHQGSYSEGAQ----MNGIQPEEIGR---LREEIEELKRNQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----AQKDILIKVLDDGITKLNBAQKSLLVS---SQSFNNASGKLLALDSQLTNDFSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KSSYFQSQVDKIRKEAYAGAAAGVVAGPFGLIISYSIAAGVVEGKL-----IPELKNKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 K-----TLLM-----DSQDKYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKAS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 DKTVEVVKNAIBTADGALDLY-NKYLDQVIPWQTFDETIKELSRFKQEYSQAASVLVGDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmodium yoelii yoelii.
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=73239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107906 MW; 2E748F2C1BC2B942 CRC64;
-!- SIMILARITY: Belongs to the VDP/USO1/YBL047C family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Coiled coil (Potential).
Asp/Glu-rich (acidic).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR008938; ARM.
InterPro; IPR00825; Armadillo.
InterPro; IPR006955; Armadillo.
InterPro; IPR006953; Usol_pil5_C.
Pfam; PF04871; Usol_pil5_C; 1.
Pfam; PF04871; Usol_pil5_C; 1.
Pfam; PF04871; ARM REPRAT; UNKNOWN 1.
Coiled coil; Golgi gtack; Membrane; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.0%; Score 120.5; DB 1;
23.7%; Pred. No. 36;
tive 51; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1611 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Globular head
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIM; 603344; -.
GO; GO:0000139; C:Golgi membrane; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein transport; Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D86326; BAA25300.1; -.
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Best Local Similarity 23.78
Matches 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               276 EAAKKMINTCNE 287
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DQDQKILSLKNK 926
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01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Myosin heavy chain, cardiac muscle isoform (Fragment).
Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1102 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        282 INTCNEYOKRHG---KKTL--FEVPE 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     931 LNHVNDTEK-HGTEEHQTLONKEVPK 955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dev. Dyn. 225:384-391(2002).
                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 21.5 les 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE=Spleen;
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MYSC_CHICK
P29616;
01-APR-1993 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             initiative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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MYSC_CHICK
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                836 VKLCKKIFLLKYYTTKDRSNYDKKYE-----NMMRHLQSEKNNLLNIIEEKKYEQE 886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KDILIK-VLDDGITKLNEAQKSLLVSSQSFNNASGKLLALDSQLTNDFSE-KSSYFQSQV 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D-----KIRKEAYAGAAAGVVAGPFGLIISYSIAAGVVEG-----KLIPELKN 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VGDIKTLLM------DSQDKYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQ 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KLKSVQNFFTTLSNTVKQANKDIDA-AKL-----KLTTEIAAIGEIKTETETRFY 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KTVEVVKNAIETADGA-LDLYNKYLDQVIPWQTPDETIK-ELSRFKQEY----SQAASVL
                                                                                                                                                                                                                                               Carucci D.J.;
"Genome sequence and comparative analysis of the model rodent malaria
               Carlton J.M., Angluoli S.V., Suh B.B., Kooij T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.B., Selengut J.D., Koo H.L., Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L., Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V., Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M., Plorens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., Van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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MEDLINE=22388557; PubMed=12477932;
MEDLINE=22388657; PubMed=12477932;
Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                          CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1611;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match

Local Similarity 22.3%; Pred. No. 66;

Es 75; Conservative 60; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1611 AA; 188293 MW; CD0493CC4A9BC5D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1057 FDSLKKEFEKSFDEVQI-ILKEMIQKEKEYTNSYNK 1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    264 VD------YDDLMLSLLKEAAKKMINTCNEYQK 290
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                                                                                                                                                                                                                                                                                              parasite Plasmodium yoelii yoelii.";
Nature 419:512-519(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                preliminary data.
EMBL, AABLO1001787; EAA17620.1;
Hypothetical protein. 188293 MW;
SEQUENCE 1611 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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NCBI_TaxID=8355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 40
Q6GNE7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  729 VOSOTKETLOSVLPOITIVSQOSYSEWLQ---EPRERTSQLLS-----QOTEKEGSSE 778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 KDILIKVLDDGITKLNEAQKSLLVSSQSFNNASGKLLALDSQLTNDFSEK----SSYFQS 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169 QVDKIRKEAYAGAAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNKLKSVQNFFTTLSNT 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  779 LOLOLKQAED-----SQSDLQVECEKYRTILGQTEAMLKALONSVEEEEQVWKAKFSS 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  229 VKQANKDIDAAKLKLTT---EIAAIGEIKTET----ETTRFYVDYDDLMLSLLKEAAKKM 281
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McKernen K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 VVKNAIETADGALDLYNKYLD-QVIPWQ------TFDETIKELSRFKQEYSQAASV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22341132; PubMed=12454917;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 1012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.0%; Score 120; DB 2; Length 10
21.5%; Pred. No. 41;
ative 58; Mismatches 124; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Klein S., Strausberg R.; Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases. Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases. EMBL; BC073565; AAH713565.j. .

InterPro; IPR009053; Prefoldin. InterPro; IPR007794; Rib_recept_KP. Pfam; PF05104; Rib_recept_KP. Hypothetical protein. InterPro; IPR007054; Rib_reg; I. SEQUENCE 1012 AA; I12965 MW; CF23AB8E0D9EDARA CRC64;
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----GEIKTETET----TR 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            146 GKLLAL----DSQLTNDFSEKSSYFQ-----SQVDKIRKEAYAGAAAGVVAGPFGLI 193
                                                                                                                                                                                                                              ET--IKELSRFKQEYSQAASVLVGDIKTLLMDSQDKYFEATQTVYEWCGVATQLLAAYIL 99
151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 194 ISYSIAAGVVEGKLIPELKNKLKSVQNFFTTLSNTV-------KQANKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 LFDEYNEKKASAQKDILIKVLDDGITKLNEAQKSLLV------SSQSFNNAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1201 BELKKLIDTTKKÇLTKBFETKKSELEKLISLPDANNVDKKDELSIFG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 TEIVADKTVEVVKNAIETADGAL-----DLYNKYLD------QVIPWQTFD
                             | :: ||::| ::| |::| |::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::|
                                                                                                                                                                                              206 KLIPELKNKLKSVONFFTTLSNTVKOANKDI------DAAKLKLTTEIAAIGEI
---LDDGITKLNEAQKSLLVSSQSFNNASGKLLAL
                                                                                               D-----SQLTNDFSEKSSYFQSQVDKIRKEAYAGAAAGVVAGPFGLIISYSIAAGVVEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.0%; Score 120; DB 2; Length 1828;
19.8%; Pred. No. 82;
ive 53; Mismatches 111; Indels 156; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycoplasma hominis.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 28 Potential.
29 1828 variable membrane protein.
1828 AA; 205343 MW; 6A0D98F6491A1570 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Boesen T.;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
BMBL, A4529113; CAF32691.1; -
InterPro; IPR003900; KID repeat.
InterPro; IPR010935; SMC_hinge.
InterPro; IPR010938; tRNA_binding_arm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        262 FYVDYDDLMLSLLKEAAKKMINTCNEYQKRHGKKTLFEV 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1828 AA
                                                                                                                                                                                                                                                                                                        254 KTETETTRFYVDYDDLMLSLLKEAAKK 280
                                                                                                                                                                                                                                                                                                                                   | ::| || :: || :: || 179 HEESKTLRFQLELSQLKADFERKLAEK 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Potential.
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     108 KASAQKDILIKV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF02524; KID; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicu
NCBI_TaxID=2098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=vmp;
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                                                                                                                                                         609
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                                                                                                          152
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Q700S8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 ASVLVGDIKT-----LLMDSQDKYPEATQTVYEWCGVATQLLAAYILLFD----EYNEK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           432 MTRLWNDLTTCKTCSENGEFVRQLEEKESLISQLSRGKTSFTQQIEELRRQLEEETKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002028; Myosin tail.
Pfam, PR01576; Myosin tail.1.
Actin-binding; ATP-binding; Coiled coil; Direct protein sequencing;
Multigene family; Muscle protein; Myosin; Thick filament.
                                                                                                                                         SEQUENCE OF 65-1102 FROM N.A.
STRAIN=Broiler; TISSUE=Heart;
MEDININE=92130260; PubMed=1774788;
Stewart A.F.R., Camoretti-Mercado B., Perlman D., Gupta M.,
Jakovcic S., Zak R.;
"Structural and phylogenetic analysis of the chicken ventricular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Amino-acid sequence of the short subfragment-2 in adult chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          subfragment (S2).
SIMILARITY: Contains 1 myosin-like globular head domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 1102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.0%; Score 120; DB 1; Length 110
19.0%; Pred. No. 45;
ive 73; Mismatches 132; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2293668D049825DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A -> T (in Ref. 1).
V -> A (in Ref. 1).
CS -> FAL (in Ref. 1).
H -> Q (in Ref. 1).
T -> R (in Ref. 1).
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                                                                                                                                                                                                                                                                                                                                                                                                     IISSUE=Heart;
MEDLINE=93039740; PubMed=1418675;
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J. Mol. Evol. 33:357-366(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cardiac muscle myosin.";
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135 13
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                                                                                  NCBI_TaxID=9031;
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Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
Goffard N., Prangeul L., Aigle M., Anthouard V., Babbour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Bospons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
Pellonz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
Mincker P., Souciet J.L.;
Nature 430:35-44(2004).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 7.9%; Score 119.5; DB 2; Length 1 Similarity 21.3%; Pred. No. 27; 69; Conservative 56; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genoscope;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR382121; CAH02873.1; -.
SEQUENCE 655 AA; 74898 MW; 8024192DF56618EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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SEQUENCE FROM N.A.
TISSUE=Human skeletal muscle;
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                                                                 STRAIN=NRRL Y-1140;
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                           SEQUENCE FROM N.A.
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01-0CT-2004 (TrEMBLrel. 28, Last sequence update)
01-0CT-2004 (TrEMBLrel. 28, Last sequence update)
Similar to sp|P34237 Saccharomyces cerevisiae YKL179c.
ORFNames-KLLAOA064029;
KLUyveromyces lactis (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetels; Saccharomycetels; Saccharomycetels; Saccharomycetels; Saccharomycetels; Saccharomycetes; NCBI_TAXID=28985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.0%; Score 120; DB 2; Length 1828;
19.9%; Pred. No. 82;
tive 53; Mismatches 111; Indels 156;
                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 28 Potential.
29 1828 variable membrane protein.
1828 AA; 205343 MW; 6AOD98F6491A1570 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Gene and protein structure of the Mycoplasma hominis vi
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases
EMBL; AJ629113; CAF32691.1; -
----DAQKTLDEI 1393
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                                                                                                                                                                                                                        (TrEMBLrel. 27, Created)
(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
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1363 AKTELSDLITSSSNQAPADAIS--
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ses 79; Conservative
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                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                Mycoplasma hominis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=2098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=4195;
                                                                                                                                                                                                   CAF32691;
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                                                                                                                                                             CAF32691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              646 DKKEEEVKKTLEQHDDIVTHYKNMIREQDLQLEELRQOVSTLKCONEQLQTAVTQQVSQI 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                K-----TLLM------DSQDKYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKAS-- 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KSSYFQSQVDKIRKEAYAGAAAGVVAGPFGLIISYSIAAGVVEGKL-----IPELKNKL 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KSVQNFFTTLSNTVKQANKDIDAAKLKLTTEIAAIGEIKTETETTRFYVDYDDLMLSLLK 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QQHKDQYNLLKIQLGKDNQHQGSYSEGAQ----MNGIQPEEIGR----LREEIEBLKRNQE 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----AQKDILIKVLDDGITKLNEAQKSLLVS---SQSFNNASGKLLALDSQLTNDFSE 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S., Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla B., Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V., Barnay S., Blanchin S., Beckerich J.M., Beyne B., Bleykasten C., Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A., Despons L., Fabre B., Fairhead C., Ferry-Dumazet H., Groppi A., Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R., Kerrest A., Koszul R., Lesur I., Ma L., Muller H., Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DKTVEVVKNAIETADGALDLY-NKYLDQVIPWQTFDETIKELSRFKQEYSQAASVLVGDI
Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
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01-OCT-2004 (TrEMBLrel. 28, Created)
01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to sp|P25386 Saccharomyces cerevisiae YDL058w USO1.
ORFNames=DEHAQC096589;
Debaryomyces hansenii (Yeast) (Torulaspora hansenii).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 973;
               Robo G., Han M., Wiemann S.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
R EMBL, AL832010; CAD89317.1.
R GO; GO:0005737; C:cytcplasm; IEA.
GO; GO:0005737; C:cytcplasm; IEA.
GO; GO:0006856; P:protein transporter activity; IEA.
R GO; GO:000686; P:intracellular protein transport; IEA.
R InterPro; IPR006955; Wool_pll5_C.
R InterPro; IPR006955; Wool_pll5_C.
R InterPro; IPR006955; Wool_pll5_C.
R InterPro; IPR006955; Wool_pll5_C.
R Pfam; PF04871; Usol_pll5_C; 1.
R Pfam; PF04869; Usol_pll5_C; 1.
R PROSITE; PS50176; ARM_REPEAT; 1.
Hypothetical protein.
SEQUENCE 973 AA; 109186 MW; 9DD0279FC2CC6BFD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.9%; Score 119.5; DB 2; Length 9 Local Similarity 23.7%; Pred. No. 42; New 74; Conservative 51; Mismatches 136; Indels
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Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A., Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B., Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A., Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J., "Genome evolution in yeasts.";

"Genome evolution in yeasts.";
Nature 430:35-44(2004).
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Similar to an Arabidopsis thialiana chromosome BAC genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genoscope;
Submitted (JUL-2004) to the EMBL/JUL-2004;
EMBL; CR382135; CAG86127.1; -.
APATHINGE 2042 AA; 233328 MW; 959292DEDBEE1158 CRC64;
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895 AA; 100520 MW; BA4F7EFDF70FFAA3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 119.5; DB 2;
; Pred. No. 1e+02;
60; Mismatches 124;
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11.1%; Pred. No. 4
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01-0CT-2000 (TrEMBLrel. 15, Last seq
01-0CT-2002 (TrEMBLrel. 22, Last ann
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Best Local Similarity 21.15,
14; Conservative
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Best Local Similarity
Matches 59; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN=CBS767;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ehydrogenase (p. . .; IEA.
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a M., Walunas T.,
                                                                                                                       *OKRHGKKTLFE 299
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IDR----KKNIFE 1189
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S) entry which is
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69 NASLSDFDVQMSSISYELIDFAKEM-----SELSESNLAVVEBITASMNQVNHTIED 120
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DKIRKEAYAGAAAGVVAGPFGLIISYSIAAGVVEGKLIPELKNKLK-----SVQ 219
                                          220 NFFITLSN--TVKQANKDIDAAKLK------LTTEIAAI--GEIKTETETTRFYVD- 265
                                                                                                                                                                     244 ELVITULGKDVTVDEVNAAMKAASNESFGYTEEPLVSSDIIGISFGSLFDATQTKVLTVDG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 -MDSQDKYFEATQTVYEWCGVATQLLAAYILLFDEYNEKKASAQKDILIKV--LDDGITK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127 LNEAQKSLLVSSQSFNNASGKLLA-----LDSQLTNDFSEKSSYFQSQVDKIRKEAYA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180 GAAAGVVAGPFGLII------SYSIAAGVVEGKLIPELKNKLKSVQNFFTT 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             225 LSNTVKQANKDID---AAKLKLTTEIAAIGEIKTETETTRFYVDYDDLMLSLLKEAAKKM 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 VVKNAIETADGALDLYNKYLDQVIPWQTFDETIKELSRFKQEYSQAASVLVGDIKTLL-- 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 IIKXVEERLEG-----NKTLE----PKVEYPIHVKLLKNYKKLFSN-EGIMSSSAKTLLDI 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The genome sequence of Clostridium tetani, the causative agent of tetanus disease.";
Proc. Natl. Acad. Sci. U.S.A. 100:1316-1321(2003).
EMBL; AE015940; AA035729.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brueggemann H., Baeumer S., Fricke W.F., Wiezer A., Liesegang H., Decker I., Herzberg C., Martinez-Arias R., Merkl R., Henne A., Gottschalk G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clostridium tetani.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
NCBI_TaxID=1513;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete proteome.
SEQUENCE 495 AA; 55854 MW; 4167C6BD598557CB CRC64;
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GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:0004871; F:signal transducer activity; IEA.
GO; GO:000593; P:signal transduction; IEA.
InterPro; IPR004089; Chmtaxis transd.
InterPro; IPR004089; Chmtaxis transd.
InterPro; IPR004089; McPhemotaxis.
PERM; PRF00015; MCP8ignal; 1.
PRINTS; PR00260; CHEMTRNSDUCR.
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PROSITE; PS50111; CHEMOTAXIS_TRANSDUC_2; 1.
                                                                                                                                                                                                                                                                       -----YDDLM--LSLLKEAAKKMI 282
                                                                                                                                                                                                                                                                                                                                      304 KOLVKTVAWÝDNEMSYTSOLIRTLKKFV 331
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Db 240 IQNTSREGKKSMDNTISSTEKMSKKIDAI-----TYTTKSNVD------MLEDSVRS 285
Qy 282 INTCNE 287

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Db 286 IYTINE 291
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